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Sir:

Transmitted herewith for filing is the patent application of:

Inventors: Markus Pompejus *et al.*

For: *"Corynebacterium Glutamicum Genes Encoding Proteins Involved in Carbon Metabolism and Energy Production"*

Enclosed are:

- ☒ 63 pages of specification, 5 pages of claims and 1 page of abstract.
- ☒ 13 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 22 pages of Table 4;
- ☒ 156 pages of Appendix A;
- ☒ 52 pages of Appendix B;
- ☒ 1106 pages of Sequence Listing;
- ☒ Zip Disk Containing Sequence Listing;
- ☒ Transmittal Letter for Zip Disk Containing Sequence Listing,
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney; and
- ☒ A pre-paid acknowledgment postcard.

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☒ Address all future communications (May only be completed by applicant, or attorney or agent of record) to **Elizabeth A. Hanley, Esq. at Customer Number: 000959** whose address is:

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CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION

Related Applications

This application claims priority to prior U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial No. 60/143208, filed July 9, 1999, and U.S. Provisional Patent Application Serial No. 60/151572, filed August 31, 1999. This application also claims priority to prior German Patent Application No. 19931412.8, filed July 8, 1999, German Patent Application No. 19931413.6, filed July 8, 1999, German Patent Application No. 19931419.5, filed July 8, 1999, German Patent Application No. 19931420.9, filed July 8, 1999, German Patent Application No. 19931424.1, filed July 8, 1999, German Patent Application No. 19931428.4 , filed July 8, 1999, German Patent Application No. 19931431.4, filed July 8, 1999, German Patent Application No. 19931433.0, filed July 8, 1999, German Patent Application No. 19931434.9, filed July 8, 1999, German Patent Application No. 19931510.8, filed July 8, 1999, German Patent Application No. 19931562.0, filed July 8, 1999, German Patent Application No. 19931634.1, filed July 8, 1999, German Patent Application No. 19932180.9, filed July 9, 1999, German Patent Application No. 19932227.9, filed July 9, 1999, German Patent Application No. 19932230.9, filed July 9, 1999, German Patent Application No. 19932924.9, filed July 14, 1999, German Patent Application No. 19932973.7, filed July 14, 1999, German Patent Application No. 19933005.0, filed July 14, 1999, German Patent Application No. 19940765.7, filed August 27, 1999, German Patent Application No. 19942076.9, filed September 3, 1999, German Patent Application No. 19942079.3, filed September 3, 1999, German Patent Application No. 19942086.6, filed September 3, 1999, German Patent Application No. 19942087.4, filed September 3, 1999, German Patent Application No. 19942088.2, filed September 3, 1999, German Patent Application No. 19942095.5, filed September 3, 1999, German Patent Application No. 19942123.4, filed September 3, 1999, and German Patent Application No. 19942125.0, filed September 3, 1999. The entire contents of all of the aforementioned application are hereby expressly incorporated herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids,

nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as sugar metabolism and oxidative phosphorylation (SMP) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SMP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the SMP nucleic acids of the invention, or modification of the sequence of the SMP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a Corynebacterium or Brevibacterium species).

The SMP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium*

diphtheriae (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The SMP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered Corynebacterium or Brevibacterium species.

e.g.e.g. The SMP proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama et al, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and $FADH_2$ to compounds containing high energy phosphate bonds via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) Biology of Prokaryotes, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least due to the presence of a greater number of viable cells, each producing the desired fine chemical. Also, many of the degradation products produced during sugar metabolism are utilized by the cell as precursors or intermediates in the production of other desirable products, such as fine chemicals. So, by increasing the ability of the cell to metabolize sugars, the number of these degradation products available to the cell for other processes should also be increased.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as SMP proteins, which are capable of, for example, performing a function involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Nucleic acid molecules encoding an SMP protein are referred to herein as SMP nucleic acid molecules. In a preferred embodiment, the SMP protein participates in the conversion of carbon molecules and degradation products thereof to energy which is utilized by the cell for metabolic processes. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SMP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SMP-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in

Appendix A or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, *e.g.*, sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an SMP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of Appendix B (*e.g.*, an entire amino acid sequence selected from those sequences set forth in Appendix B). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an SMP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to perform a function involved in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid

molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SMP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an SMP protein by culturing the host cell in a suitable medium. The SMP protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an SMP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SMP sequence as a transgene. In another embodiment, an endogenous SMP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered SMP gene. In another embodiment, an endogenous or introduced SMP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SMP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated SMP protein or portion thereof is capable of performing a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In another preferred embodiment, the isolated SMP

protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The invention also provides an isolated preparation of an SMP protein. In preferred embodiments, the SMP protein comprises an amino acid sequence of Appendix B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated SMP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated SMP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98,%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of SMP proteins also have one or more of the SMP bioactivities described herein.

The SMP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-SMP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SMP protein alone. In other preferred embodiments, this fusion protein performs a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a

substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an SMP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SMP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates SMP protein activity or SMP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* carbon metabolism pathways or for the production of energy through processes such as oxidative phosphorylation, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates SMP protein activity can be an agent which stimulates SMP protein activity or SMP nucleic acid expression. Examples of agents which stimulate SMP protein activity or SMP nucleic acid expression include small molecules, active SMP proteins, and nucleic acids encoding SMP proteins that have been introduced into the cell. Examples of agents which inhibit SMP activity or expression include small molecules and antisense SMP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SMP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides SMP nucleic acid and protein molecules which are involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where overexpression or optimization of a glycolytic pathway protein has a direct impact on the yield, production, and/or efficiency of production of, *e.g.*, pyruvate from modified *C. glutamicum*), or may have an indirect impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of proteins involved in oxidative phosphorylation results in alterations in the amount of energy available to perform necessary metabolic processes and other cellular functions, such as nucleic acid and protein biosynthesis and transcription/translation). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino aids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α-ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β-carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B_1) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B_2) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B_6' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate

biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-alanine and for the condensation to panthotenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B_5), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α-ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B_{12}) and porphyrines belong to a group of chemicals characterized by a tetrapyrole ring system. The biosynthesis of vitamin B_{12} is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B_6, pantothenate, and biotin. Only Vitamin B_{12} is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language

"purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from

ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α, α-1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) J. Japan 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Sugar and Carbon Molecule Utilization and Oxidative Phosphorylation

Carbon is a critically important element for the formation of all organic compounds, and thus is a nutritional requirement not only for the growth and division of *C. glutamicum*, but also for the overproduction of fine chemicals from this microorganism. Sugars, such as mono-, di-, or polysaccharides, are particularly good carbon sources, and thus standard growth media typically contain one or more of: glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch, or cellulose (Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim). Alternatively, more complex forms of sugar may be utilized in the media, such as molasses, or other by-products of sugar refinement. Other compounds aside from the sugars may be used as alternate carbon sources, including alcohols (*e.g.*, ethanol or methanol), alkanes, sugar alcohols, fatty acids, and organic acids (*e.g.*, acetic acid or lactic acid). For a review of carbon sources and their utilization by microorganisms in culture, see: Ullman's Encyclopedia of

Industrial Chemistry (1987) vol. A9, "Enzymes", VCH: Weinheim; Stoppok, E. and Buchholz, K. (1996) "Sugar-based raw materials for fermentation applications" in Biotechnology (Rehm, H.J. *et al.*, eds.) vol. 6, VCH: Weinheim, p. 5-29; Rehm, H.J. (1980) Industrielle Mikrobiologie, Springer: Berlin; Bartholomew, W.H., and Reiman, H.B. (1979). Economics of Fermentation Processes, in: Peppler, H.J. and Perlman, D., eds. Microbial Technology 2nd ed., vol. 2, chapter 18, Academic Press: New York; and Kockova-Kratachvilova, A. (1981) Characteristics of Industrial Microorganisms, in: Rehm, H.J. and Reed, G., eds. Handbook of Biotechnology, vol. 1, chapter 1, Verlag Chemie: Weinheim.

After uptake, these energy-rich carbon molecules must be processed such that they are able to be degraded by one of the major sugar metabolic pathways. Such pathways lead directly to useful degradation products, such as ribose-5-phosphate and phosphoenolpyruvate, which may be subsequently converted to pyruvate. Three of the most important pathways in bacteria for sugar metabolism include the Embden-Meyerhoff-Pamas (EMP) pathway (also known as the glycolytic or fructose bisphosphate pathway), the hexosemonophosphate (HMP) pathway (also known as the pentose shunt or pentose phosphate pathway), and the Entner-Doudoroff (ED) pathway (for review, see Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York, and Stryer, L. (1988) Biochemistry, Chapters 13-19, Freeman: New York, and references therein).

The EMP pathway converts hexose molecules to pyruvate, and in the process produces 2 molecules of ATP and 2 molecules of NADH. Starting with glucose-1-phosphate (which may be either directly taken up from the medium, or alternatively may be generated from glycogen, starch, or cellulose), the glucose molecule is isomerized to fructose-6-phosphate, is phosphorylated, and split into two 3-carbon molecules of glyceraldehyde-3-phosphate. After dehydrogenation, phosphorylation, and successive rearrangements, pyruvate results.

The HMP pathway converts glucose to reducing equivalents, such as NADPH, and produces pentose and tetrose compounds which are necessary as intermediates and precursors in a number of other metabolic pathways. In the HMP pathway, glucose-6-phosphate is converted to ribulose-5-phosphate by two successive dehydrogenase reactions (which also release two NADPH molecules), and a carboxylation step. Ribulose-5-phosphate may also be converted to xyulose-5-phosphate and ribose-5-phosphate; the former can undergo a series of biochemical steps to glucose-6-phosphate, which may enter the EMP pathway, while the latter is commonly utilized as an intermediate in other biosynthetic pathways within the cell.

The ED pathway begins with the compound glucose or gluconate, which is subsequently phosphorylated and dehydrated to form 2-dehydro-3-deoxy-6-P-gluconate. Glucuronate and galacturonate may also be converted to 2-dehydro-3-deoxy-6-P-gluconate through more complex biochemical pathways. This product molecule is subsequently cleaved into glyceraldehyde-3-P and pyruvate; glyceraldehyde-3-P may itself also be converted to pyruvate.

The EMP and HMP pathways share many features, including intermediates and enzymes. The EMP pathway provides the greatest amount of ATP, but it does not produce ribose-5-phosphate, an important precursor for, *e.g.*, nucleic acid biosynthesis, nor does it produce erythrose-4-phosphate, which is important for amino acid biosynthesis. Microorganisms that are capable of using only the EMP pathway for glucose utilization are thus not able to grow on simple media with glucose as the sole carbon source. They are referred to as fastidious organisms, and their growth requires inputs of complex organic compounds, such as those found in yeast extract.

In contrast, the HMP pathway produces all of the precursors necessary for both nucleic acid and amino acid biosynthesis, yet yields only half the amount of ATP energy that the EMP pathway does. The HMP pathway also produces NADPH, which may be used for redox reactions in biosynthetic pathways. The HMP pathway does not directly produce pyruvate, however, and thus these microorganisms must also possess this portion of the EMP pathway. It is therefore not surprising that a number of microorganisms, particularly the facultative anerobes, have evolved such that they possess both of these pathways.

The ED pathway has thus far has only been found in bacteria. Although this pathway is linked partly to the HMP pathway in the reverse direction for precursor formation, the ED pathway directly forms pyruvate by the aldolase cleavage of 3-ketodeoxy-6-phosphogluconate. The ED pathway can exist on its own and is utilized by the majority of strictly aerobic microorganisms. The net result is similar to that of the HMP pathway, although one mole of ATP can be formed only if the carbon atoms are converted into pyruvate, instead of into precursor molecules.

The pyruvate molecules produced through any of these pathways can be readily converted into energy via the Krebs cycle (also known as the citric acid cycle, the citrate cycle, or the tricarboxylic acid cycle (TCA cycle)). In this process, pyruvate is first decarboxylated, resulting in the production of one molecule of NADH, 1 molecule of acetyl-CoA, and 1 molecule of CO_2. The acetyl group of acetyl CoA then reacts with the 4 carbon unit, oxaolacetate, leading to the formation of citric acid, a 6 carbon organic acid. Dehydration and two additional CO_2 molecules are released. Ultimately, oxaloacetate is regenerated and can serve again as an acetyl acceptor, thus completing

the cycle. The electrons released during the oxidation of intermediates in the TCA cycle are transferred to NAD^+ to yield NADH.

During respiration, the electrons from NADH are transferred to molecular oxygen or other terminal electron acceptors. This process is catalyzed by the respiratory chain, an electron transport system containing both integral membrane proteins and membrane associated proteins. This system serves two basic functions: first, to accept electrons from an electron donor and to transfer them to an electron acceptor, and second, to conserve some of the energy released during electron transfer by the synthesis of ATP. Several types of oxidation-reduction enzymes and electron transport proteins are known to be involved in such processes, including the NADH dehydrogenases, flavin-containing electron carriers, iron sulfur proteins, and cytochromes. The NADH dehydrogenases are located at the cytoplasmic surface of the plasma membrane, and transfer hydrogen atoms from NADH to flavoproteins, in turn accepting electrons from NADH. The flavoproteins are a group of electron carriers possessing a flavin prosthetic group which is alternately reduced and oxidized as it accepts and transfers electrons. Three flavins are known to participate in these reactions: riboflavin, flavin-adenine dinucleotide (FAD) and flavin-mononucleotide (FMN). Iron sulfur proteins contain a cluster of iron and sulfur atoms which are not bonded to a heme group, but which still are able to participate in dehydration and rehydration reactions. Succinate dehydrogenase and aconitase are exemplary iron-sulfur proteins; their iron-sulfur complexes serve to accept and transfer electrons as part of the overall electron-transport chain. The cytochromes are proteins containing an iron porphyrin ring (heme). There are a number of different classes of cytochromes, differing in their reduction potentials. Functionally, these cytochromes form pathways in which electrons may be transferred to other cytochromes having increasingly more positive reduction potentials. A further class of non-protein electron carriers is known: the lipid-soluble quinones (*e.g.*, coenzyme Q). These molecules also serve as hydrogen atom acceptors and electron donors.

The action of the respiratory chain generates a proton gradient across the cell membrane, resulting in proton motive force. This force is utilized by the cell to synthesize ATP, via the membrane-spanning enzyme, ATP synthase. This enzyme is a multiprotein complex in which the transport of H^+ molecules through the membrane results in the physical rotation of the intracellular subunits and concomitant phosphorylation of ADP to form ATP (for review, see Fillingame, R.H. and Divall, S. (1999) *Novartis Found. Symp.* 221: 218-229, 229-234).

Non-hexose carbon substrates may also serve as carbon and energy sources for cells. Such substrates may first be converted to hexose sugars in the gluconeogenesis

pathway, where glucose is first synthesized by the cell and then is degraded to produce energy. The starting material for this reaction is phosphoenolpyruvate (PEP), which is one of the key intermediates in the glycolytic pathway. PEP may be formed from substrates other than sugars, such as acetic acid, or by decarboxylation of oxaloacetate (itself an intermediate in the TCA cycle). By reversing the glycolytic pathway (utilizing a cascade of enzymes different than those of the original glycolysis pathway), glucose-6-phosphate may be formed. The conversion of pyruvate to glucose requires the utilization of 6 high energy phosphate bonds, whereas glycolysis only produces 2 ATP in the conversion of glucose to pyruvate. However, the complete oxidation of glucose (glycolysis, conversion of pyruvate into acetyl CoA, citric acid cycle, and oxidative phosphorylation) yields between 36-38 ATP, so the net loss of high energy phosphate bonds experienced during gluconeogenesis is offset by the overall greater gain in such high-energy molecules produced by the oxidation of glucose.

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III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SMP nucleic acid and protein molecules, which participate in the conversion of sugars to useful degradation products and energy (*e.g.*, ATP) in *C. glutamicum* or which may participate in the production of useful energy-rich molecules (*e.g.*, ATP) by other processes, such as oxidative phosphorylation. In one embodiment, the SMP molecules participate in the metabolism of carbon compounds such as sugars or the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. In a preferred embodiment, the activity of the SMP molecules of the present invention to contribute to carbon metabolism or energy production in *C. glutamicum* has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SMP molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic and energetic pathways in which the SMP proteins of the invention participate are modulated in yield, production, and/or efficiency of production, which either directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "SMP protein" or "SMP polypeptide" includes proteins which are capable of performing a function involved in the metabolism of carbon compounds such as sugars and the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Examples of SMP proteins include those encoded by the SMP genes set forth in Table 1 and Appendix A. The terms "SMP gene" or "SMP nucleic acid sequence" include nucleic acid sequences encoding an SMP

protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SMP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The term "degradation product" is art-recognized and includes breakdown products of a compound. Such products may themselves have utility as precursor (starting point) or intermediate molecules necessary for the biosynthesis of other compounds by the cell. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the SMP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and $FADH_2$ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as

ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) Biology of Prokaryotes, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least due to the presence of a greater number of viable cells, each producing the desired fine chemical. Further, a number of the degradation and intermediate compounds produced during sugar metabolism are necessary precursors and intermediates for other biosynthetic pathways throughout the cell. For example, many amino acids are synthesized directly from compounds normally resulting from glycolysis or the TCA cycle (*e.g.*, serine is synthesized from 3-phosphoglycerate, an intermediate in glycolysis). Thus, by increasing the efficiency of conversion of sugars to useful energy molecules, it is also possible to increase the amount of useful degradation products as well.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* SMP DNAs and the predicted amino acid sequences of the *C.*

glutamicum SMP proteins are shown in Appendices A and B, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins having a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

An SMP protein or a biologically active portion or fragment thereof of the invention can participate in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or can have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SMP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SMP-encoding nucleic acid (*e.g.*, SMP DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3'end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated

from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SMP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SMP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of Appendix A). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an SMP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of Appendix A correspond to the *Corynebacterium glutamicum* SMP DNAs of the invention. This DNA comprises sequences encoding SMP proteins (*i.e.*, the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix A.

For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA, RXN, or RXS number having the designation "RXA," "RXN," or "RXS" followed by 5 digits (*i.e.*, RXA00013,RXN00043, or RXS0735). Each of these sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be distinguished by their differing RXA, RXN, or RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA, RXN, or RXS designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequence in Appendix B designated RXA00013 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA00013 in Appendix A, and the amino acid sequence in Appendix B designated RXN00043 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00043 in Appendix A. Each of the RXARXN and RXS nucleotide and amino acid sequences of the invention has also been assigned a SEQ ID NO, as indicated in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXAdesignation. For example, SEQ ID NO:11, designated, as indicated on Table 1, as "F RXA01312", is an F-designated gene, as are SEQ ID NOs: 29, 33, and 39 (designated on Table 1 as "F RXA02803", "F RXA02854", and "F RXA01365", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version

relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an SMP protein. The nucleotide sequences determined from the cloning of the SMP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning SMP homologues in other cell types and organisms, as well as SMP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide

sequence of Appendix A can be used in PCR reactions to clone SMP homologues. Probes based on the SMP nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SMP protein, such as by measuring a level of an SMP-encoding nucleic acid in a sample of cells, *e.g.*, detecting SMP mRNA levels or determining whether a genomic SMP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is able to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. Protein members of such sugar metabolic pathways or energy producing systems, as described herein, may play a role in the production and secretion of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of an SMP protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SMP protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B.

Portions of proteins encoded by the SMP nucleic acid molecules of the invention are preferably biologically active portions of one of the SMP proteins. As used herein, the term "biologically active portion of an SMP protein" is intended to include a portion, *e.g.*, a domain/motif, of an SMP protein that participates in the metabolism of carbon compounds such as sugars, or in energy-generating pathways in *C. glutamicum*, or has

an activity as set forth in Table 1. To determine whether an SMP protein or a biologically active portion thereof can participate in the metabolism of carbon compounds or in the production of energy-rich molecules in *C. glutamicum*, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an SMP protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the SMP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SMP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy of the genetic code and thus encode the same SMP protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 58% identical to the nucleotide sequence designated RXA00014 (SEQ ID NO:41), a nucleotide sequence which is greater than and/or at least % identical to the nucleotide sequence designated RXA00195 (SEQ ID NO:399), and a nucleotide sequence which is greater than and/or at least 42% identical to the nucleotide sequence designated RXA00196 (SEQ ID NO:401). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the

lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* SMP nucleotide sequences shown in Appendix A, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SMP proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the SMP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SMP protein, preferably a *C. glutamicum* SMP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the SMP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SMP that are the result of natural variation and that do not alter the functional activity of SMP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SMP DNA of the invention can be isolated based on their homology to the *C. glutamicum* SMP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C.

Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* SMP protein.

In addition to naturally-occurring variants of the SMP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded SMP protein, without altering the functional ability of the SMP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SMP proteins (Appendix B) without altering the activity of said SMP protein, whereas an "essential" amino acid residue is required for SMP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having SMP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SMP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SMP proteins that contain changes in amino acid residues that are not essential for SMP activity. Such SMP proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the SMP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Appendix B and is capable of participate in the metabolism of carbon compounds such as sugars, or in the biosynthesis of high-energy compounds in *C. glutamicum*, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in

the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the sequence selected from Appendix B), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an SMP protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SMP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an SMP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SMP activity described herein to identify mutants that retain SMP activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding SMP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which

are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire SMP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SMP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of NO. 3 (RXA01626) comprises nucleotides 1 to 345). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SMP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SMP disclosed herein (*e.g.*, the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SMP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SMP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SMP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-

methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SMP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave SMP mRNA transcripts to thereby inhibit translation of SMP

mRNA. A ribozyme having specificity for an SMP-encoding nucleic acid can be designed based upon the nucleotide sequence of an SMP cDNA disclosed herein (*i.e.*, SEQ ID NO. 3 (RXA01626) in Appendix A). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an SMP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, SMP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, SMP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SMP nucleotide sequence (*e.g.*, an SMP promoter and/or enhancers) to form triple helical structures that prevent transcription of an SMP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SMP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, $lacI^q$-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, arny, SPO2, λ-P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MFα, AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by those of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, SMP proteins, mutant forms of SMP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of SMP proteins in prokaryotic or eukaryotic cells. For example, SMP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge),

algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* –mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SMP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant SMP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315), pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λgt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the

pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming Streptomyces, while plasmids pUB110, pC194, or pBD214 are suited for transformation of Bacillus species. Several plasmids of use in the transfer of genetic information into Corynebacterium include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the SMP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ, pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the SMP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the SMP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the

spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). .

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α-fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in

a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SMP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an SMP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular*

Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SMP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SMP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the SMP gene. Preferably, this SMP gene is a *Corynebacterium glutamicum* SMP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SMP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous SMP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous SMP protein). In the homologous recombination vector, the altered portion of the SMP gene is flanked at its 5' and 3' ends by additional nucleic acid of the SMP gene to allow for homologous recombination to occur between the exogenous SMP gene carried by the vector and an endogenous SMP gene in a microorganism. The additional flanking SMP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SMP gene has homologously recombined with the endogenous SMP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.

For example, inclusion of an SMP gene on a vector placing it under control of the lac operon permits expression of the SMP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous SMP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced SMP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SMP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SMP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SMP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described SMP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SMP protein. Accordingly, the invention further provides methods for producing SMP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SMP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SMP protein) in a suitable medium until SMP protein is produced. In another embodiment, the method further comprises isolating SMP proteins from the medium or the host cell.

C. Isolated SMP Proteins

Another aspect of the invention pertains to isolated SMP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of SMP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SMP protein having less than about 30% (by dry weight) of non-SMP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SMP protein, still more preferably less than about 10% of non-SMP protein, and most preferably less

than about 5% non-SMP protein. When the SMP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SMP protein having less than about 30% (by dry weight) of chemical precursors or non-SMP chemicals, more preferably less than about 20% chemical precursors or non-SMP chemicals, still more preferably less than about 10% chemical precursors or non-SMP chemicals, and most preferably less than about 5% chemical precursors or non-SMP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the SMP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SMP protein in a microorganism such as *C. glutamicum.*

An isolated SMP protein or a portion thereof of the invention can participate in the metabolism of carbon compounds such as sugars, or in the production of energy compounds (*e.g.*, by oxidative phosphorylation) utilized to drive unfavorable metabolic pathways, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SMP protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the SMP protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more

preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred SMP proteins of the present invention also preferably possess at least one of the SMP activities described herein. For example, a preferred SMP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A, and which can perform a function involved in the metabolism of carbon compounds such as sugars or in the generation of energy molecules (*e.g.*, ATP) by processes such as oxidative phosphorylation in *Corynebacterium glutamicum*, or which has one or more of the activities set forth in Table 1.

In other embodiments, the SMP protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the SMP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B and which has at least one of the SMP activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B.

Biologically active portions of an SMP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an SMP protein, *e.g.*, the an amino acid sequence shown in Appendix B or the amino acid sequence of a protein homologous to an SMP protein, which include fewer amino acids than a full length SMP protein or the full length protein which is homologous to an SMP protein, and exhibit at

least one activity of an SMP protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SMP protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SMP protein include one or more selected domains/motifs or portions thereof having biological activity.

SMP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the SMP protein is expressed in the host cell. The SMP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an SMP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SMP protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-SMP antibody, which can be produced by standard techniques utilizing an SMP protein or fragment thereof of this invention.

The invention also provides SMP chimeric or fusion proteins. As used herein, an SMP "chimeric protein" or "fusion protein" comprises an SMP polypeptide operatively linked to a non-SMP polypeptide. An "SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an SMP protein, whereas a "non-SMP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the SMP protein, *e.g.*, a protein which is different from the SMP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SMP polypeptide and the non-SMP polypeptide are fused in-frame to each other. The non-SMP polypeptide can be fused to the N-terminus or C-terminus of the SMP polypeptide. For example, in one embodiment the fusion protein is a GST-SMP fusion protein in which the SMP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SMP proteins. In another embodiment, the fusion protein is an SMP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an SMP protein can be increased through use of a heterologous signal sequence.

Preferably, an SMP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the

different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, Ausubel *et al.*, eds. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An SMP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SMP protein.

Homologues of the SMP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the SMP protein. As used herein, the term "homologue" refers to a variant form of the SMP protein which acts as an agonist or antagonist of the activity of the SMP protein. An agonist of the SMP protein can retain substantially the same, or a subset, of the biological activities of the SMP protein. An antagonist of the SMP protein can inhibit one or more of the activities of the naturally occurring form of the SMP protein, by, for example, competitively binding to a downstream or upstream member of the sugar molecule metabolic cascade or the energy-producing pathway which includes the SMP protein.

In an alternative embodiment, homologues of the SMP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the SMP protein for SMP protein agonist or antagonist activity. In one embodiment, a variegated library of SMP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of SMP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SMP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of SMP sequences therein. There are a variety of methods which can be used to produce libraries of potential SMP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding

the desired set of potential SMP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the SMP protein coding can be used to generate a variegated population of SMP fragments for screening and subsequent selection of homologues of an SMP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an SMP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SMP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SMP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SMP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated SMP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of SMP protein

regions required for function; modulation of an SMP protein activity; modulation of the metabolism of one or more sugars; modulation of high-energy molecule production in a cell (*i.e.*, ATP, NADPH); and modulation of cellular production of a desired compound, such as a fine chemical.

The SMP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in C. *glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated

with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The SMP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and energy-releasing processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the SMP nucleic acid molecules of the invention may result in the production of SMP proteins having functional differences from the wild-type SMP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an SMP protein, either by interacting with the protein itself or a substrate or binding partner of the SMP protein, or by modulating the transcription or translation of an SMP nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more SMP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SMP protein is assessed.

There are a number of mechanisms by which the alteration of an SMP protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. The degradation of high-energy carbon molecules such as sugars, and the conversion of compounds such as NADH and $FADH_2$ to more useful forms via oxidative phosphorylation results in a number of compounds which themselves may be desirable

fine chemicals, such as pyruvate, ATP, NADH, and a number of intermediate sugar compounds. Further, the energy molecules (such as ATP) and the reducing equivalents (such as NADH or NADPH) produced by these metabolic pathways are utilized in the cell to drive reactions which would otherwise be energetically unfavorable. Such unfavorable reactions include many biosynthetic pathways for fine chemicals. By improving the ability of the cell to utilize a particular sugar (*e.g.*, by manipulating the genes encoding enzymes involved in the degradation and conversion of that sugar into energy for the cell), one may increase the amount of energy available to permit unfavorable, yet desired metabolic reactions (*e.g.*, the biosynthesis of a desired fine chemical) to occur.

Further, modulation of one or more pathways involved in sugar utilization permits optimization of the conversion of the energy contained within the sugar molecule to the production of one or more desired fine chemicals. For example, by reducing the activity of enzymes involved in, for example, gluconeogenesis, more ATP is available to drive desired biochemical reactions (such as fine chemical biosyntheses) in the cell. Also, the overall production of energy molecules from sugars may be modulated to ensure that the cell maximizes its energy production from each sugar molecule. Inefficient sugar utilization can lead to excess CO_2 production and excess energy, which may result in futile metabolic cycles. By improving the metabolism of sugar molecules, the cell should be able to function more efficiently, with a need for fewer carbon molecules. This should result in an improved fine chemical product: sugar molecule ratio (improved carbon yield), and permits a decrease in the amount of sugars that must be added to the medium in large-scale fermentor culture of such engineered *C. glutamicum.*

The mutagenesis of one or more SMP genes of the invention may also result in SMP proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum.* For example, by increasing the efficiency of utilization of one or more sugars (such that the conversion of the sugar to useful energy molecules is improved), or by increasing the efficiency of conversion of reducing equivalents to useful energy molecules (*e.g.*, by improving the efficiency of oxidative phosphorylation, or the activity of the ATP synthase), one can increase the amount of these high-energy compounds available to the cell to drive normally unfavorable metabolic processes. These processes include the construction of cell walls, transcription, translation, and the biosynthesis of compounds necessary for growth and division of the cells (*e.g.*, nucleotides, amino acids, vitamins, lipids, etc.) (Lengeler *et al.* (1999) Biology of Prokaryotes, Thieme Verlag: Stuttgart, p. 88-109; 913-918; 875-899). By improving the growth and multiplication of these engineered cells, it is possible to

increase both the viability of the cells in large-scale culture, and also to improve their rate of division, such that a relatively larger number of cells can survive in fermentor culture. The yield, production, or efficiency of production may be increased, at least due to the presence of a greater number of viable cells, each producing the desired fine chemical.

Further, many of the degradation products produced during sugar metabolism are themselves utilized by the cell as precursors or intermediates for the production of a number of other useful compounds, some of which are fine chemicals. For example, pyruvate is converted into the amino acid alanine, and ribose-5-phosphate is an integral part of, for example, nucleotide molecules. The amount and efficiency of sugar metabolism, then, has a profound effect on the availability of these degradation products in the cell. By increasing the ability of the cell to process sugars, either in terms of efficiency of existing pathways (*e.g.*, by engineering enzymes involved in these pathways such that they are optimized in activity), or by increasing the availability of the enzymes involved in such pathways (*e.g.*, by increasing the number of these enzymes present in the cell), it is possible to also increase the availability of these degradation products in the cell, which should in turn increase the production of many different other desirable compounds in the cell (*e.g.*, fine chemicals).

The aforementioned mutagenesis strategies for SMP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SMP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l $MgSO_4 \times 7H_2O$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(NH_4)_2SO_4$, 1 g/l NaCl, 2 g/l $MgSO_4 \times 7H_2O$, 0.2 g/l $CaCl_2$, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $FeSO_4 \times H_2O$, 10 mg/l $ZnSO_4 \times 7\ H_2O$, 3 mg/l $MnCl_2 \times 4\ H_2O$, 30 mg/l H_3BO_3 20 mg/l $CoCl_2 \times 6\ H_2O$, 1 mg/l $NiCl_2 \times 6\ H_2O$, 3 mg/l $Na_2MoO_4 \times 2\ H_2O$, 500 mg/l complexing agent (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.,* Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see *e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g. Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli and C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be

overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other Corynebacterium or Brevibacterium species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) From Genes to Clones – Introduction to Gene Technology. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which

specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for Corynebacteria are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Procaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(NH_4)_2SO_4$, NH_4OH, nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A

Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH_4OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD_{600} of O.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining

methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum* cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on

a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. *et al.* (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci.* USA 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to SMP nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SMP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped

BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP

(global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the

synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing

polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S-methionine, ^{35}S-cysteine, ^{14}C-labelled amino acids, ^{15}N-amino acids, $^{15}NO_3$ or $^{15}NH_4^+$ or ^{13}C-labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic)

situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an SMP protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an SMP protein involved in the production of a fine chemical.

3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.

9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.

10. A vector comprising the nucleic acid molecule of claim 1.

11. The vector of claim 10, which is an expression vector.

12. A host cell transfected with the expression vector of claim 11.

13. The host cell of claim 12, wherein said cell is a microorganism.

14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.

16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.

18. An isolated SMP polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.

23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.

26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.

27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.

28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum, Corynebacterium herculis, Corynebacterium, lilium, Corynebacterium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium acetophilum, Corynebacterium ammoniagenes, Corynebacterium fujiokense, Corynebacterium nitrilophilus, Brevibacterium ammoniagenes, Brevibacterium butanicum, Brevibacterium divaricatum, Brevibacterium flavum, Brevibacterium healii, Brevibacterium ketoglutamicum, Brevibacterium ketosoreductum, Brevibacterium lactofermentum, Brevibacterium linens, Brevibacterium paraffinolyticum,* and those strains set forth in Table 3.

30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

32. The method of claim 25, wherein said fine chemical is an amino acid.

33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.

34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.

35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of the sequences set forth in Appendix A or Appendix B in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.

37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION

Abstract of the Disclosure

Isolated nucleic acid molecules, designated SMP nucleic acid molecules, which encode novel SMP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SMP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SMP proteins, mutated SMP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SMP genes in this organism.

TABLE 1: GENES IN THE APPLICATION

HMP:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
1	2	RXS02735	VV0074	14576	15280	6-Phosphoglucolactonase
3	4	RXA01626	GR00452	4270	3926	L-ribulose-phosphate 4-epimerase
5	6	RXA02245	GR00654	13639	14295	RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5 1 3 1)
7	8	RXA01015	GR00290	346	5	RIBOSE 5-PHOSPHATE ISOMERASE (EC 5 3 1 6)

TCA:

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
9	10	RXN01312	VV0082	20803	18785	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1 3 99.1)
11	12	F RXA01312	GR00380	2690	1614	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1 3.99 1)
13	14	RXN00231	VV0083	15484	14015	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (EC 1 2 1 16)
15	16	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99 1)
17	18	RXA01535	GR00427	1354	2760	FUMARATE HYDRATASE PRECURSOR (EC 4.2 1 2)
19	20	RXA00517	GR00131	1407	2447	MALATE DEHYDROGENASE (EC 1 1 1 37) (EC 1 1 1.82)
21	22	RXA01350	GR00392	1844	2827	MALATE DEHYDROGENASE (EC 1 1 1 37)

EMB-Pathway

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
23	24	RXA02149	GR00639	17786	18754	GLUCOKINASE (EC 2 7 1 2)
25	26	RXA01814	GR00515	2571	910	PHOSPHOGLUCOMUTASE (EC 5.4 2 2) / PHOSPHOMANNOMUTASE (EC 5.4 2 8)
27	28	RXN02803	VV0086	1	657	PHOSPHOGLUCOMUTASE (EC 5 4 2 2) / PHOSPHOMANNOMUTASE (EC 5 4.2.8)
29	30	F RXA02803	GR00784	2	400	PHOSPHOGLUCOMUTASE (EC 5 4 2 2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
31	32	RXN03076	VV0043	1624	35	PHOSPHOGLUCOMUTASE (EC 5 4 2 2) / PHOSPHOMANNOMUTASE (EC 5.4.2 8)
33	34	F RXA02854	GR10002	1588	5	PHOSPHOGLUCOMUTASE (EC 5 4.2 2) / PHOSPHOMANNOMUTASE (EC 5 4 2.8)
35	36	RXA00511	GR00129	1	513	PHOSPHOGLUCOMUTASE (EC 5 4 2 2) / PHOSPHOMANNOMUTASE (EC 5 4 2 8)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
37	38	RXN01365	VV0091	1476	103	PHOSPHOGLUCOMUTASE (EC 5 4 2 2) / PHOSPHOMANNOMUTASE (EC 5 4 2 8)
39	40	F RXA01365	GR00397	897	4	PHOSPHOGLUCOMUTASE (EC 5 4 2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2 8)
41	42	RXA00098	GR00014	6525	8144	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5 3.1.9)
43	44	RXA01989	GR00578	1	630	GLUCOSE-6-PHOSPHATE ISOMERASE A (GPI A) (EC 5.3.1 9)
45	46	RXA00340	GR00059	1549	2694	PHOSPHOGLYCERATE MUTASE (EC 5.4.2 1)
47	48	RXA02492	GR00720	2201	2917	PHOSPHOGLYCERATE MUTASE (EC 5 4.2 1)
49	50	RXA00381	GR00082	1451	846	PHOSPHOGLYCERATE MUTASE (EC 5 4.2.1)
51	52	RXA02122	GR00636	6511	5813	PHOSPHOGLYCERATE MUTASE (EC 5 4.2.1)
53	54	RXA00206	GR00032	6171	5134	6-PHOSPHOFRUCTOKINASE (EC 2 7 1 11)
55	56	RXA01243	GR00359	2302	3261	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
57	58	RXA01882	GR00538	1165	2154	1-PHOSPHOFRUCTOKINASE (EC 2 7.1 56)
59	60	RXA01702	GR00479	1397	366	FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1 2 13)
61	62	RXA02258	GR00654	26451	27227	TRIOSEPHOSPHATE ISOMERASE (EC 5 3.1 1)
63	64	RXN01225	VV0064	6382	4943	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
65	66	F RXA01225	GR00354	5302	6741	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE HOMOLOG
67	68	RXA02256	GR00654	23934	24935	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1 2 1 12)
69	70	RXA02257	GR00654	25155	26369	PHOSPHOGLYCERATE KINASE (EC 2.7 2 3)
71	72	RXA00235	GR00036	2365	1091	ENOLASE (EC 4 2 1 11)
73	74	RXA01093	GR00306	1552	122	PYRUVATE KINASE (EC 2 7 1 40)
75	76	RXN02675	VV0098	72801	70945	PYRUVATE KINASE (EC 2 7 1 40)
77	78	F RXA02675	GR00754	2	364	PYRUVATE KINASE (EC 2.7.1 40)
79	80	F RXA02695	GR00755	2949	4370	PYRUVATE KINASE (EC 2 7 1 40)
81	82	RXA00682	GR00179	5299	3401	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7 9 2)
83	84	RXA00683	GR00179	6440	5349	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2 7 9 2)
85	86	RXN00635	VV0135	22708	20972	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2 2)
87	88	F RXA02807	GR00788	88	552	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2 2.2)
89	90	F RXA00635	GR00167	3	923	PYRUVATE DEHYDROGENASE (CYTOCHROME) (EC 1.2.2 2)
91	92	RXN03044	VV0019	1391	2221	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4 1)
93	94	F RXA02852	GR00852	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1 2.4 1)
95	96	F RXA00268	GR00041	125	955	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1 2 4 1)
97	98	RXN03086	VV0049	2243	2650	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1 2.4 1)
99	100	F RXA02887	GR10022	411	4	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4 1)
101	102	RXN03043	VV0019	1	1362	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4 1)
103	104	F RXA02897	GR10039	1291	5	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2 4 1)
105	106	RXN03083	VV0047	88	1110	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8 1.4)
107	108	F RXA02853	GR10001	89	1495	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1 8.1.4)
109	110	RXA02259	GR00654	27401	30172	PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
111	112	RXN02326	VV0047	4500	5315	PYRUVATE CARBOXYLASE (EC 6 4 1 1)
113	114	F RXA02326	GR00668	5338	4523	PYRUVATE CARBOXYLASE
115	116	RXN02327	VV0047	3533	4492	PYRUVATE CARBOXYLASE (EC 6 4 1 1)
117	118	F RXA02327	GR00668	6305	5346	PYRUVATE CARBOXYLASE
119	120	RXN02328	VV0047	1842	3437	PYRUVATE CARBOXYLASE (EC 6 4 1.1)
121	122	F RXA02328	GR00668	7783	6401	PYRUVATE CARBOXYLASE (EC 6 4 1 1)
123	124	RXN01048	VV0079	12539	11316	MALIC ENZYME (EC 1.1 1 39)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
125	126	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1 1 39)
127	128	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1 1.39)
129	130	RXA02694	GR00755	1879	2820	L-LACTATE DEHYDROGENASE (EC 1.1 1.27)
131	132	RXN00296	VV0176	35763	38606	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1 1.2.4)
133	134	F RXA00296	GR00048	3	2837	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1 1 2 4)
135	136	RXA01901	GR00544	4158	5417	L-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1 2.3)
137	138	RXN01952	VV0105	9954	11666	D-LACTATE DEHYDROGENASE (EC 1.1 1 28)
139	140	F RXA01952	GR00562	1	216	D-LACTATE DEHYDROGENASE (EC 1 1 1.28)
141	142	F RXA01955	GR00562	4611	6209	D-LACTATE DEHYDROGENASE (EC 1.1 1 28)
143	144	RXA00293	GR00047	2645	1734	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1 1.1 95)
145	146	RXN01130	VV0157	6138	5536	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1 1 1 95)
147	148	F RXA01130	GR00315	2	304	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1 1.95)
149	150	RXN03112	VV0085	509	6	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1 1.1 95)
151	152	F RXA01133	GR00316	568	1116	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1 1 95)
153	154	RXN00871	VV0127	3127	2240	IOLB PROTEIN
155	156	F RXA00871	GR00239	2344	3207	IOLB PROTEIN D-FRUCTOSE 1,6-BISPHOSPHATE = GLYCERONE-CC PHOSPHATE + D- GLYCERALDEHYDE 3-PHOSPHATE
157	158	RXN02829	VV0354	287	559	IOLS PROTEIN
159	160	F RXA02829	GR00816	287	562	IOLS PROTEIN
161	162	RXN01468	VV0019	7474	8298	NAGD PROTEIN
163	164	F RXA01468	GR00422	1250	2074	PUTATIVE N-GLYCERALDEHYDE-2-PHOSPHOTRANSFERASE
165	166	RXA00794	GR00211	3993	2989	GLPX PROTEIN
167	168	RXN02920	VV0213	6135	5224	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1 1.95)
169	170	F RXA02379	GR00690	1390	686	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1 1.1 95)
171	172	RXN02688	VV0098	59053	58385	PHOSPHOGLYCERATE MUTASE (EC 5 4 2 1)
173	174	RXN03087	VV0052	3216	3428	PYRUVATE CARBOXYLASE (EC 6.4 1 1)
175	176	RXN03186	VV0377	310	519	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1 2 4 1)
177	178	RXN03187	VV0382	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1 2 4 1)
179	180	RXN02591	VV0098	14370	12541	PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] (EC 4.1.1.32)
181	182	RXS01260	VV0009	3477	2296	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
183	184	RXS01261	VV0009	3703	3533	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8 1.4)

Glycerol metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
185	186	RXA02640	GR00749	1400	2926	GLYCEROL KINASE (EC 2 7.1.30)
187	188	RXN01025	VV0143	5483	4488	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1.1.1.94)
189	190	F RXA01025	GR00293	939	1853	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1 1 1.94)
191	192	RXA01851	GR00525	3515	1830	AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1 1 99 5)
193	194	RXA01242	GR00359	1526	2302	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
195	196	RXA02288	GR00661	992	147	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
197	198	RXN01891	VV0122	24949	24086	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
199	200	F RXA01891	GR00541	1736	918	GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
201	202	RXA02414	GR00703	3808	3062	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
203	204	RXN01580	VV0122	22091	22807	Glycerophosphoryl diester phosphodiesterase

Acetate metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
205	206	RXA01436	GR00418	2547	1357	ACETATE KINASE (EC 2 7.2.1)
207	208	RXA00686	GR00179	8744	7941	ACETATE OPERON REPRESSOR
209	210	RXA00246	GR00037	4425	3391	ALCOHOL DEHYDROGENASE (EC 1 1 1 1)
211	212	RXA01571	GR00438	1360	1959	ALCOHOL DEHYDROGENASE (EC 1 1 1 1)
213	214	RXA01572	GR00438	1928	2419	ALCOHOL DEHYDROGENASE (EC 1 1 1 1)
215	216	RXA01758	GR00498	3961	2945	ALCOHOL DEHYDROGENASE (EC 1 1 1 1)
217	218	RXA02539	GR00726	11676	10159	ALDEHYDE DEHYDROGENASE (EC
219	220	RXN03061	VV0034	108	437	ALDEHYDE DEHYDROGENASE (EC 1.2 1 3)
221	222	RXN03150	VV0155	10678	10055	ALDEHYDE DEHYDROGENASE (EC 1 2 1 3)
223	224	RXN01340	VV0033	3	860	ALDEHYDE DEHYDROGENASE (EC 1 2 1 3)
225	226	RXN01498	VV0008	1598	3160	ALDEHYDE DEHYDROGENASE (EC 1.2.1 3)
227	228	RXN02674	VV0315	15614	14163	ALDEHYDE DEHYDROGENASE (EC 1 2.1 3)
229	230	RXN00868	VV0127	2230	320	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4 1 3 18)
231	232	RXN01143	VV0077	9372	8254	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4 1 3 18)
233	234	RXN01146	VV0264	243	935	ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4 1 3 18)
235	236	RXN01144	VV0077	8237	7722	ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 4.1.3 18)

Butanediol, diacetyl and acetoin formation

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
237	238	RXA02474	GR00715	8082	7309	(S,S)-butane-2,3-diol dehydrogenase (EC 1 1 1 76)
239	240	RXA02453	GR00710	6103	5351	ACETOIN(DIACETYL) REDUCTASE (EC 1.1.1 5)
241	242	RXS01758	VV0112	27383	28399	ALCOHOL DEHYDROGENASE (EC 1.1 1.1)

HMP-Cycle

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
243	244	RXA02737	GR00763	3312	1771	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1 1 1 49)
245	246	RXA02738	GR00763	4499	3420	TRANSALDOLASE (EC 2.2.1.2)
247	248	RXA02739	GR00763	6769	4670	TRANSKETOLASE (EC 2.2.1.1)
249	250	RXA00965	GR00270	1232	510	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1 1.44)
251	252	RXN00999	VV0106	2817	1366	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1 1 1 44)
253	254	F RXA00999	GR00283	3012	4448	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1 1 1 44)

Nucleotide sugar conversion

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
255	256	RXN02596	VV0098	48784	47582	UDP-GALACTOPYRANOSE MUTASE (EC 5 4 99 9)
257	258	F RXA02596	GR00742	1	489	UDP-GALACTOPYRANOSE MUTASE (EC 5 4 99.9)
259	260	F RXA02642	GR00749	5383	5880	UDP-GALACTOPYRANOSE MUTASE (EC 5.4 99.9)
261	262	RXA02572	GR00737	2	646	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1 1 1 22)
263	264	RXA02485	GR00718	2345	3445	UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (EC 1.1 1 158)
265	266	RXA01216	GR00352	2302	1202	UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2 7.7 23)
267	268	RXA01259	GR00367	987	130	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2 7.7 9)
269	270	RXA02028	GR00616	573	998	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9)
271	272	RXA01262	GR00367	8351	7191	GDP-MANNOSE 6-DEHYDROGENASE (EC 1 1.1.132)
273	274	RXA01377	GR00400	3935	5020	MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7 13)
275	276	RXA02063	GR00626	3301	4527	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (EC 2.7.7 27)
277	278	RXN00014	VV0048	8848	9627	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7 7 24)
279	280	F RXA00014	GR00002	4448	5227	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2 7 7.24)
281	282	RXA01570	GR00438	427	1281	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7.7.24)
283	284	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLYLTRANSFERASE (EC 2.7 7 40)
285	286	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2 1 46)

Inositol and ribitol metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
287	288	RXA01887	GR00539	4219	3209	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1 1 18)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
289	290	RXN00013	VV0048	7966	8838	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3 1 3 25)
291	292	F RXA00013	GR00002	3566	4438	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 1 (EC 3.1 3 25)
293	294	RXA01099	GR00306	6328	5504	INOSITOL MONOPHOSPHATE PHOSPHATASE
295	296	RXN01332	VV0273	579	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1 18)
297	298	F RXA01332	GR00388	552	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1 18)
299	300	RXA01632	GR00454	2338	3342	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
301	302	RXA01633	GR00454	3380	4462	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
303	304	RXN01406	VV0278	2999	1977	MYO-INOSITOL 2-DEHYDROGENASE (EC 1 1.1 18)
305	306	RXN01630	VV0050	48113	47037	MYO-INOSITOL 2-DEHYDROGENASE (EC 1 1.1 18)
307	308	RXN00528	VV0079	23406	22318	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5 5 1 4)
309	310	RXN03057	VV0028	7017	7688	MYO-INOSITOL 2-DEHYDROGENASE (EC 1 1.1 18)
311	312	F RXA02902	GR10040	10277	10948	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1 1 99 28)
313	314	RXA00251	GR00038	931	224	RIBITOL 2-DEHYDROGENASE (EC 1.1 1.56)

Utilization of sugars

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
315	316	RXN02654	VV0090	12206	13090	GLUCOSE 1-DEHYDROGENASE (EC 1 1 1 47)
317	318	F RXA02654	GR00752	7405	8289	GLUCOSE 1-DEHYDROGENASE II (EC 1 1 1.47)
319	320	RXN01049	VV0079	9633	11114	GLUCONOKINASE (EC 2 7 1 12)
321	322	F RXA01049	GR00296	1502	492	GLUCONOKINASE (EC 2 7 1.12)
323	324	F RXA01050	GR00296	1972	1499	GLUCONOKINASE (EC 2 7 1 12)
325	326	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
327	328	RXN00872	VV0127	6557	5604	FRUCTOKINASE (EC 2 7 1 4)
329	330	F RXA00872	GR00240	565	1086	FRUCTOKINASE (EC 2.7.1.4)
331	332	RXN00799	VV0009	58477	56834	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3 2 1 21) (EC 3.2.1.37)
333	334	F RXA00799	GR00214	1	1584	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1.21) (EC 3 2.1 37)
335	336	RXA00032	GR00003	12028	10520	MANNITOL 2-DEHYDROGENASE (EC 1 1 1 67)
337	338	RXA02528	GR00725	6880	7854	FRUCTOSE REPRESSOR
339	340	RXN00316	VV0006	7035	8180	Hypothetical Oxidoreductase (EC 1.1.1 -)
341	342	F RXA00309	GR00053	316	5	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99 28)
343	344	RXN00310	VV0006	6616	7050	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
345	346	F RXA00310	GR00053	735	301	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1 99.28)
347	348	RXA00041	GR00007	1246	5	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3 2.1 26)
349	350	RXA02026	GR00615	725	6	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
351	352	RXA02061	GR00626	1842	349	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2 1 26)
353	354	RXN01369	VV0124	595	1776	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3 1 8)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
355	356	F RXA01369	GR00398	3	503	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5 3.1 8)
357	358	F RXA01373	GR00399	595	1302	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5 3 1 8)
359	360	RXA02611	GR00743	1	1752	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4 1 18)
361	362	RXA02612	GR00743	1793	3985	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)
363	364	RXN01884	VV0184	1	1890	GLYCOGEN DEBRANCHING ENZYME (EC 2 4 1 25) (EC 3.2 1 33)
365	366	F RXA01884	GR00539	3	1475	GLYCOGEN DEBRANCHING ENZYME (EC 2.4 1 25) (EC 3.2.1.33)
367	368	RXA01111	GR00306	16981	17427	GLYCOGEN OPERON PROTEIN GLGX (EC 3 2 1.-)
369	370	RXN01550	VV0143	14749	16260	GLYCOGEN PHOSPHORYLASE (EC 2 4 1 1)
371	372	F RXA01550	GR00431	3	1346	GLYCOGEN PHOSPHORYLASE (EC 2.4.1 1)
373	374	RXN02100	VV0318	2	2326	GLYCOGEN PHOSPHORYLASE (EC 2 4.1 1)
375	376	F RXA02100	GR00631	3	920	GLYCOGEN PHOSPHORYLASE (EC 2 4 1.1)
377	378	F RXA02113	GR00633	2	1207	GLYCOGEN PHOSPHORYLASE (EC 2 4.1.1)
379	380	RXA02147	GR00639	15516	16532	ALPHA-AMYLASE (EC 3.2 1.1)
381	382	RXA01478	GR00422	10517	12352	GLUCOAMYLASE G1 AND G2 PRECURSOR (EC 3 2 1 3)
383	384	RXA01888	GR00539	4366	4923	GLUCOSE-RESISTANCE AMYLASE REGULATOR
385	386	RXN01927	VV0127	50623	49244	XYLULOSE KINASE (EC 2 7.1 17)
387	388	F RXA01927	GR00555	3	1118	XYLULOSE KINASE (EC 2 7.1 17)
389	390	RXA02729	GR00762	747	4	RIBOKINASE (EC 2 7 1 15)
391	392	RXA02797	GR00778	1739	2641	RIBOKINASE (EC 2 7 1 15)
393	394	RXA02730	GR00762	1768	731	RIBOSE OPERON REPRESSOR
395	396	RXA02551	GR00729	2193	2552	6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2 1 86)
397	398	RXA01325	GR00385	5676	5005	DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4 1 2 4)
399	400	RXA00195	GR00030	543	1103	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1 1.-)
401	402	RXA00196	GR00030	1094	1708	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1 1 -)
403	404	RXN01562	VV0191	1230	3137	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
405	406	F RXA01562	GR00436	2	1039	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
407	408	F RXA01705	GR00480	971	1573	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE
409	410	RXN00879	VV0099	8763	6646	4-ALPHA-GLUCANOTRANSFERASE (EC 2 4.1 25)
411	412	F RXA00879	GR00242	5927	3828	4-ALPHA-GLUCANOTRANSFERASE (EC 2 4.1.25), amylomaltase
413	414	RXN00043	VV0119	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3 5.1 25)
415	416	F RXA00043	GR00007	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3 5.1 25)
417	418	RXN01752	VV0127	35265	33805	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2 4 1 -)
419	420	F RXA01839	GR00520	1157	510	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
421	422	RXA01859	GR00529	1473	547	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2 4 1 -)
423	424	RXA00042	GR00007	2037	1279	GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3 1.10)
425	426	RXA01482	GR00422	17271	15397	GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16)
427	428	RXN03179	VV0336	2	667	URONATE ISOMERASE (EC 5 3.1 12)
429	430	F RXA02872	GR10013	675	4	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3 1.12)
431	432	RXN03180	VV0337	672	163	URONATE ISOMERASE (EC 5 3.1.12)
433	434	F RXA02873	GR10014	672	163	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)
435	436	RXA02292	GR00662	1611	2285	GALACTOSIDE O-ACETYLTRANSFERASE (EC 2.3 1 18)
437	438	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLYLTRANSFERASE (EC 2.7 7 40)
439	440	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
441	442	RXA02440	GR00709	5097	4258	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
443	444	RXN01569	VV0009	41086	42444	dTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1 1 1 133)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
445	446	F RXA01569	GR00438	2	427	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1 1 1 133)
447	448	F RXA02055	GR00624	7122	8042	DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1 133)
449	450	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4 2.1 46)
451	452	RXA02054	GR00624	6103	7119	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2 1 46)
453	454	RXN00427	VV0112	7004	6219	dTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2 - - -)
455	456	F RXA00427	GR00098	1591	2022	DTDP-RHAMNOSYL TRANSFERASE RFBF (EC 2.- - -)
457	458	RXA00327	GR00057	10263	9880	PROTEIN ARAJ
459	460	RXA00328	GR00057	11147	10656	PROTEIN ARAJ
461	462	RXA00329	GR00057	12390	11167	PROTEIN ARAJ
463	464	RXN01554	VV0135	28686	26545	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR (EC 3 2.1.39)
465	466	RXN03015	VV0063	289	8	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1 1 1 22)
467	468	RXN03056	VV0028	6258	6935	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.- - -)
469	470	RXN03030	VV0009	57006	56443	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR (EC 3.2.1 21) (EC 3 2.1.37)
471	472	RXN00401	VV0025	12427	11489	5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC 4 2 1 41)
473	474	RXN02125	VV0102	23242	22442	ALDOSE REDUCTASE (EC 1.1 1 21)
475	476	RXN00200	VV0181	1679	5116	arabinosyl transferase subunit B (EC 2.4.2.-)
477	478	RXN01175	VV0017	39688	38303	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4 1 2 15)
479	480	RXN01376	VV0091	5610	4750	PUTATIVE GLYCOSYL TRANSFERASE WBIF
481	482	RXN01631	VV0050	47021	46143	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5 - - -)
483	484	RXN01593	VV0229	13274	12408	NAGD PROTEIN
485	486	RXN00337	VV0197	20369	21418	GALACTOKINASE (EC 2 7.1.6)
487	488	RXS00584	VV0323	5516	6640	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4 1 2 15)
489	490	RXS02574				BETA-HEXOSAMINIDASE A PRECURSOR (EC 3 2 1 52)
491	492	RXS03215				GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1 1.99 28)
493	494	F RXA01915	GR00549	1	1008	GLUCOSE--FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1 1 99.28)
495	496	RXS03224				CYCLOMALTODEXTRINASE (EC 3 2.1 54)
497	498	F RXA00038	GR00006	1417	260	CYCLOMALTODEXTRINASE (EC 3 2.1.54)
499	500	RXC00233				protein involved in sugar metabolism
501	502	RXC00236				Membrane Lipoprotein involved in sugar metabolism
503	504	RXC00271				Exported Protein involved in ribose metabolism
505	506	RXC00338				protein involved in sugar metabolism
507	508	RXC00362				Membrane Spanning Protein involved in metabolism of diols
509	510	RXC00412				Amino Acid ABC Transporter ATP-Binding Protein involved in sugar metabolism
511	512	RXC00526				ABC Transporter ATP-Binding Protein involved in sugar metabolism
513	514	RXC01004				Membrane Spanning Protein involved in sugar metabolism
515	516	RXC01017				Cytosolic Protein involved in sugar metabolism
517	518	RXC01021				Cytosolic Kinase involved in metabolism of sugars and thiamin
519	520	RXC01212				ABC Transporter ATP-Binding Protein involved in sugar metabolism
521	522	RXC01306				Membrane Spanning Protein involved in sugar metabolism
523	524	RXC01366				Cytosolic Protein involved in sugar metabolism
525	526	RXC01372				Cytosolic Protein involved in sugar metabolism
527	528	RXC01659				protein involved in sugar metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
529	530	RXC01663				protein involved in sugar metabolism
531	532	RXC01693				protein involved in sugar metabolism
533	534	RXC01703				Cytosolic Protein involved in sugar metabolism
535	536	RXC02254				Membrane Associated Protein involved in sugar metabolism
537	538	RXC02255				Cytosolic Protein involved in sugar metabolism
539	540	RXC02435				protein involved in sugar metabolism
541	542	F RXA02435	GR00709	825	268	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
543	544	RXC03216				protein involved in sugar metabolism

TCA-cycle

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
545	546	RXA02175	GR00641	10710	9418	CITRATE SYNTHASE (EC 4 1 3 7)
547	548	RXA02621	GR00746	2647	1829	CITRATE LYASE BETA CHAIN (EC 4 1 3.6)
549	550	RXN00519	VV0144	5585	3372	ISOCITRATE DEHYDROGENASE (NADP) (EC 1 1 1.42)
551	552	F RXA00521	GR00133	2	1060	ISOCITRATE DEHYDROGENASE [NADP] (EC 1 1 1 42)
553	554	RXN02209	VV0304	1	1671	ACONITATE HYDRATASE (EC 4.2 1.3)
555	556	F RXA02209	GR00648	3	1661	ACONITATE HYDRATASE (EC 4 2 1 3)
557	558	RXN02213	VV0305	1378	2151	ACONITATE HYDRATASE (EC 4.2 1 3)
559	560	F RXA02213	GR00649	1330	2046	ACONITATE HYDRATASE (EC 4.2.1 3)
561	562	RXA02056	GR00625	3	2870	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1 2 4 2)
563	564	RXA01745	GR00495	2	1495	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2 3.1 61)
565	566	RXA00782	GR00206	3984	3103	SUCCINYL-COA SYNTHETASE ALPHA CHAIN (EC 6 2 1 5)
567	568	RXA00783	GR00206	5280	4009	SUCCINYL-COA SYNTHETASE BETA CHAIN (EC 6 2.1 5)
569	570	RXN01695	VV0139	11307	12806	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1 1.99 16)
571	572	F RXA01615	GR00449	8608	9546	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1 1 99.16)
573	574	F RXA01695	GR00474	4388	4179	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1 1 99 16)
575	576	RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
577	578	RXN01048	VV0079	12539	11316	MALIC ENZYME (EC 1 1 1 39)
579	580	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1 1 1.39)
581	582	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
583	584	RXN03101	VV0066	2	583	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2 3.1.61)
585	586	RXN02046	VV0025	15056	14640	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2 3.1 61)
587	588	RXN00389	VV0025	11481	9922	oxoglutarate semialdehyde dehydrogenase (EC 1 2 1.-)

Glyoxylate bypass

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
589	590	RXN02399	VV0176	19708	18365	ISOCITRATE LYASE (EC 4.1 3 1)
591	592	F RXA02399	GR00699	478	1773	ISOCITRATE LYASE (EC 4.1 3 1)
593	594	RXN02404	VV0176	20259	22475	MALATE SYNTHASE (EC 4.1 3 2)
595	596	F RXA02404	GR00700	3798	1663	MALATE SYNTHASE (EC 4 1.3 2)
597	598	RXA01089	GR00304	3209	3958	GLYOXYLATE-INDUCED PROTEIN
599	600	RXA01886	GR00539	3203	2430	GLYOXYLATE-INDUCED PROTEIN

Methylcitrate-pathway

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
601	602	RXN03117	VV0092	3087	1576	2-methylisocitrate synthase (EC 5 3 3 -)
603	604	F RXA00406	GR00090	978	4	2-methylisocitrate synthase (EC 5 3 3 -)
605	606	F RXA00514	GR00130	1983	1576	2-methylisocitrate synthase (EC 5 3 3 -)
607	608	RXA00512	GR00130	621	4	2-methylcitrate synthase (EC 4 1 3.31)
609	610	RXA00518	GR00131	3069	2773	2-methylcitrate synthase (EC 4.1 3.31)
611	612	RXA01077	GR00300	4647	6017	2-methylisocitrate synthase (EC 5 3 3.-)
613	614	RXN03144	VV0141	2	901	2-methylisocitrate synthase (EC 5 3.3 -)
615	616	F RXA02322	GR00668	415	5	2-methylisocitrate synthase (EC 5 3 3 -)
617	618	RXA02329	GR00669	607	5	2-methylisocitrate synthase (EC 5 3 3 -)
619	620	RXA02332	GR00671	1906	764	2-methylcitrate synthase (EC 4 1 3.31)
621	622	RXN02333	VV0141	901	1815	methylisocitrate lyase (EC 4.1 3 30)
623	624	F RXA02333	GR00671	2120	1902	methylisocitrate lyase (EC 4.1 3 30)
625	626	RXA00030	GR00003	9590	9979	LACTOYLGLUTATHIONE LYASE (EC 4 4.1.5)

Methyl-Malonyl-CoA-Mutases

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
627	628	RXN00148	VV0167	9849	12059	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5 4 99.2)
629	630	F RXA00148	GR00023	2002	5	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5 4 99.2)
631	632	RXA00149	GR00023	3856	2009	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)

Others

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
633	634	RXN00317	VV0197	26879	27532	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3 1.3.18)
635	636	F RXA00317	GR00055	344	6	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1 3.18)
637	638	RXA02196	GR00645	3956	3264	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)
639	640	RXN02461	VV0124	14236	14643	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3 1 3 18)

Redox Chain

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
641	642	RXN01744	VV0174	2350	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10 3.-)
643	644	F RXA00055	GR00008	11753	11890	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1 10 3.-)
645	646	F RXA01744	GR00494	2113	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1 10.3.-)
647	648	RXA00379	GR00082	212	6	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
649	650	RXA00385	GR00083	773	435	CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCDA
651	652	RXA01743	GR00494	806	6	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (EC 1 10 3 -)
653	654	RXN02480	VV0084	31222	29567	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)
655	656	F RXA01919	GR00550	288	4	CYTOCHROME C OXIDASE SUBUNIT I (EC 1 9.3.1)
657	658	F RXA02480	GR00717	1449	601	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1 9 3 1)
659	660	F RXA02481	GR00717	1945	1334	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1 9.3.1)
661	662	RXA02140	GR00639	7339	8415	CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1 9 3 1)
663	664	RXA02142	GR00639	9413	10063	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9 3 1)
665	666	RXA02144	GR00639	11025	12248	RIESKE IRON-SULFUR PROTEIN
667	668	RXA02740	GR00763	7613	8542	PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR
669	670	RXA02743	GR00763	13534	12497	CYTOCHROME AA3 CONTROLLING PROTEIN
671	672	RXA01227	GR00355	1199	1519	FERREDOXIN
673	674	RXA01865	GR00532	436	122	FERREDOXIN
675	676	RXA00680	GR00179	2632	2315	FERREDOXIN VI
677	678	RXA00679	GR00179	2302	1037	FERREDOXIN--NAD(+) REDUCTASE (EC 1 18.1.3)
679	680	RXA00224	GR00032	24965	24015	ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT
681	682	RXA00225	GR00032	25783	24998	ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT
683	684	RXN00606	VV0192	11299	9026	NADH DEHYDROGENASE I CHAIN L (EC 1.6 5.3)
685	686	F RXA00606	GR00160	121	1869	NADH DEHYDROGENASE I CHAIN L (EC 1 6.5.3)
687	688	RXN00595	VV0192	8642	7113	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
689	690	F RXA00608	GR00160	2253	3017	NADH DEHYDROGENASE I CHAIN M (EC 1 6 5.3)
691	692	RXA00913	GR00249	3	2120	NADH DEHYDROGENASE I CHAIN L (EC 1.6 5 3)
693	694	RXA00909	GR00247	2552	3406	NADH DEHYDROGENASE I CHAIN L (EC 1 6.5.3)
695	696	RXA00700	GR00182	846	43	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2
697	698	RXN00483	VV0086	44824	46287	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5 3) (EC 1 6 99.3)
699	700	F RXA00483	GR00119	19106	20569	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR (EC 1.6.5 3) (EC 1 6.99 3)
701	702	RXA01534	GR00427	1035	547	NADH-DEPENDENT FMN OXYDOREDUCTASE

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
703	704	RXA00288	GR00046	2646	1636	QUINONE OXIDOREDUCTASE (EC 1 6 5 5)
705	706	RXA02741	GR00763	9585	8620	QUINONE OXIDOREDUCTASE (EC 1 6.5 5)
707	708	RXN02560	VV0101	9922	10788	NADPH-FLAVIN OXIDOREDUCTASE (EC 1 6 99.-)
709	710	F RXA02560	GR00731	6339	7160	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6 99 -)
711	712	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1 3 99.1)
713	714	RXN03014	VV0058	1273	368	NADH DEHYDROGENASE I CHAIN M (EC 1 6 5 3)
715	716	F RXA00910	GR00248	3	1259	Hydrogenase subunits
717	718	RXN01895	VV0117	955	5	NADH DEHYDROGENASE (EC 1 6 99 3)
719	720	F RXA01895	GR00543	2	817	DEHYDROGENASE
721	722	RXA00703	GR00183	2556	271	FORMATE DEHYDROGENASE ALPHA CHAIN (EC 1 2 1 2)
723	724	RXN00705	VV0005	6111	5197	FDHD PROTEIN
725	726	F RXA00705	GR00184	1291	407	FDHD PROTEIN
727	728	RXN00388	VV0025	2081	3091	CYTOCHROME C BIOGENESIS PROTEIN CCSA
729	730	F RXA00388	GR00085	969	667	essential protein similar to cytochrome c
731	732	F RXA00386	GR00084	514	5	RESC PROTEIN, essential protein similar to cytochrome c biogenesis protein
733	734	RXA00945	GR00259	1876	2847	putative cytochrome oxidase
735	736	RXN02556	VV0101	5602	6759	FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1 6 99 7)
737	738	F RXA02556	GR00731	2019	3176	FLAVOHEMOPROTEIN
739	740	RXA01392	GR00408	2297	3373	GLUTATHIONE S-TRANSFERASE (EC 2.5 1.18)
741	742	RXA00800	GR00214	2031	3134	GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1 2.1 1)
743	744	RXA02143	GR00639	10138	11025	QCRC PROTEIN, menaquinol·cytochrome c oxidoreductase
745	746	RXN03096	VV0058	405	4	NADH DEHYDROGENASE I CHAIN M (EC 1 6 5.3)
747	748	RXN02036	VV0176	32683	33063	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6 5 3)
749	750	RXN02765	VV0317	3552	2794	Hypothetical Oxidorductase
751	752	RXN02206	VV0302	1784	849	Hypothetical Oxidoreductase
753	754	RXN02554	VV0101	4633	4010	Hypothetical Oxidoreductase (EC 1.1 1 -)

ATP-Synthase

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
755	756	RXN01204	VV0121	1270	461	ATP SYNTHASE A CHAIN (EC 3 6.1.34)
757	758	F RXA01204	GR00345	394	1155	ATP SYNTHASE A CHAIN (EC 3.6.1 34)
759	760	RXA01201	GR00344	675	2315	ATP SYNTHASE ALPHA CHAIN (EC 3.6 1.34)
761	762	RXN01193	VV0175	5280	3832	ATP SYNTHASE BETA CHAIN (EC 3.6 1.34)
763	764	F RXA01193	GR00343	15	755	ATP SYNTHASE BETA CHAIN (EC 3.6 1 34)
765	766	F RXA01203	GR00344	3355	3993	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
767	768	RXN02821	VV0121	324	85	ATP SYNTHASE C CHAIN (EC 3.6 1.34)
769	770	F RXA02821	GR00802	139	318	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
771	772	RXA01200	GR00344	2	610	ATP SYNTHASE DELTA CHAIN (EC 3 6.1 34)
773	774	RXA01194	GR00343	770	1141	ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
775	776	RXA01202	GR00344	2375	3349	ATP SYNTHASE GAMMA CHAIN (EC 3 6 1 34)
777	778	RXN02434	VV0090	4923	3274	ATP-BINDING PROTEIN

Cytochrome metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
779	780	RXN00684	VV0005	29864	28581	CYTOCHROME P450 116 (EC 1.14 -.-)
781	782	RXN00387	VV0025	1150	2004	Hypothetical Cytochrome c Biogenesis Protein

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat corboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," *Biochem. Biophys. Res. Commun.*, 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," *Appl. Microbiol. Biotechnol.*, 51(2):223-228 (1999)
AB018530	dtsR		Kimura, E. et al. "Molecular cloning of a novel gene, dtsR, which rescues the detergent sensitivity of a mutant derived from *Brevibacterium lactofermentum*," *Biosci. Biotechnol. Biochem.*, 60(10):1565-1570 (1996)
AB018531	dtsR1; dtsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," *Microbiology,* 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," *Mol. Cells.,* 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," *Appl. Environ. Microbiol.,* 65(4)1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete[i])	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," *J. Bacteriol.*, 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzmye); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," *FEMS Microbiol.*, 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol aceteyl transferase	
AJ224946	mqo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," *Eur. J. Biochem.*, 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," *Biochemistry*, 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," *Mol. Microbiol.*, 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," *Microbiology,* 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-trypophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," *J. Bacteriol.*, 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," *FEMS Microbiol. Lett.*, 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," *J. Bacteriol.*, 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," *PNAS USA,* 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," *FEMS Microbiol. Lett.,* 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," *J. Microbiol. Biotechnol.,* 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," *Appl. Environ. Microbiol.,* 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," *J. Bacteriol.,* 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," *J. Bacteriol.,* 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," *J. Bacteriol.,* 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene,* 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3'end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene,* 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," *Gene,* 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.,* 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.*, 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," *J. Bacteriol.*, 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," *Arch. Microbiol.*, 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," *Appl. Environ. Microbiol.*, 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; clgIIR	Putative type II 5-cytosoine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," *J. Bacteriol.*, 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," *Gene,* 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of Methylobacillus flagellatum and Corynebacterium glutamicum," *Gene,* 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A Corynebacterium glutamicum gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," *Arch. Microbiol.,* 166(2);76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A Corynebacterium glutamicum gene conferring multidrug resistance in the heterologous host Escherichia coli," *J. Bacteriol.,* 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the Brevibacterium lactofermentum tryptophan operon," *Nucleic Acids Res.,* 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of Corynebacterium glutamicum and possible mechanisms for modulation of its expression," *Mol. Gen. Genet.,* 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: Molecular cloning, nucleotide sequence, and expression," *Mol. Gen. Genet.,* 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," *Plant. Mol. Biol.,* 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the Corynebacterium glutamicum fda gene: structural comparison of C. glutamicum fructose-1, 6-biphosphate aldolase to class I and class II aldolases," *Mol. Microbiol.,*
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from Corynebacterium glutamicum," *Nucleic Acids Res.,* 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," *Mol. Microbiol.,* 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," *Nucleic Acids Res.,* 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," *Mol. Microbiol.,* 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," *Mol. Microbiol.,* 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspertate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," *Mol. Gen. Genet.,* 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomeras," *J. Bacteriol.,* 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," *Mol. Microbiol.,* 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," *Mol. Microbiol.,* 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Ps1 protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," *Mol. Microbiol.,* 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," *Microbiol.,* 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," *Mol. Microbiol.,* 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," *Mol. Microbiol.,* 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," *Appl. Environ. Microbiol.,* 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," *J. Bacteriol.,* 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," *Biochem. Biophys. Res. Commun.,* 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," *Appl. Microbiol. Biotechnol.,* 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," *J. Bacteriol.,* 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek,* 64:285-305 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek,* 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," *DNA Seq.,* 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase: sequence analysis," *Microbiology,* 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," *Microbiol.,* 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronemeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," *J. Bacteriol.,* 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," *Microbiology,* 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus Corynebacterium deduced from analyses of small-subunit ribosomal DNA sequences," *Int. J. Syst. Bacteriol.,* 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.,* 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.,* 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus Corynebacterium based on 16S rRNA gene sequences," *Int. J. Syst. Bacteriol.,* 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of Corynebacterium glutamicumproline reveals the presence of aroP, which encodes the aromatic amino acid transporter," *J. Bacteriol.,* 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," *Microbiology,* 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," *Microbiology,* 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," *J. Bacteriol.,* 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of Corynebacterium glutamicum," *J. Biol. Chem.,* 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the Corynebacterium glutamicum betP gene, encoding the transport system for the compatible solute glycine betaine," *J. Bacteriol.,* 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of Corynebacterium glutamicum, encoding two enzymes involved in L-lysine synthesis," *Biotechnol. Lett.,* 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum," *Mol. Microbiol.,* 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," *Appl. Environ. Microbiol.*, 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," *Gene,* 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.,* 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," *Nucleic Acids Res.,* 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.,* 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," *Mol. Microbiol.,* 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," *Mol. Gen. Genet.,* 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," *Arch. Microbiol.,* 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," *Microbiology,* 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," *Appl. Microbiol. Biotechnol.,* 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," *Microbiol.*, 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," *FEMS Microbiol. Lett.*, 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," *Virology*, 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," *J. Bacteriol.*,175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," *J. Bacteriol.*, 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," *Appl. Environ. Microbiol.*, 60(7)2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," *Gene*, 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," *Gene*, 170(1):91-94 (1996)

[1] A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							

Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japen.

TABLE 4: ALIGNMENT RESULTS

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rxa00013	996	GB_GSS4:AQ713475	581	AQ713475	HS_5402_B2_A12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=978 Col=24 Row=B, genomic survey sequence	Homo sapiens	37,148	13-Jul-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M 10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
rxa00014	903	GB_BA1:MTCY3A2	25830	Z83867	Mycobacterium tuberculosis H37Rv complete genome, segment 136/162.	Mycobacterium tuberculosis	58,140	17-Jun-98
		GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	57,589	8-Aug-97
		GB_BA1:SAPURCLUS	9120	X92429	S.alboniger napH, pur7, pur10, pur6, pur4, pur5 and pur3 genes.	Streptomyces anulatus	55,667	28-Feb-96
rxa00030	513	GB_EST21 C89713	767	C89713	C89713 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSG229, mRNA sequence.	Dictyostelium discoideum	45,283	20-Apr-98
		GB_EST28:AI497294	484	AI497294	fb63g03.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:AFP4_MYOOC P80961 ANTIFREEZE PROTEIN LS-12 ,, mRNA sequence.	Danio rerio	42,991	11-MAR-1999
		GB_EST21:C92167	637	C92167	C92167 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSD179, mRNA sequence.	Dictyostelium discoideum	44,444	12-Jul-99
rxa00032	1632	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	39,689	12-MAY-1998
		GB_BA2:AF018073	9810	AF018073	Rhodobacter sphaeroides operon regulator (smoC), periplasmic sorbitol-binding protein (smoE), sorbitol/mannitol transport inner membrane protein (smoF), sorbitol/mannitol transport inner membrane protein (smoG), sorbitol/mannitol transport ATP-binding transport protein (smoK), sorbitol dehydrogenase (smoS), mannitol dehydrogenase (mtlK), and periplasmic mannitol-binding protein (smoM) genes, complete cds.	Rhodobacter sphaeroides	48,045	22-OCT-1997
		GB_BA2:AF045245	5930	AF045245	Klebsiella pneumoniae D-arabinitol transporter (dalT), D-arabinitol kinase (dalK), D-arabinitol dehydrogenase (dalD), and repressor (dalR) genes, complete cds.	Klebsiella pneumoniae	38,514	16-Jul-98
rxa00041	1342	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene	Corynebacterium glutamicum	99,031	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown	99,031	07-OCT-1996
		GB_IN1:LMFL5883	31934	AL117384	Leishmania major Friedlin chromosome 23 cosmid L5883, complete sequence.	Leishmania major	43,663	21-OCT-1999
rxa00042	882	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	94,767	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	94,767	07-OCT-1996
		GB_IN1:CEU33051	4899	U33051	Caenorhabditis elegans sur-2 mRNA, complete cds	Caenorhabditis elegans	40,276	23-Jan-96
rxa00043	1287	GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776	Unknown	97,591	07-OCT-1996
		EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	97,591	08-OCT-1997 (Rel. 52, Created)
		GB_PR3:AC005174	39769	AC005174	Homo sapiens clone UWGC:g1564a012 from 7p14-15, complete sequence.	Homo sapiens	35,879	24-Jun-98

TABLE 4: ALIGNMENT RESULTS

rxa00098	1743	GB_BA1:MSU88433	1928	U88433	Mycobacterium smegmatis phosphoglucose isomerase gene, complete cds	Mycobacterium smegmatis	62,658	19-Apr-97
		GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	37,638	27-Jul-98
		GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome, segment 44/162	Mycobacterium tuberculosis	36,784	17-Jun-98
rxa00148	2334	GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	Mycobacterium tuberculosis	67,457	17-Jun-98
		GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456	Mycobacterium tuberculosis	40,883	03-DEC-1996
		GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175	Mycobacterium tuberculosis	67,457	10-DEC-1996
rxa00149	1971	GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456	Mycobacterium tuberculosis	35,883	03-DEC-1996
		GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175	Mycobacterium tuberculosis	51,001	10-DEC-1996
		GB_BA1:MTCY277	38300	Z79701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162	Mycobacterium tuberculosis	51,001	17-Jun-98
rxa00195	684	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome, segment 126/162.	Mycobacterium tuberculosis	35,735	19-Jun-98
		GB_BA1:MSGB1529CS	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequence	Mycobacterium leprae	57,014	15-Jun-96
		GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162	Mycobacterium tuberculosis	41,892	19-Jun-98
rxa00196	738	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome, segment 126/162.	Mycobacterium tuberculosis	41,841	19-Jun-98
		GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	36,599	19-Jun-98
		GB_RO:RATCBRQ	10752	M55532	Rat carbohydrate binding receptor gene, complete cds.	Rattus norvegicus	36,212	27-Apr-93
rxa00202	1065	GB_EST11.AA253618	313	AA253618	mw95c10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE.678450 5', mRNA sequence.	Mus musculus	38,816	13-MAR-1997
		GB_EST26.AI390284	490	AI390284	mw96a03 y1 Soares mouse NML Mus musculus cDNA clone IMAGE·678508 5' similar to TR:O09171 O09171 BETAINE-HOMOCYSTEINE METHYLTRANSFERASE,, mRNA sequence	Mus musculus	42,239	2-Feb-99
		GB_EST26:AI390280	467	AI390280	mw95c10.y1 Soares mouse NML Mus musculus cDNA clone IMAGE 678450 5', mRNA sequence.	Mus musculus	37,307	2-Feb-99
rxa00206	1161	GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	58,312	17-Sep-97
		GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162	Mycobacterium tuberculosis	36,632	23-Jun-99
		GB_BA1:SC6E10	23990	AL109661	Streptomyces coelicolor cosmid 6E10	Streptomyces coelicolor A3(2)	38,616	5-Aug-99
rxa00224	1074	GB_BA1:BJU32230	1769	U32230	Bradyrhizobium japonicum electron transfer flavoprotein small subunit (etfS) nd large subunit (etfL) genes, complete cds.	Bradyrhizobium japonicum	48,038	25-MAY-1996
		GB_BA1.PDEETFAB	2440	L14864	Paracoccus denitrificans electron transfer flavoprotein alpha and beta subunit genes, complete cds's.	Paracoccus denitrificans	48,351	27-OCT-1993
		GB_HTG3:AC009689	177954	AC009689	Homo sapiens chromosome 4 clone 104_F_7 map 4, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	38,756	28-Aug-99
rxa00225	909	GB_RO:AF060178	2057	AF060178	Mus musculus heparan sulfate 2-sulfotransferase (Hs2st) mRNA, complete cds.	Mus musculus	39,506	18-Jun-98
		GB_GSS11:AQ325043	734	AQ325043	mgxb0020J01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0020J01r, genomic survey sequence.	Magnaporthe grisea	38,333	8-Jan-99
		GB_EST31:AI676413	551	AI676413	etmEST0167 EtH1 Eimeria tenella cDNA clone etmc074 5', mRNA sequence	Eimeria tenella	35,542	19-MAY-1999
rxa00235	1398	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	65,759	17-Jun-98
		GB_BA2:AF061753	3721	AF061753	Nitrosomonas europaea CTP synthase (pyrG) gene, partial cds, and enolase (eno) gene, complete cds.	Nitrosomonas europaea	58,941	31-Aug-98
		GB_BA2:AF086791	37867	AF086791	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (rnh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds, and unknown genes.	Zymomonas mobilis	61,239	4-Nov-98
rxa00246	1158	GB_BA2:AF012550	2690	AF012550	Acinetobacter sp. BD413 ComP (comP) gene, complete cds	Acinetobacter sp. BD413	53,726	27-Sep-99

TABLE 4: ALIGNMENT RESULTS

		GB_PAT:E03856	1506	E03856	gDNA encoding alcohol dehydrogenase.	Bacillus stearothermophilus	51,688	29-Sep-97
		GB_BA1:BACADHT	1688	D90421	B.stearothermophilus adhT gene for alcohol dehydrogenase.	Bacillus stearothermophilus	51,602	7-Feb-99
rxa00251	831	GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162	Mycobacterium tuberculosis	42,875	17-Jun-98
		GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	40,380	18-Jun-98
		GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome, segment 144/162.	Mycobacterium tuberculosis	41,789	18-Jun-98
rxa00288	1134	GB_BA2:AF050114	1038	AF050114	Pseudomonas sp. W7 alginate lyase gene, complete cds	Pseudomonas sp. W7	49,898	03-MAR-1999
		GB_GSS3:B16984	469	B16984	344A14.TVC CIT978SKA1 Homo sapiens genomic clone A-344A14, genomic survey sequence.	Homo sapiens	39,355	4-Jun-98
		GB_IN2:AF144549	7887	AF144549	Aedes albopictus ribosomal protein L34 (rpl34) gene, complete cds	Aedes albopictus	36,509	3-Jun-99
rxa00293	1035	GB_EST1:T28483	313	T28483	EST46182 Human Kidney Homo sapiens cDNA 3' end similar to flavin-containing monooxygenase 1 (HT:1956), mRNA sequence.	Homo sapiens	42,997	6-Sep-95
		GB_PR1:HUMFMO1	2134	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds	Homo sapiens	37,915	8-Nov-94
		GB_EST32:AI734238	512	AI734238	zb73c05.y5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:309224 5' similar to gb:M64082 DIMETHYLANILINE MONOOXYGENASE (HUMAN),, mRNA sequence	Homo sapiens	41,502	14-Jun-99
rxa00296	2967	GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 92 unordered pieces.	Drosophila melanogaster	33,890	02-DEC-1999
		GB_EST15:AA531468	414	AA531468	nj63d12 s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE.997175, mRNA sequence	Homo sapiens	40,821	20-Aug-97
		GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPCI-98 11.H.20 map 12B-12C strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 92 unordered pieces.	Drosophila melanogaster	30,963	02-DEC-1999
rxa00310	558	GB_VI:VMVY16780	186986	Y16780	variola minor virus complete genome	variola minor virus	35,883	2-Sep-99
		GB_VI:VARCG	186103	L22579	Variola major virus (strain Bangladesh-1975) complete genome.	Variola major virus	34,664	12-Jan-95
		GB_VI:VVCGAA	185578	X69198	Variola virus DNA complete genome	Variola virus	36,000	13-DEC-1996
rxa00317	777	GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
		GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
		GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.	Homo sapiens	36,340	09-OCT-1998
rxa00327	507	GB_BA1:LCATPASEB	1514	X64542	L.casei gene for ATPase beta-subunit.	Lactobacillus casei	34,664	11-DEC-1992
		GB_BA1:LCATPASEB	1514	X64542	L casei gene for ATPase beta-subunit.	Lactobacillus casei	39,308	11-DEC-1992
rxa00328	615	GB_BA1:STYPUTPE	1887	L01138	Salmonella (S2980) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
		GB_BA1:STYPUTPF	1887	L01139	Salmonella (S2983) proline permease (putP) gene, 5' end	Salmonella sp.	39,623	09-MAY-1996
		GB_BA1:STYPUTPI	1889	L01142	Salmonella (S3015) proline permease (putP) gene, 5' end	Salmonella sp.	42,906	09-MAY-1996
rxa00329	1347	GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence	Homo sapiens	38,142	16-MAY-1998
		GB_PR4:AC004916	129014	AC004916	Homo sapiens clone DJ0891L14, complete sequence	Homo sapiens	38,549	17-Jul-99
		GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence	Homo sapiens	35,865	16-MAY-1998
rxa00340	1269	GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome, segment 99/162	Mycobacterium tuberculosis	38,940	24-Jun-99
		GB_GSS12:AQ412290	238	AQ412290	RPCI-11-195H2.TV RPCI-11 Homo sapiens genomic clone RPCI-11-195H2, genomic survey sequence.	Homo sapiens	36,555	23-MAR-1999
		GB_PL2:AF112871	2394	AF112871	Astasia longa small subunit ribosomal RNA gene, complete sequence	Astasia longa	36,465	28-Jun-99

TABLE 4: ALIGNMENT RESULTS

rxa00379	307	GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99
		GB_HTG1:CEY56A3	224746	AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99
		GB_PR2:HS134O19	86897	AL034555	Human DNA sequence from clone 134O19 on chromosome 1p36 11-36 33, complete sequence.	Homo sapiens	40,604	23-Nov-99
rxa00381	729	GB_GSS4:AQ730532	416	AQ730532	HS_2149_A1_C06_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2149 Col=11 Row=E, genomic survey sequence.	Homo sapiens	35,766	15-Jul-99
		GB_EST23:AI120939	561	AI120939	ub74f05 r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN), gb.M19381 Mouse calmodulin (MOUSE),, mRNA sequence.	Mus musculus	41,113	2-Sep-98
		GB_EST23:AI120939	561	AI120939	ub74f05 r1 Soares mouse mammary gland NMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN), gb:M19381 Mouse calmodulin (MOUSE);, mRNA sequence.	Mus musculus	41,113	2-Sep-98
rxa00385	362	GB_EST32:AI726450	565	AI726450	BNLGHi5857 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF015913) Skb1Hs [Homo sapiens], mRNA sequence.	Gossypium hirsutum	41,152	11-Jun-99
		GB_GSS4:AQ740856	768	AQ740856	HS_2274_A2_A07_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2274 Col=14 Row=A, genomic survey sequence.	Homo sapiens	41,360	16-Jul-99
		GB_PR1:HSPAIP	1587	X91809	H sapiens mRNA for GAIP protein.	Homo sapiens	36,792	29-MAR-1996
rxa00388	1134	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome, segment 28/162	Mycobacterium tuberculosis	51,852	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224	Mycobacterium tuberculosis	51,852	03-DEC-1996
		GB_HTG1.AP000471	72466	AP000471	Homo sapiens chromosome 21 clone B2308H15 map 21q22 3, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	36,875	13-Sep-99
rxa00427	909	GB_BA1:MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126	Mycobacterium tuberculosis	60,022	10-DEC-1996
		GB_BA1.MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome, segment 156/162	Mycobacterium tuberculosis	60,022	17-Jun-98
		GB_HTG1:CEY48C3	270193	Z92855	Caenorhabditis elegans chromosome II clone Y48C3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	28,013	29-MAY-1999
rxa00483	1587	GB_PR2:HSAF001550	173882	AF001550	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence	Homo sapiens	38,226	22-Aug-97
		GB_BA1:LLCPJW565	12828	Y12736	Lactococcus lactis cremoris plasmid pJW565 DNA, abiiM, abiiR genes and orfX	Lactococcus lactis subsp. cremoris	37,492	01-MAR-1999
		GB_HTG2:AC006754	206217	AC006754	Caenorhabditis elegans clone Y40B10, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Caenorhabditis elegans	36,648	23-Feb-99
rxa00511	615	GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11 2-qter contains STS.	Homo sapiens	39,831	23-Nov-99
		GB_PR3:HSE127C11	38423	Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11 2-qter contains STS.	Homo sapiens	36,409	23-Nov-99
rxa00512	718	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162	Mycobacterium tuberculosis	56,232	17-Jun-98
		GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase	Mycobacterium smegmatis	56,143	20-Sep-91
		GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	48,563	14-Jul-99
rxa00517	1164	GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
		GB_HTG2:AC006911	298804	AC006911	Caenorhabditis elegans clone Y94H6x, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99

TABLE 4: ALIGNMENT RESULTS

		GB_EST29:AI602158	481	AI602158	UI-R-AB0-vy-a-01-0-UI.s2 UI-R-AB0 Rattus norvegicus cDNA clone UI-R-AB0-vy-a-01-0-UI 3', mRNA sequence.	Rattus norvegicus	40,833	21-Apr-99
rxa00518	320	GB_BA2:ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	49,688	14-Jul-99
		GB_BA2:STU51879	8371	U51879	Salmonella typhimurium propionate catabolism operon RpoN activator protein homolog (prpR), carboxyphosphonoenolpyruvate phosphonomutase homolog (prpB), citrate synthase homolog (prpC), prpD and prpE genes, complete cds.	Salmonella typhimurium	50,313	5-Aug-99
		GB_BA2:AE000140	12498	AE000140	Escherichia coli K-12 MG1655 section 30 of 400 of the complete genome	Escherichia coli	49,688	12-Nov-98
rxa00606	2378	GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,333	7-Jun-99
		GB_EST13:AA363046	329	AA363046	EST72922 Ovary II Homo sapiens cDNA 5' end, mRNA sequence	Homo sapiens	34,347	21-Apr-97
		GB_EST32:AU068253	376	AU068253	AU068253 Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence.	Oryza sativa	41,899	7-Jun-99
rxa00635	1860	GB_BA1:PAORF1	1440	X13378	Pseudomonas amyloderamosa DNA for ORF 1.	Pseudomonas amyloderamosa	53,912	14-Jul-95
		GB_BA1:PAORF1	1440	X13378	Pseudomonas amyloderamosa DNA for ORF 1.	Pseudomonas amyloderamosa	54,422	14-Jul-95
rxa00679	1389	GB_PL2.AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence	Arabidopsis thaliana	38,244	13-Nov-99
		GB_PL1:AT81KBGEN	81493	X98130	A thaliana 81kb genomic sequence.	Arabidopsis thaliana	36,091	12-MAR-1997
		GB_PL2:AC010871	80381	AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana	37,135	13-Nov-99
rxa00680	441	GB_PR3:AC004058	38400	AC004058	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence	Homo sapiens	36,165	30-Sep-98
		GB_PL1:AT81KBGEN	81493	X98130	A.thaliana 81kb genomic sequence.	Arabidopsis thaliana	38,732	12-MAR-1997
		GB_PL1:AB026648	43481	AB026648	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone MLJ15, complete sequence.	Arabidopsis thaliana	38,732	07-MAY-1999
rxa00682	2022	GB_HTG3.AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
		GB_HTG3:AC010325	197110	AC010325	Homo sapiens chromosome 19 clone CITB-E1_2568A17, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens	37,976	15-Sep-99
		GB_PR4:AC008179	181745	AC008179	Homo sapiens clone NH0576F01, complete sequence	Homo sapiens	37,143	28-Sep-99
rxa00683	1215	GB_BA2:AE000896	10707	AE000896	Methanobacterium thermoautotrophicum from bases 1189349 to 1200055 (section 102 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	38,429	15-Nov-97
		GB_IN1:DMBR7A4	212734	AL109630	Drosophila melanogaster clone BACR7A4	Drosophila melanogaster	36,454	30-Jul-99
		GB_EST35:AV163010	273	AV163010	AV163010 Mus musculus head C57BL/6J 13-day embryo Mus musculus cDNA clone 3110006J22, mRNA sequence.	Mus musculus	41,758	8-Jul-99
rxa00686	927	GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25 1-25 3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
		GB_HTG2:HSDJ137K2	190223	AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25 1-25 3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,031	03-DEC-1999
		GB_EST12:AA284399	431	AA284399	zs57b04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE.701551 5', mRNA sequence.	Homo sapiens	39,205	14-Aug-97
rxa00700	927	GB_EST34:AI785570	454	AI785570	uj44d03.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1922789 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN),, mRNA sequence.	Mus musculus	41,943	2-Jul-99

TABLE 4: ALIGNMENT RESULTS

		GB_EST25:AI256147	684	AI256147	ui95e12.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE.1890190 3' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN),, mRNA sequence	Mus musculus	40,791	12-Nov-98
		GB_BA1:CARCG12	2079	X14979	C. aurantiacus reaction center genes 1 and 2	Chloroflexus aurantiacus	37,721	23-Apr-91
rxa00703	2409	GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2	Streptomyces coelicolor A3(2)	56,646	2-Aug-99
		GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome, segment 126/162	Mycobacterium tuberculosis	37,369	19-Jun-98
		GB_BA2:REU60056	2520	U60056	Ralstonia eutropha formate dehydrogenase-like protein (cbbBc) gene, complete cds.	Ralstonia eutropha	51,087	16-OCT-1996
rxa00705	1038	GB_GSS15:AQ604477	505	AQ604477	HS_2116_B1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2116 Col=13 Row=N, genomic survey sequence.	Homo sapiens	39,617	10-Jun-99
		GB_EST11.AA224340	443	AA224340	zr14e07.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648804 3', mRNA sequence.	Homo sapiens	35,129	11-MAR-1998
		GB_EST5:N30648	291	N30648	yw77b02.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258219 3', mRNA sequence.	Homo sapiens	43,986	5-Jan-96
rxa00782	1005	GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome, segment 44/162.	Mycobacterium tuberculosis	63,327	17-Jun-98
		GB_BA1.MLCL373	37304	AL035500	Mycobacterium leprae cosmid L373.	Mycobacterium leprae	62,300	27-Aug-99
		GB_BA2:AF128399	2842	AF128399	Pseudomonas aeruginosa succinyl-CoA synthetase beta subunit (sucC) and succinyl-CoA synthetase alpha subunit (sucD) genes, complete cds	Pseudomonas aeruginosa	53,698	25-MAR-1999
rxa00783	1395	GB_HTG2.AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
		GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK.42_F_20 map 17, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	35,135	28-Jul-99
		GB_PR3:AC005017	137176	AC005017	Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence	Homo sapiens	35,864	8-Aug-98
rxa00794	1128	GB_BA1.MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	40,331	24-Jun-99
		GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,170	27-Aug-99
		GB_PR2:HS151B14	128942	Z82188	Human DNA sequence from clone 151B14 on chromosome 22 Contains SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) gene,pseudogene similar to ribosomal protein L39,RAC2 (RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 (P21-RAC2)) gene ESTs, STSs, GSSs and CpG islands, complete sequence.	Homo sapiens	37,455	16-Jun-99
rxa00799	1767	GB_PL2:AF016327	616	AF016327	Hordeum vulgare Barperm1 (perm1) mRNA, partial cds.	Hordeum vulgare	41,311	01-OCT-1997
		GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21 3, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	36,845	30-Nov-99
		GB_HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,845	30-Nov-99
rxa00800	1227	GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis H37Rv complete genome, segment 100/162	Mycobacterium tuberculosis	63,101	17-Jun-98
		GB_BA1:AB019513	4417	AB019513	Streptomyces coelicolor genes for alcohol dehydrogenase and ABC transporter, complete cds.	Streptomyces coelicolor	41,312	13-Nov-98
		GB_PL1:SCSFAARP	7008	X68020	S cerevisiae SFA and ARP genes.	Saccharomyces cerevisiae	36,288	29-Nov-94
rxa00825	1056	GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome, segment 154/162.	Mycobacterium tuberculosis	39,980	17-Jun-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	39,435	27-Aug-99
		GB_BA2.AF169031	1141	AF169031	Xanthomonas oryzae pv. oryzae putative sugar nucleotide epimerase/dehydratase gene, partial cds.	Xanthomonas oryzae pv. oryzae	46,232	14-Sep-99
rxa00871								

TABLE 4: ALIGNMENT RESULTS

rxa00872	1077	GB_IN1:CEF23H12	35564	Z74472	Caenorhabditis elegans cosmid F23H12, complete sequence.	Caenorhabditis elegans	34,502	08-OCT-1999
		GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces	Homo sapiens	35,714	24-MAY-1999
		GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.	Homo sapiens	35,714	24-MAY-1999
rxa00879	2241	GB_BA1:MTV049	40360	AL022021	Mycobacterium tuberculosis H37Rv complete genome, segment 81/162	Mycobacterium tuberculosis	36,981	19-Jun-98
		GB_PL2:CDU236897	1827	AJ236897	Candida dubliniensis ACT1 gene, exons 1-2.	Candida dubliniensis	38,716	1-Sep-99
		GB_PL1:CAACT1A	3206	X16377	Candida albicans act1 gene for actin	Candida albicans	36,610	10-Apr-93
rxa00909	955	GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome	Rhodobacter capsulatus	51,586	12-MAY-1998
		GB_BA1:RMPHA	7888	X93358	Rhizobium meliloti pha[A,B,C,D,E,F,G] genes.	Sinorhizobium meliloti	48,367	12-MAR-1999
		GB_EST16:C23528	317	C23528	C23528 Japanese flounder spleen Paralichthys olivaceus cDNA clone HB5(2), mRNA sequence.	Paralichthys olivaceus	41,640	28-Sep-99
rxa00913	2118	GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK 44_O_1 map 18, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99
		GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK.44_O_1 map 18, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.	Homo sapiens	34,457	5-Jun-99
		GB_EST18:AA709478	406	AA709478	vv34a05 r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE 1224272 5', mRNA sequence	Mus musculus	42,065	24-DEC-1997
rxa00945	1095	GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999
		GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone CITB-H1_2022B6, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces	Homo sapiens	36,448	31-OCT-1999
rxa00965		GB_BA1.MTCY05A6	38631	Z96072	Mycobacterium tuberculosis H37Rv complete genome, segment 120/162	Mycobacterium tuberculosis	36,218	17-Jun-98
rxa00999	1575	GB_PAT:E13660	1916	E13660	gDNA encoding 6-phosphogluconate dehydrogenase	Corynebacterium glutamicum	98,349	24-Jun-98
		GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	38,520	17-Jun-98
		GB_BA1:MLCB1788	39228	AL008609	Mycobacterium leprae cosmid B1788.	Mycobacterium leprae	64,355	27-Aug-99
rxa01015	442	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	39,860	17-Jun-98
		GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome, segment 108/162	Mycobacterium tuberculosis	39,120	17-Jun-98
rxa01025	1119	GB_BA1.SC7A1	32039	AL034447	Streptomyces coelicolor cosmid 7A1.	Streptomyces coelicolor	55,287	15-DEC-1998
		GB_BA1:MSGB1723CS	38477	L78825	Mycobacterium leprae cosmid B1723 DNA sequence.	Mycobacterium leprae	56,847	15-Jun-96
		GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	Mycobacterium leprae	56,676	17-Sep-97
rxa01048	1347	GB_BA2:AF017444	3067	AF017444	Sinorhizobium meliloti NADP-dependent malic enzyme (tme) gene, complete cds.	Sinorhizobium meliloti	53,660	2-Nov-97
		GB_BA1:BSUB0013	218470	Z99116	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730.	Bacillus subtilis	37,255	26-Nov-97
		GB_VI.HSV2HG52	154746	Z86099	Herpes simplex virus type 2 (strain HG52), complete genome	human herpesvirus 2	38,081	04-DEC-1998
rxa01049	1605	GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97
		GB_HTG2.AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97

TABLE 4: ALIGNMENT RESULTS

		GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	26,180	2-Sep-97
rxa01077	1494	GB_PR3:HSDJ653C5	85237	AL049743	Human DNA sequence from clone 653C5 on chromosome 1p21 3-22.3 Contains CA repeat(D1S435), STSs and GSSs, complete sequence	Homo sapiens	36,462	23-Nov-99
		GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes	Escherichia coli	41,808	1-Jul-95
		GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome, approximately 61 to 62 minutes.	Escherichia coli	36,130	1-Jul-95
rxa01089	873	GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18.TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence	Homo sapiens	36,528	14-Jul-98
		GB_GSS8:AQ042907	392	AQ042907	CIT-HSP-2318D17.TR CIT-HSP Homo sapiens genomic clone 2318D17, genomic survey sequence	Homo sapiens	35,969	14-Jul-98
		GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18.TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	44,545	14-Jul-98
rxa01093	1554	GB_BA1:CORPYKI	2795	L27126	Corynebacterium pyruvate kinase gene, complete cds.	Corynebacterium glutamicum	100,000	07-DEC-1994
		GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome, segment 72/162.	Mycobacterium tuberculosis	63,771	17-Jun-98
		GB_BA1:MIU65430	1439	U65430	Mycobacterium intracellulare pyruvate kinase (pykF) gene, complete cds.	Mycobacterium intracellulare	67,061	23-DEC-1996
rxa01099	948	GB_BA2:AF045998	780	AF045998	Corynebacterium glutamicum inositol monophosphate phosphatase (impA) gene, complete cds	Corynebacterium glutamicum	99,615	19-Feb-98
		GB_BA2.AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase (hisA) gene, complete cds	Corynebacterium glutamicum	100,000	12-MAR-1998
		GB_GSS1:FR0005503	619	Z89313	F.rubripes GSS sequence, clone 079B16aE8, genomic survey sequence	Fugu rubripes	37,785	01-MAR-1997
rxa01111	541	GB_PR3:AC004063	177014	AC004063	Homo sapiens chromosome 4 clone B32I8, complete sequence	Homo sapiens	35,835	10-Jul-98
		GB_PR3:HS1178I21	62268	AL109852	Human DNA sequence from clone RP5-1178I21 on chromosome X, complete sequence.	Homo sapiens	37,873	01-DEC-1999
		GB_HTG3 AC009301	163369	AC009301	Homo sapiens clone NH0062F14, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Homo sapiens	37,240	13-Aug-99
rxa01130	687	GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces	Homo sapiens	38,416	22-Aug-99
		GB_HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99
		GB_IN1:DMC66A1	34127	AL031227	Drosophila melanogaster cosmid 66A1.	Drosophila melanogaster	38,416	05-OCT-1998
rxa01193	1572	GB_BA1:CGASO19	1452	X76875	C.glutamicum (ASO 19) ATPase beta-subunit gene	Corynebacterium glutamicum	99,931	27-OCT-1994
		EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	99,242	07-OCT-1997 (Rel. 52, Created)
		GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,153	09-MAR-1995
rxa01194	495	EM_PAT:E09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in	Corynebacterium glutamicum	100,000	07-OCT-1997 (Rel. 52, Created)
		GB_BA1:CGASO19	1452	X76875	C.glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	100,000	27-OCT-1994
		GB_VI:HEPCRE4B	414	X60570	Hepatitis C genomic RNA for putative envelope protein (RE4B isolate)	Hepatitis C virus	36,769	5-Apr-92
rxa01200								
rxa01201	1764	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes	Streptomyces lividans	66,269	01-MAY-1995
		GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome, segment 57/162	Mycobacterium tuberculosis	65,437	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

		GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,302	09-MAR-1995
rxa01202	1098	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	57,087	01-MAY-1995
		GB_BA1:SLATPSYNA	8560	Z22606	S.lividans i protein and ATP synthase genes.	Streptomyces lividans	38,298	01-MAY-1995
		GB_BA1:MCSQSSHC	5538	Y09978	M capsulatus orfx, orfy, orfz, sqs and shc genes.	Methylococcus capsulatus	37,626	26-MAY-1998
rxa01204	933	GB_PL1:AP000423	154478	AP000423	Arabidopsis thaliana chloroplast genomic DNA, complete sequence, strain:Columbia.	Chloroplast Arabidopsis thaliana	38,395	15-Sep-99
		GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114I16, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces.	Homo sapiens	35,459	04-DEC-1999
		GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114I16, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces.	Homo sapiens	36,117	04-DEC-1999
rxa01216	1124	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	Mycobacterium tuberculosis	39,064	17-Jun-98
		GB_BA2.AF017435	4301	AF017435	Methylobacterium extorquens methanol oxidation genes, glmU-like gene, partial cds, and orfL2, orfL1, orfR genes, complete cds.	Methylobacterium extorquens	42,671	10-MAR-1998
		GB_BA1:CCRFLBDBA	4424	M69228	C.crescentus flagellar gene promoter region.	Caulobacter crescentus	41,054	26-Apr-93
rxa01225	1563	GB_BA2.AF058302	25306	AF058302	Streptomyces roseofulvus frenolicin biosynthetic gene cluster, complete sequence.	Streptomyces roseofulvus	36,205	2-Jun-98
		GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 04.B.9 map 43E12-44F1 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 150 unordered pieces.	Drosophila melanogaster	39,922	17-Aug-99
		GB_HTG3.AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BACR04B09 (D576) RPCI-98 04.B.9 map 43E12-44F1 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 150 unordered pieces	Drosophila melanogaster	39,922	17-Aug-99
rxa01227	444	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds	Saccharopolyspora erythraea	64,908	13-MAR-1996
		GB_BA1.MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome, segment 51/162.	Mycobacterium tuberculosis	62,838	17-Jun-98
		GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348	Mycobacterium tuberculosis	61,712	10-DEC-1996
rxa01242	900	GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence	Homo sapiens	35,373	09-OCT-1998
		GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99
		GB_HTG3:AC010722	160723	AC010722	Homo sapiens clone NH0122L09, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Homo sapiens	39,863	25-Sep-99
rxa01243	1083	GB_GSS10:AQ255057	583	AQ255057	mgxb0008N01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0008N01r, genomic survey sequence	Magnaporthe grisea	38,722	23-OCT-1998
		GB_IN1.CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence	Caenorhabditis elegans	35,448	23-Nov-98
		GB_IN1:CEK05D4	19000	Z92804	Caenorhabditis elegans cosmid K05D4, complete sequence	Caenorhabditis elegans	35,694	23-Nov-98
rxa01259	981	GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	100,000	1-Feb-99
		GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPCI98-11N6, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces	Drosophila melanogaster	37,178	16-OCT-1999
		GB_HTG4:AC010567	143287	AC010567	Drosophila melanogaster chromosome 3L/69C1 clone RPCI98-11N6, ***SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	37,178	16-OCT-1999
rxa01262	1284	GB_BA2:AF172324	14263	AF172324	Escherichia coli GalF (galF) gene, partial cds; O-antigen repeat unit transporter Wzx (wzx), WbnA (wbnA), O-antigen polymerase Wzy (wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbnE), UDP-Glc-4-epimerase GalE (galE), 6-phosphogluconate dehydrogenase Gnd (gnd), UDP-Glc-6-dehydrogenase Ugd (ugd), and WbnF (wbnF) genes, complete cds, and chain length determinant Wzz (wzz) gene, partial cds.	Escherichia coli	59,719	29-OCT-1999

TABLE 4: ALIGNMENT RESULTS

		GB_BA2:ECU78086	4759	U78086	Escherichia coli hypothetical uridine-5'-diphosphoglucose dehydrogenase (ugd) and O-chain length regulator (wzz) genes, complete cds	Escherichia coli	59,735	5-Nov-97
		GB_BA1:D90841	20226	D90841	E.coli genomic DNA, Kohara clone #351(45.1-45 5 min)	Escherichia coli	37,904	21-MAR-1997
rxa01311	870	GB_PR3:AC004103	144368	AC004103	Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.	Homo sapiens	37,340	18-Apr-98
		GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	Homo sapiens	36,385	25-Sep-99
		GB_HTG3:AC007383	215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	36,385	25-Sep-99
rxa01312	2142	GB_BA2:AE000487	13889	AE000487	Escherichia coli K-12 MG1655 section 377 of 400 of the complete genome.	Escherichia coli	39,494	12-Nov-98
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.	Mycobacterium tuberculosis	46,252	23-Jun-99
		GB_BA1:U00022	36411	U00022	Mycobacterium leprae cosmid L308.	Mycobacterium leprae	46,368	01-MAR-1994
rxa01325	795	GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
		GB_HTG4:AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.	Homo sapiens	36,016	2-Nov-99
		GB_HTG4.AC009245	215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.	Homo sapiens	39,618	2-Nov-99
rxa01332	576	GB_HTG6:AC007186	225851	AC007186	Drosophila melanogaster chromosome 2 clone BACR03D06 (D569) RPCI-98 03.D.6 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 91 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999
		GB_HTG6:AC007147	202291	AC007147	Drosophila melanogaster chromosome 2 clone BACR19N18 (D572) RPCI-98 19 N 18 map 32A-32A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 22 unordered pieces.	Drosophila melanogaster	35,366	07-DEC-1999
		GB_HTG3:AC010207	207890	AC010207	Homo sapiens clone RPCI11-375I20, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Homo sapiens	34,821	16-Sep-99
rxa01350	1107	GB_BA2.AF109682	990	AF109682	Aquaspirillum arcticum malate dehydrogenase (MDH) gene, complete cds	Aquaspirillum arcticum	58,487	19-OCT-1999
		GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces.	Caenorhabditis elegans	37,963	25-Feb-99
		GB_HTG2:AC006759	103725	AC006759	Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS***, 8 unordered pieces.	Caenorhabditis elegans	37,963	25-Feb-99
rxa01365	1497	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome, segment 139/162	Mycobacterium tuberculosis	38,011	17-Jun-98
		GB_BA1:XANXANAB	3410	M83231	Xanthomonas campestris phosphoglucomutase and phosphomannomutase (xanA) and phosphomannose isomerase and GDP-mannose pyrophosphorylase (xanB) genes, complete cds.	Xanthomonas campestris	47,726	26-Apr-93
		GB_GSS10:AQ194038	697	AQ194038	RPCI11-47D24.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-47D24, genomic survey sequence.	Homo sapiens	36,599	20-Apr-99
rxa01369	1305	GB_BA1:MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162.	Mycobacterium tuberculosis	36,940	17-Jun-98
		GB_GSS3:B10037	974	B10037	T27A19-T7 TAMU Arabidopsis thaliana genomic clone T27A19, genomic survey sequence.	Arabidopsis thaliana	35,284	14-MAY-1997
		GB_GSS3:B09549	1097	B09549	T21A19-T7.1 TAMU Arabidopsis thaliana genomic clone T21A19, genomic survey sequence.	Arabidopsis thaliana	38,324	14-MAY-1997
rxa01377	1209	GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,778	10-Feb-99
		GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	Homo sapiens	32,658	16-Nov-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.	Homo sapiens	38,395	16-Nov-99
rxa01392	1200	GB_BA2:AF072709	8366	AF072709	Streptomyces lividans amplifiable element AUD4. putative transcriptional regulator, putative ferredoxin, putative cytochrome P450 oxidoreductase, and putative oxidoreductase genes, complete cds; and unknown genes.	Streptomyces lividans	55,221	8-Jul-98
		GB_BA1:CGLYSEG	2374	X96471	C glutamicum lysE and lysG genes.	Corynebacterium glutamicum	100,000	24-Feb-97
		GB_PR4 AC005906	185952	AC005906	Homo sapiens 12p13.3 BAC RPCI11-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	36,756	30-Jan-99
rxa01436	1314	GB_BA1:CGPTAACKA	3657	X89084	C glutamicum pta gene and ackA gene.	Corynebacterium glutamicum	100,000	23-MAR-1999
		GB_BA1:D90861	14839	D90861	E coli genomic DNA, Kohara clone #405(52.0-52 3 min)	Escherichia coli	53,041	29-MAY-1997
		GB_PAT.E02087	1200	E02087	DNA encoding acetate kinase protein form Escherichia coli	Escherichia coli	54,461	29-Sep-97
rxa01468	948	GB_GSS1.HPU60627	280	U60627	Helicobacter pylori feoB-like DNA sequence, genomic survey sequence.	Helicobacter pylori	39,286	9-Apr-97
		GB_EST31:AI701691	349	AI701691	we81c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347494 3' similar to gb.L19686_rna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN),, mRNA sequence	Homo sapiens	39,412	3-Jun-99
		GB_EST15:AA480256	389	AA480256	ne31f04.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE.898975 3' similar to gb:L19686_rna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN);, mRNA sequence.	Homo sapiens	39,574	14-Aug-97
rxa01478	1959	GB_BA1.SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	54,141	16-Aug-99
		GB_BA1:SCE36	12581	AL049763	Streptomyces coelicolor cosmid E36.	Streptomyces coelicolor	38,126	05-MAY-1999
		GB_BA1 CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	41,852	9-Apr-97
rxa01482	1998	GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	62,149	20-Aug-98
		GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	38,303	01-MAR-1994
		GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome, segment 146/162	Mycobacterium tuberculosis	38,179	18-Jun-98
rxa01534								
rxa01535	1530	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	66,208	27-Aug-99
		GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome, segment 48/162	Mycobacterium tuberculosis	38,553	24-Jun-99
		GB_BA1:PAU72494	4368	U72494	Pseudomonas aeruginosa fumarase (fumC) and Mn superoxide dismutase (sodA) genes, complete cds.	Pseudomonas aeruginosa	52,690	23-OCT-1996
rxa01550	1635	GB_BA1:D90907	132419	D90907	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885	Synechocystis sp.	56,487	7-Feb-99
		GB_IN2:AF073177	9534	AF073177	Drosophila melanogaster glycogen phosphorylase (GlyP) gene, complete cds.	Drosophila melanogaster	55,100	1-Jul-99
		GB_IN2:AF073179	3159	AF073179	Drosophila melanogaster glycogen phosphorylase (Glp1) mRNA, complete cds.	Drosophila melanogaster	56,708	27-Apr-99
rxa01562								
rxa01569	1482	GB_BA1:D78182	7836	D78182	Streptococcus mutans DNA for dTDP-rhamnose synthesis pathway, complete cds.	Streptococcus mutans	44,050	5-Feb-99
		GB_BA2:AF079139	4342	AF079139	Streptomyces venezuelae pikCD operon, complete sequence	Streptomyces venezuelae	38,587	28-OCT-1998
		GB_BA2:AF087022	1470	AF087022	Streptomyces venezuelae cytochrome P450 monooxygenase (picK) gene, complete cds.	Streptomyces venezuelae	38,621	15-OCT-1998
rxa01570	978	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	59,035	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

		GB_BA2:AF097519	4594	AF097519	Klebsiella pneumoniae dTDP-D-glucose 4,6 dehydratase (rmlB), glucose-1-phosphate thymidylyl transferase (rmlA), dTDP-4-keto-L-rhamnose reductase (rmlD), dTDP-4-keto-6-deoxy-D-glucose 3,5-epimerase (rmlC), and rhamnosyl transferase (wbbL) genes, complete cds.	Klebsiella pneumoniae	59,714	4-Nov-98
		GB_BA2:NGOCPSPS	8905	L09189	Neisseria meningitidis dTDP-D-glucose 4,6-dehydratase (rfbB), glucose-1-phosphate thymidyl transferase (rfbA) and rfbC genes, complete cds and UPD-glucose-4-epimerase (galE) pseudogene	Neisseria meningitidis	58,384	30-Jul-96
rxa01571	723	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,500	7-Aug-98
		GB_BA1.AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	35,655	7-Aug-98
rxa01572	615	GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	57,843	7-Aug-98
		GB_BA1:AB011413	12070	AB011413	Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	Streptomyces griseus	38,119	7-Aug-98
rxa01606	2799	GB_VI:CFU72240	4783	U72240	Choristoneura fumiferana nuclear polyhedrosis virus ETM protein homolog, 79 kDa protein homolog, 15 kDa protein homolog and GTA protein homolog genes, complete cds	Choristoneura fumiferana nucleopolyhedrovirus	37,115	29-Jan-99
		GB_GSS10.AQ213248	408	AQ213248	HS_3249_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3249 Col=3 Row=B, genomic survey sequence.	Homo sapiens	34,559	18-Sep-98
		GB_GSS8:AQ070145	285	AQ070145	HS_3027_B1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=P, genomic survey sequence	Homo sapiens	40,351	5-Aug-98
rxa01626	468	GB_PR4:AF152510	2490	AF152510	Homo sapiens protocadherin gamma A3 short form protein (PCDH-gamma-A3) variable region sequence, complete cds.	Homo sapiens	34,298	14-Jul-99
		GB_PR4:AF152323	4605	AF152323	Homo sapiens protocadherin gamma A3 (PCDH-gamma-A3) mRNA, complete cds	Homo sapiens	34,298	22-Jul-99
		GB_PR4:AF152509	2712	AF152509	Homo sapiens PCDH-gamma-A3 gene, aberrantly spliced, mRNA sequence.	Homo sapiens	34,298	14-Jul-99
rxa01632	1128	GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 map 36E-36E strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
		GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13 N 2 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999
		GB_GSS8:B99182	415	B99182	CIT-HSP-2280I13.TR CIT-HSP Homo sapiens genomic clone 2280I13, genomic survey sequence.	Homo sapiens	36,111	26-Jun-98
rxa01633	1206	GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200	Bacillus subtilis	36,591	26-Nov-97
		GB_BA1:BSUB0009	208780	Z99112	Bacillus subtilis complete genome (section 9 of 21) from 1598421 to 1807200.	Bacillus subtilis	34,941	26-Nov-97
		GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48I10 (D505) RPCI-98 48.I.10 map 49E6-49F8 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Drosophila melanogaster	37,037	2-Aug-99
rxa01695	1623	GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate.quinone oxidoreductase.	Corynebacterium glutamicum	100,000	11-Aug-98
		GB_BA1:MTCY24A1	20270	Z95207	Mycobacterium tuberculosis H37Rv complete genome; segment 124/162.	Mycobacterium tuberculosis	38,626	17-Jun-98
		GB_IN1:DMU15974	2994	U15974	Drosophila melanogaster kinesin-like protein (klp68d) mRNA, complete cds.	Drosophila melanogaster	36,783	18-Jul-95

TABLE 4: ALIGNMENT RESULTS

rxa01702	1155	GB_BA1:CGFDA	3371	X17313	Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4.1.2.13)	Corynebacterium glutamicum	99,913	12-Sep-93
		GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome, segment 18/162.	Mycobacterium tuberculosis	38,786	17-Jun-98
		GB_BA1:MLCB4	36310	AL023514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	38,238	27-Aug-99
rxa01743	901	GB_IN2:CELC27H5	35840	U14635	Caenorhabditis elegans cosmid C27H5	Caenorhabditis elegans	35,334	13-Jul-95
		GB_EST24:AI167112	579	AI167112	xylem est.878 Poplar xylem Lambda ZAPII library Populus balsamifera subsp. trichocarpa cDNA 5', mRNA sequence.	Populus balsamifera subsp. trichocarpa	39,222	03-DEC-1998
		GB_GSS9:AQ102635	347	AQ102635	HS_3048_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=15 Row=L, genomic survey sequence.	Homo sapiens	40,653	27-Aug-98
rxa01744	1662	GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162	Mycobacterium tuberculosis	36,650	17-Jun-98
		GB_GSS1:AF009226	665	AF009226	Mycobacterium tuberculosis cytochrome D oxidase subunit I (appC) gene, partial sequence, genomic survey sequence	Mycobacterium tuberculosis	63,438	31-Jul-97
		GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	53,088	26-Nov-98
rxa01745	836	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome, segment 98/162	Mycobacterium tuberculosis	62,081	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22	Mycobacterium leprae	61,364	22-Aug-97
		GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	52,323	12-Nov-98
rxa01758	1140	GB_PR3:HS57G9	113872	Z95116	Human DNA sequence from BAC 57G9 on chromosome 22q12 1 Contains ESTs, CA repeat, GSS.	Homo sapiens	39,209	23-Nov-99
		GB_PL2:YSCH9666	39057	U10397	Saccharomyces cerevisiae chromosome VIII cosmid 9666	Saccharomyces cerevisiae	40,021	5-Sep-97
		GB_PL2:YSCH9986	41664	U00027	Saccharomyces cerevisiae chromosome VIII cosmid 9986	Saccharomyces cerevisiae	34,375	29-Aug-97
rxa01814	1785	GB_BA1:ABCCELB	2058	L24077	Acetobacter xylinum phosphoglucomutase (celB) gene, complete cds	Acetobacter xylinus	62,173	21-Sep-94
		GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome, segment 133/162	Mycobacterium tuberculosis	39,749	17-Jun-98
		GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162	Mycobacterium tuberculosis	40,034	17-Jun-98
rxa01851	1809	GB_GSS9:AQ142579	529	AQ142579	HS_2222_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=5 Row=P, genomic survey sequence	Homo sapiens	38,068	24-Sep-98
		GB_IN2.AC005889	108924	AC005889	Drosophila melanogaster, chromosome 2L, region 30A3- 30A6, P1 clones DS06958 and DS03097, complete sequence.	Drosophila melanogaster	36,557	30-OCT-1998
		GB_GSS1:AG008814	637	AG008814	Homo sapiens genomic DNA, 21q region, clone. B137B7BB68, genomic survey sequence.	Homo sapiens	35,316	7-Feb-99
rxa01859	1050	GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence, Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,364	03-OCT-1999
		GB_HTG5:AC008031	158889	AC008031	Trypanosoma brucei chromosome II clone RPCI93-25N14, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Trypanosoma brucei	35,334	15-Nov-99
		GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnaN) gene, partial cds; microcystin synthetase gene cluster, complete sequence, Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,529	03-OCT-1999
rxa01865	438	GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	59,862	13-MAR-1996
		GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162	Mycobacterium tuberculosis	61,949	17-Jun-98
		GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348	Mycobacterium tuberculosis	59,908	10-DEC-1996
rxa01882	1113	GB_PR1:HUMADRA2C	1491	J03853	Human kidney alpha-2-adrenergic receptor mRNA, complete cds	Homo sapiens	36,899	27-Apr-93
		GB_PR4:HSU72648	4850	U72648	Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.	Homo sapiens	36,899	23-Nov-98

TABLE 4: ALIGNMENT RESULTS

		GB_GSS3:B42200	387	B42200	HS-1055-B1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=5 Row=B, genomic survey sequence.	Homo sapiens	34,805	18-OCT-1997
rxa01884	1913	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome, segment 69/162	Mycobacterium tuberculosis	37,892	17-Jun-98
		GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	40,413	29-MAR-1999
		GB_BA1:D90908	122349	D90908	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234	Synechocystis sp.	47,792	7-Feb-99
rxa01886	897	GB_GSS9:AQ116291	572	AQ116291	RPCI11-49P6.TK.1 RPCI-11 Homo sapiens genomic clone RPCI-11-49P6, genomic survey sequence.	Homo sapiens	43,231	20-Apr-99
		GB_BA2.AE001721	17632	AE001721	Thermotoga maritima section 33 of 136 of the complete genome.	Thermotoga maritima	39,306	2-Jun-99
		GB_EST16:AA567090	596	AA567090	GM01044.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM01044 5prime, mRNA sequence	Drosophila melanogaster	42,807	28-Nov-98
rxa01887	1134	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102 unordered pieces.	Homo sapiens	36,417	03-DEC-1999
		GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102 unordered pieces.	Homo sapiens	37,667	03-DEC-1999
		GB_BA2:ALW243431	26953	AJ243431	Acinetobacter lwoffii wzc, wzb, wza, weeA, weeB, wceC, wzx, wzy, weeD, weeE, weeF, weeG, weeH, weeI, weeJ, weeK, galU, ugd, pgi, galE, pgm (partial) and mip (partial) genes (emulsan biosynthetic gene cluster), strain RAG-1.	Acinetobacter lwoffii	39,640	01-OCT-1999
rxa01888	658	GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCI-98 02.L.12 map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 113 unordered pieces	Drosophila melanogaster	32,969	2-Aug-99
		GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPCI-98 02 L 12 map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 113 unordered pieces	Drosophila melanogaster	32,969	2-Aug-99
		GB_EST36:AI881527	598	AI881527	606070C09.y1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence.	Zea mays	43,617	21-Jul-99
rxa01891	887	GB_VI:HIV232971	621	AJ232971	Human immunodeficiency virus type 1 subtype C nef gene, patient MP83	Human immunodeficiency virus type 1	40,040	05-MAR-1999
		GB_PL1:AFCHSE	6158	Y09542	A.fumigatus chsE gene	Aspergillus fumigatus	37,844	1-Apr-97
		GB_PR3.AF064858	193387	AF064858	Homo sapiens chromosome 21q22.3 BAC 28F9, complete sequence	Homo sapiens	37,136	2-Jun-98
rxa01895	1051	GB_BA1:CGL238250	1593	AJ238250	Corynebacterium glutamicum ndh gene.	Corynebacterium glutamicum	100,000	24-Apr-99
		GB_BA2.AF038423	1376	AF038423	Mycobacterium smegmatis NADH dehydrogenase (ndh) gene, complete cds.	Mycobacterium smegmatis	65,254	05-MAY-1998
		GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome, segment 84/162.	Mycobacterium tuberculosis	40,058	17-Jun-98
rxa01901	1383	GB_BA1:MSGB38COS	37114	L01095	M. leprae genomic DNA sequence, cosmid B38 bfr gene, complete cds	Mycobacterium leprae	59,551	6-Sep-94
		GB_BA1:SCE63	37200	AL035640	Streptomyces coelicolor cosmid E63.	Streptomyces coelicolor	39,468	17-MAR-1999
		GB_PR3:AF093117	147216	AF093117	Homo sapiens chromosome 7qtelo BAC E3, complete sequence	Homo sapiens	39,291	02-OCT-1998
rxa01927	1503	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	38,384	11-MAY-1999
		GB_BA1:ASXYLA	1905	X59466	Arthrobacter Sp. N.R R.L. B3728 xylA gene for D-xylose(D-glucose) isomerase	Arthrobacter sp.	56,283	04-MAY-1992
		GB_HTG3:AC009500	176060	AC009500	Homo sapiens clone NH0511A20, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces.	Homo sapiens	37,593	24-Aug-99
rxa01952	1836	GB_BA2:AE000739	13335	AE000739	Aquifex aeolicus section 71 of 109 of the complete genome	Aquifex aeolicus	36,309	25-MAR-1998
		GB_EST28:AI519629	612	AI519629	LD39282.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD39282 5prime, mRNA sequence	Drosophila melanogaster	41,941	16-MAR-1999
		GB_EST21:AA949396	767	AA949396	LD28277.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD28277 5prime, mRNA sequence	Drosophila melanogaster	39,855	25-Nov-98

TABLE 4: ALIGNMENT RESULTS

rxa01989	630	GB_BA1:BSPGIA	1822	X16639	Bacillus stearothermophilus pgiA gene for phosphoglucoisomerase isoenzyme A (EC 5.3.1.9).	Bacillus stearothermophilus	66,292	20-Apr-95
		GB_BA1:BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.	Bacillus subtilis	37,255	26-Nov-97
		GB_BA2:AF132127	8452	AF132127	Streptococcus mutans sorbitol phosphoenolpyruvate:sugar phosphotransferase operon, complete sequence and unknown gene.	Streptococcus mutans	63,607	28-Sep-99
rxa02026	720	GB_BA1:SXSCRBA	3161	X67744	S.xylosus scrB and scrR genes.	Staphylococcus xylosus	67,778	28-Nov-96
		GB_BA1:BSUB0020	212150	Z99123	Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.	Bacillus subtilis	35,574	26-Nov-97
		GB_BA1:BSGENR	97015	X73124	B.subtilis genomic region (325 to 333).	Bacillus subtilis	51,826	2-Nov-93
rxa02028	526	GB_BA1:MTCI237	27030	Z94752	Mycobacterium tuberculosis H37Rv complete genome; segment 46/162.	Mycobacterium tuberculosis	54,476	17-Jun-98
		GB_PL2:SCE9537	66030	U18778	Saccharomyces cerevisiae chromosome V cosmids 9537, 9581, 9495, 9867, and lambda clone 5898.	Saccharomyces cerevisiae	36,100	1-Aug-97
		GB_GSS13:AQ501177	767	AQ501177	V26G9 mTn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae genomic 5', genomic survey sequence.	Saccharomyces cerevisiae	32,039	29-Apr-99
rxa02054	1140	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	61,896	27-Aug-99
		GB_BA1:MTY13E12	43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	Mycobacterium tuberculosis	59,964	17-Jun-98
		GB_BA1:MTU43540	3453	U43540	Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein (rfbA), and rmlC genes, complete cds.	Mycobacterium tuberculosis	59,659	14-Aug-97
rxa02056	2891	GB_PAT:E14601	4394	E14601	Brevibacterium lactofermentum gene for alpha-ketoglutaric acid dehydrogenase.	Corynebacterium glutamicum	98,928	28-Jul-99
		GB_BA1:D84102	4394	D84102	Corynebacterium glutamicum DNA for 2-oxoglutarate dehydrogenase, complete cds.	Corynebacterium glutamicum	98,928	6-Feb-99
		GB_BA1:MTV006	22440	AL021006	Mycobacterium tuberculosis H37Rv complete genome; segment 54/162.	Mycobacterium tuberculosis	39,265	18-Jun-98
rxa02061	1617	GB_HTG7:AC005883	211682	AC005883	Homo sapiens chromosome 17 clone RP11-958E11 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	37,453	08-DEC-1999
		GB_PL2:ATAC003033	84254	AC003033	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	19-DEC-1997
		GB_PL2:ATAC002334	75050	AC002334	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711	04-MAR-1998
rxa02063	1350	GB_BA1:SCGLGC	1518	X89733	S.coelicolor DNA for glgC gene.	Streptomyces coelicolor	56,972	12-Jul-99
		GB_GSS4:AQ687350	786	AQ687350	nbxb0074H11r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0074H11r, genomic survey sequence.	Oryza sativa	40,696	1-Jul-99
		GB_EST38:AW028530	444	AW028530	wv27f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2530795 3' similar to WP:T03G11.6 CE04874 ;, mRNA sequence.	Homo sapiens	36,795	27-OCT-1999
rxa02100	2348	GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	40,156	10-DEC-1996
		GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	55,218	17-Jun-98
		GB_BA1:SCO001205	9589	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism clusterI.	Streptomyces coelicolor	38,475	29-MAR-1999
rxa02122	822	GB_BA1:D90858	13548	D90858	E.coli genomic DNA, Kohara clone #401(51.3-51.6 min.).	Escherichia coli	38,586	29-MAY-1997
		GB_EST37:AI948595	469	AI948595	wq07d12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470583 3', mRNA sequence.	Homo sapiens	37,259	6-Sep-99
		GB_HTG3:AC010387	220665	AC010387	Homo sapiens chromosome 5 clone CITB-H1_2074D8, *** SEQUENCING IN PROGRESS ***, 77 unordered pieces.	Homo sapiens	38,868	15-Sep-99
rxa02140	1200	GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
		GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	51,399	15-Jun-96
		GB_RO:AF093099	2482	AF093099	Mus musculus transcription factor TBLYM (Tblym) mRNA, complete cds.	Mus musculus	36,683	01-OCT-1999
rxa02142	774	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,292	17-Jun-98
		GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,058	24-MAR-1999

TABLE 4: ALIGNMENT RESULTS

		GB_BA1:AB016787	5550	AB016787	Pseudomonas putida genes for cytochrome o ubiquinol oxidase A-E and 2 ORFs, complete cds.	Pseudomonas putida	47,403	5-Aug-99
rxa02143	1011	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,317	17-Jun-98
		GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
		GB_BA1:MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.	Mycobacterium leprae	38,159	15-Jun-96
rxa02144	1347	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	55,530	17-Jun-98
		GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
		GB_HTG3:AC011500_0	300851	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	39,659	18-Feb-00
rxa02147	1140	GB_EST28:AI492095	485	AI492095	tg07a01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108040 3', mRNA sequence.	Homo sapiens	39,798	30-MAR-1999
		GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
		GB_EST10:AA157467	376	AA157467	zo50e01.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.	Homo sapiens	36,436	11-DEC-1996
rxa02149	1092	GB_PR3:HSBK277P6	61698	AL117347	Human DNA sequence from clone 277P6 on chromosome 1q25.3-31.2, complete sequence.	Homo sapiens	36,872	23-Nov-99
		GB_BA2:EMB065R075	360	AF116423	Rhizobium etli mutant MB045 RosR-transcriptionally regulated sequence.	Rhizobium etli	43,175	06-DEC-1999
		GB_EST34:AI789323	574	AI789323	uk53g05.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1972760 5' similar to WP:K11H12.8 CE12160 ;, mRNA sequence.	Mus musculus	39,715	2-Jul-99
rxa02175	1416	GB_BA1:CGGLTG	3013	X66112	C.glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	100,000	17-Feb-95
		GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.	Mycobacterium tuberculosis	64,331	17-Jun-98
		GB_BA1:MLCB57	38029	Z99494	Mycobacterium leprae cosmid B57.	Mycobacterium leprae	62,491	10-Feb-99
rxa02196	816	GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	38,791	31-MAY-1995
		GB_GSS8:AQ012162	763	AQ012162	127PB037070197 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 127PB037070197, genomic survey sequence.	Rhodobacter sphaeroides	40,044	4-Jun-98
		GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete cds.	Rattus norvegicus	37,312	31-MAY-1995
rxa02209	1694	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,173	3-Apr-99
		GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	40,219	26-MAR-1998
		GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	38,253	17-Jun-98
rxa02213	874	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.	Corynebacterium glutamicum	99,096	3-Apr-99
		GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	34,937	17-Jun-98
		GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GIR10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (moxR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.	Mycobacterium avium	36,885	26-MAR-1998

TABLE 4: ALIGNMENT RESULTS

rxa02245	780	GB_BA2:RCU23145	5960	U23145	Rhodobacter capsulatus Calvin cycle carbon dioxide fixation operon fructose-1,6-/sedoheptulose-1,7-bisphosphate aldolase (cbbA) gene, partial cds, Form II ribulose-1,5-bisphosphate carboxylase/oxygenase (cbbM) gene, complete cds, and Calvin cycle operon· pentose-5-phosphate-3-epimerase (cbbE), phosphoglycolate phosphatase (cbbZ), and cbbY genes, complete cds	Rhodobacter capsulatus	48,701	28-OCT-1997
		GB_BA1:ECU82664	139818	U82664	Escherichia coli minutes 9 to 11 genomic sequence	Escherichia coli	39,119	11-Jan-97
		GB_HTG2:AC007922	158858	AC007922	Homo sapiens chromosome 18 clone hRPK 178_F_10 map 18, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.	Homo sapiens	33,118	26-Jun-99
rxa02256	1125	GB_BA1:CGGAPPGK	3804	X59403	C glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,289	05-OCT-1992
		GB_BA1:SCC54	30753	AL035591	Streptomyces coelicolor cosmid C54.	Streptomyces coelicolor	36,951	11-Jun-99
		GB_BA1.MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162	Mycobacterium tuberculosis	64,196	19-Jun-98
rxa02257	1338	GB_BA1.CGGAPPGK	3804	X59403	C.glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase	Corynebacterium glutamicum	98,873	05-OCT-1992
		GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome, segment 63/162.	Mycobacterium tuberculosis	61,273	19-Jun-98
		GB_BA2:MAU82749	2530	U82749	Mycobacterium avium glyceraldehyde-3-phosphate dehydrogenase homolog (gapdh) gene, complete cds; and phosphoglycerate kinase gene, partial cds.	Mycobacterium avium	61,772	6-Jan-98
rxa02258	900	GB_BA1·CGGAPPGK	3804	X59403	C glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase	Corynebacterium glutamicum	99,667	05-OCT-1992
		GB_BA1:CORPEPC	4885	M25819	C glutamicum phosphoenolpyruvate carboxylase gene, complete cds	Corynebacterium glutamicum	100,000	15-DEC-1995
		GB_PAT:A09073	4885	A09073	C.glutamicum ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
rxa02259	2895	GB_BA1.CORPEPC	4885	M25819	C glutamicum phosphoenolpyruvate carboxylase gene, complete cds	Corynebacterium glutamicum	100,000	15-DEC-1995
		GB_PAT:A09073	4885	A09073	C.glutamicum ppg gene for phosphoenol pyruvate carboxylase	Corynebacterium glutamicum	100,000	25-Aug-93
		GB_BA1.CGPPC	3292	X14234	Corynebacterium glutamicum phosphoenolpyruvate carboxylase gene (EC 4 1.1.31).	Corynebacterium glutamicum	99,827	12-Sep-93
rxa02288	969	GB_PR3:HSDJ94E24	243145	AL050317	Human DNA sequence from clone RP1-94E24 on chromosome 20q12, complete sequence.	Homo sapiens	36,039	03-DEC-1999
		GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
		GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
rxa02292	798	GB_BA2:AF125164	26443	AF125164	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	Bacteroides fragilis	39,747	01-DEC-1999
		GB_GSS5:AQ744695	827	AQ744695	HS_5505_A2_C06_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1081 Col=12 Row=E, genomic survey sequence	Homo sapiens	39,185	16-Jul-99
		GB_EST14:AA381925	309	AA381925	EST95058 Activated T-cells I Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	35,922	21-Apr-97
rxa02322	511	GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome, segment 49/162	Mycobacterium tuberculosis	57,677	17-Jun-98
		GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome, segment 49/162.	Mycobacterium tuberculosis	37,143	17-Jun-98
rxa02326	939	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene	Corynebacterium glutamicum	100,000	08-MAY-1998
		GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
		GB_BA1.MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome, segment 131/162	Mycobacterium tuberculosis	37,363	17-Jun-98
rxa02327	1083	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	99,259	08-MAY-1998
		GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	99,259	24-DEC-1997
		GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 131/162.	Mycobacterium tuberculosis	41,317	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

rxa02328	1719	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998
		GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
		GB_PL2:AF097728	3916	AF097728	Aspergillus terreus pyruvate carboxylase (Pyc) mRNA, complete cds.	Aspergillus terreus	52,248	29-OCT-1998
rxa02332	1266	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,460	20-Sep-91
		GB_BA2:ABU85944	1334	U85944	Antarctic bacterium DS2-3R citrate synthase (cisy) gene, complete cds.	Antarctic bacterium DS2-3R	57,154	23-Sep-97
		GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	38,164	12-Nov-98
rxa02333	1038	GB_BA1:MSGLTA	1776	X60513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,929	20-Sep-91
		GB_PR4:HUAC002299	171681	AC002299	Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 ~complete genomic sequence, complete sequence.	Homo sapiens	33,070	23-Nov-99
		GB_HTG2:AC007889	127840	AC007889	Drosophila melanogaster chromosome 3 clone BACR48E12 (D695) RPCI-98 48.E.12 map 87A-87B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 86 unordered pieces.	Drosophila melanogaster	34,897	2-Aug-99
rxa02399	1467	GB_BA1:CGACEA	2427	X75504	C.glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
		GB_BA1:CORACEA	1905	L28760	Corynebacterium glutamicum isocitrate lyase (aceA) gene	Corynebacterium glutamicum	100,000	10-Feb-95
		GB_PAT:I13693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	99,795	26-Sep-95
rxa02404	2340	GB_BA1:CGACEB	3024	X78491	C.glutamicum (ATCC 13032) aceB gene	Corynebacterium glutamicum	99,914	13-Jan-95
		GB_BA1:CORACEB	2725	L27123	Corynebacterium glutamicum malate synthase (aceB) gene, complete cds	Corynebacterium glutamicum	99,786	8-Jun-95
		GB_BA1:PFFC2	5588	Y11998	P fluorescens FC2.1, FC2 2, FC2.3c, FC2 4 and FC2.5c open reading frames.	Pseudomonas fluorescens	63,539	11-Jul-97
rxa02414	870	GB_PR4:AC007102	176258	AC007102	Homo sapiens chromosome 4 clone C0162P16 map 4p16, complete sequence.	Homo sapiens	35,069	2-Jun-99
		GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	36,885	03-OCT-1999
		GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	36,885	03-OCT-1999
rxa02435	681	GB_BA2:AF101055	7457	AF101055	Clostridium acetobutylicum atp operon, complete sequence	Clostridium acetobutylicum	39,605	03-MAR-1999
		GB_OM:RABPKA	4441	J03247	Rabbit phosphorylase kinase (alpha subunit) mRNA, complete cds.	Oryctolagus cuniculus	36,061	27-Apr-93
		GB_OM:RABPLASISM	4458	M64656	Oryctolagus cuniculus phosphorylase kinase alpha subunit mRNA, complete cds.	Oryctolagus cuniculus	36,000	22-Jun-98
rxa02440	963	GB_EST14.AA417723	374	AA417723	zv01b12 s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 746207 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;, mRNA sequence.	Homo sapiens	38,770	16-OCT-1997
		GB_EST11.AA215428	303	AA215428	zr95a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683412 3' similar to contains Alu repetitive element;, mRNA sequence.	Homo sapiens	39,934	13-Aug-97
		GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome, segment 146/162.	Mycobacterium tuberculosis	38,889	18-Jun-98
rxa02453	876	GB_EST14:AA426336	375	AA426336	zv53g02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757394 3', mRNA sequence.	Homo sapiens	38,043	16-OCT-1997
		GB_BA1:STMAACC8	1353	M55426	S.fradiae aminoglycoside acetyltransferase (aacC8) gene, complete cds.	Streptomyces fradiae	37,097	05-MAY-1993
		GB_PR3:AC004500	77538	AC004500	Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.	Homo sapiens	33,256	30-MAR-1998
rxa02474	897	GB_BA1:AB009078	2686	AB009078	Brevibacterium saccharolyticum gene for L-2.3-butanediol dehydrogenase, complete cds.	Brevibacterium saccharolyticum	96,990	13-Feb-99
		GB_OM.BTU71200	877	U71200	Bos taurus acetoin reductase mRNA, complete cds.	Bos taurus	51,659	8-Oct-97
		GB_EST2:F12685	287	F12685	HSC3DA031 normalized infant brain cDNA Homo sapiens cDNA clone c-3da03, mRNA sequence	Homo sapiens	41,509	14-Mar-95
rxa02480	1779	GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome, segment 132/162.	Mycobacterium tuberculosis	36,737	23-Jun-99
		GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10	Streptomyces coelicolor	35,511	24-MAR-1999
		GB_BA1:AP000060	347800	AP000060	Aeropyrum pernix genomic DNA, section 3/7.	Aeropyrum pernix	48,014	22-Jun-99
rxa02485								

TABLE 4: ALIGNMENT RESULTS

rxa02492	840	GB_BA1:STMPGM	921	M83661	Streptomyces coelicolor phosphoglycerate mutase (PGM) gene, complete cds	Streptomyces coelicolor	65,672	26-Apr-93
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome, segment 25/162.	Mycobacterium tuberculosis	61,436	17-Jun-98
		GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	37,893	01-MAR-1994
rxa02528	1098	GB_PR2:HS161N10	56075	AL008707	Human DNA sequence from PAC 161N10 on chromosome Xq25. Contains EST.	Homo sapiens	37,051	23-Nov-99
		GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 15.B.19 map 94F-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
		GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 15.B.19 map 94F-95A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 125 unordered pieces.	Drosophila melanogaster	36,822	2-Aug-99
rxa02539	1641	GB_BA2:RSU17129	17425	U17129	Rhodococcus erythropolis ThcA (thcA) gene, complete cds, and unknown genes.	Rhodococcus erythropolis	66,117	16-Jul-99
		GB_BA1:MTV038	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162	Mycobacterium tuberculosis	65,174	17-Jun-98
		GB_BA2:AF068264	3152	AF068264	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA)gene, partial cds, cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthesis A (pqqA) genes, complete cds; and pyrroloquinoline quinone synthesis B (pqqB) gene, partial cds.	Pseudomonas aeruginosa	65,448	18-MAR-1999
rxa02551	483	GB_BA1:BACHYPTP	17057	D29985	Bacillus subtilis wapA and orf genes for wall-associated protein and hypothetical proteins	Bacillus subtilis	53,602	7-Feb-99
		GB_BA1:BACHUTWAPA	28954	D31856	Bacillus subtilis genome containing the hut and wapA loci.	Bacillus subtilis	53,602	7-Feb-99
		GB_BA1.BSGBGLUC	4290	Z34526	B.subtilis (Marburg 168) genes for beta-glucoside permease and beta-glucosidase	Bacillus subtilis	53,602	3-Jul-95
rxa02556	1281	GB_HTG3:AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 106 unordered pieces	Homo sapiens	34,022	22-Aug-99
		GB_HTG3.AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 106 unordered pieces.	Homo sapiens	34,022	22-Aug-99
		GB_PL2:AC005292	99053	AC005292	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence.	Arabidopsis thaliana	33,858	16-Apr-99
rxa02560	990	GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence	Caenorhabditis elegans	36,420	2-Sep-99
		GB_EST32.AI731605	566	AI731605	BNLGHi10201 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AC004684) hypothetical protein [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	38,095	11-Jun-99
		GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	Caenorhabditis elegans	33,707	2-Sep-99
rxa02572	668	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome, segment 16/162	Mycobacterium tuberculosis	61,677	17-Jun-98
		GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome, segment 16/162	Mycobacterium tuberculosis	37,170	17-Jun-98
		GB_HTG1:HS24H01	46989	AL121632	Homo sapiens chromosome 21 clone LLNLc116H0124 map 21q21, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	19,820	29-Sep-99
rxa02596	1326	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	36,957	24-Jun-99
		GB_BA2:AF026540	1778	AF026540	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	67,627	30-OCT-1998
		GB_BA2:MTU96128	1200	U96128	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	Mycobacterium tuberculosis	70,417	25-MAR-1998
rxa02611	1775	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162	Mycobacterium tuberculosis	38,532	17-Jun-98
		GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	60,575	10-DEC-1996
		GB_BA1:U00014	36470	U00014	Mycobacterium leprae cosmid B1549.	Mycobacterium leprae	57,486	29-Sep-94
rxa02612	2316	GB_BA1.MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome, segment 59/162	Mycobacterium tuberculosis	38,018	17-Jun-98
		GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151	Mycobacterium tuberculosis	58,510	10-DEC-1996

TABLE 4: ALIGNMENT RESULTS

		GB_BA1:STMGLGEN	2557	L11647	Streptomyces aureofaciens glycogen branching enzyme (glgB) gene, complete cds.	Streptomyces aureofaciens	57,193	25-MAY-1995
rxa02621	942	GB_BA1:CGL133719	1839	AJ133719	Corynebacterium glutamicum yjcc gene, amtR gene and citE gene, partial.	Corynebacterium glutamicum	36,858	12-Aug-99
		GB_IN1:CEM106	39973	Z46935	Caenorhabditis elegans cosmid M106, complete sequence	Caenorhabditis elegans	37,608	2-Sep-99
		GB_EST29:AI547662	377	AI547662	UI-R-C3-sz-h-03-0-UI.s1 UI-R-C3 Rattus norvegicus cDNA clone UI-R-C3-sz-h-03-0-UI 3', mRNA sequence.	Rattus norvegicus	50,667	3-Jul-99
rxa02640	1650	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome, segment 155/162.	Mycobacterium tuberculosis	39,187	24-Jun-99
		GB_BA1:PAU49666	4495	U49666	Pseudomonas aeruginosa (orfX), glycerol dfiffusion facilitator (glpF), glycerol kinase (glpK), and Glp repressor (glpR) genes, complete cds, and (orfK) gene, partial cds.	Pseudomonas aeruginosa	59,273	18-MAY-1997
		GB_BA1.AB015974	1641	AB015974	Pseudomonas tolaasii glpK gene for glycerol kinase, complete cds.	Pseudomonas tolaasii	58,339	28-Aug-99
rxa02654	1008	GB_EST6:N65787	512	N65787	20827 Lambda-PRL2 Arabidopsis thaliana cDNA clone 232B7T7, mRNA sequence	Arabidopsis thaliana	39,637	5-Jan-98
		GB_PL2:T17H3	65839	AC005916	Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, complete sequence	Arabidopsis thaliana	33,735	5-Aug-99
		GB_RO:MMU58105	88871	U58105	Mus musculus Btk locus, alpha-D-galactosidase A (Ags), ribosomal protein (L44L), and Bruton's tyrosine kinase (Btk) genes, complete cds.	Mus musculus	35,431	13-Feb-97
rxa02666	891	GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	38,851	01-MAY-1998
		GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	Homo sapiens	41,599	01-MAY-1998
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds	Corynebacterium glutamicum	40,413	1-Jul-98
rxa02675	1980	GB_BA1:PDENQOURF	10425	L02354	Paracoccus denitrificans NADH dehydrogenase (URF4), (NQO8), (NQO9), (URF5), (URF6), (NQO10), (NQO11), (NQO12), (NQO13), and (NQO14) genes, complete cds's; biotin [acetyl-CoA carboxyl] ligase (birA) gene, complete cds	Paracoccus denitrificans	40,735	20-MAY-1993
		GB_BA1:MTCY339	42861	Z77163	Mycobacterium tuberculosis H37Rv complete genome; segment 101/162.	Mycobacterium tuberculosis	36,471	17-Jun-98
		GB_BA1:MXADEVRS	2452	L19029	Myxococcus xanthus devR and devS genes, complete cds's.	Myxococcus xanthus	38,477	27-Jan-94
rxa02694	1065	GB_BA1.BACLDH	1147	M19394	B.caldolyticus lactate dehydrogenase (LDH) gene, complete cds	Bacillus caldolyticus	57,371	26-Apr-93
		GB_BA1:BACLDHL	1361	M14788	B stearothermophilus lct gene encoding L-lactate dehydrogenase, complete cds	Bacillus stearothermophilus	57,277	26-Apr-93
		GB_PAT:A06664	1350	A06664	B.stearothermophilus lct gene.	Bacillus stearothermophilus	57,277	29-Jul-93
rxa02729	844	GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ,, mRNA sequence	Danio rerio	50,746	27-Jun-97
		GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR.G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN. ,, mRNA sequence.	Danio rerio	36,364	27-Jun-97
rxa02730	1161	GB_EST19:AA758660	233	AA758660	ah67d06 s1 Soares_testis_NHT Homo sapiens cDNA clone 1320683 3', mRNA sequence	Homo sapiens	37,059	29-DEC-1998
		GB_EST15:AA494626	121	AA494626	fa09d04.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 11A22 5' similar to TR G1171163 G1171163 G/T-MISMATCH BINDING PROTEIN ,, mRNA sequence.	Danio rerio	42,149	27-Jun-97

TABLE 4: ALIGNMENT RESULTS

		GB_PR4:AC006285	150172	AC006285	Homo sapiens, complete sequence.	Homo sapiens	37,655	15-Nov-99
rxa02737	1665	GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	99,580	24-Jun-98
		GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	38,363	19-Jun-98
		GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	39,444	27-Jul-98
rxa02738	1203	GB_PAT:E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	98,226	24-Jun-98
		GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	60,399	12-Jul-99
		GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	36,426	27-Jul-98
rxa02739	2223	GB_BA1:AB023377	2572	AB023377	Corynebacterium glutamicum tkt gene for transketolase, complete cds.	Corynebacterium glutamicum	99,640	20-Feb-99
		GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	61,573	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	61,573	01-MAR-1994
rxa02740	1053	GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48I10 (D505) RPCI-98 48.I.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Drosophila melanogaster	37,105	2-Aug-99
		GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48I10 (D505) RPCI-98 48.I.10 map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Drosophila melanogaster	37,105	2-Aug-99
		GB_HTG3:AC007150	121474	AC007150	Drosophila melanogaster chromosome 2 clone BACR16P13 (D597) RPCI-98 16.P.13 map 49E-49F strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 87 unordered pieces.	Drosophila melanogaster	38,728	20-Sep-99
rxa02741	1089	GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022I14, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	33,116	12-Jun-98
		GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022I14, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	33,116	12-Jun-98
		GB_IN1:AB006546	931	AB006546	Ephydatia fluviatilis mRNA for G protein a subunit 4, partial cds.	Ephydatia fluviatilis	36,379	23-Jun-99
rxa02743	1161	GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	48,401	04-DEC-1998
		GB_BA1:U00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	48,401	01-MAR-1994
		GB_HTG2:AC007401	83657	AC007401	Homo sapiens clone NH0501O07, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	37,128	26-Jun-99
rxa02797	1026	GB_BA1:CGBETPGEN	2339	X93514	C.glutamicum betP gene.	Corynebacterium glutamicum	38,889	8-Sep-97
		GB_GSS9:AQ148714	405	AQ148714	HS_3136_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=5 Row=A, genomic survey sequence.	Homo sapiens	34,321	08-OCT-1998
		GB_BA1:BFU64514	3837	U64514	Bacillus firmus dppABC operon, dipeptide transporter protein dppA gene, partial cds, and dipeptide transporter proteins dppB and dppC genes, complete cds.	Bacillus firmus	38,072	1-Feb-97
rxa02803	680	GB_BA1:U00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	34,462	01-MAR-1994
		GB_BA2:PSU85643	4032	U85643	Pseudomonas syringae pv. syringae putative dihydropteroate synthase gene, partial cds, regulatory protein MrsA (mrsA), triose phosphate isomerase (tpiA), transport protein SecG (secG), tRNA-Leu, tRNA-Met, and 15 kDa protein genes, complete cds.	Pseudomonas syringae pv. syringae	50,445	9-Apr-97
		GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	59,314	20-Aug-98
rxa02821	363	GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	37,607	22-Jul-99
		GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	37,607	22-Jul-99
		GB_EST33:AV117143	222	AV117143	AV117143 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 2610200J17, mRNA sequence.	Mus musculus	40,157	30-Jun-99

TABLE 4: ALIGNMENT RESULTS

rxa02829	373	GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LL0XNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
		GB_HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LL0XNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
		GB_PR3:HSU85B5	39550	Z69724	Human DNA sequence from cosmid U85B5, between markers DXS366 and DXS87 on chromosome X.	Homo sapiens	41,595	23-Nov-99
rxc03216	1141	GB_HTG3:AC008184	151720	AC008184	Drosophila melanogaster chromosome 2 clone BACR04D05 (D540) RPCI-98 04.D.5 map 36E5-36F2 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Drosophila melanogaster	39,600	2-Aug-99
		GB_EST15:AA477537	411	AA477537	zu36g12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740134 5' similar to contains Alu repetitive element;contains element HGR repetitive element ;, mRNA sequence.	Homo sapiens	37,260	9-Nov-97
		GB_EST26:AI330662	412	AI330662	fa91d08.y1 zebrafish fin day1 regeneration Danio rerio cDNA 5', mRNA sequence.	Danio rerio	37,805	28-DEC-1998
rxs03215	1038	GB_BA1:SC3F9	19830	AL023862	Streptomyces coelicolor cosmid 3F9.	Streptomyces coelicolor A3(2)	48,657	10-Feb-99
		GB_BA1:SLLINC	36270	X79146	S.lincolnensis (78-11) Lincomycin production genes.	Streptomyces lincolnensis	39,430	15-MAY-1996
		GB_HTG5:AC009660	204320	AC009660	Homo sapiens chromosome 15 clone RP11-424J10 map 15, *** SEQUENCING IN PROGRESS ***, 41 unordered pieces.	Homo sapiens	35,151	04-DEC-1999
rxs03224	1288	GB_PR3:AC004076	41322	AC004076	Homo sapiens chromosome 19, cosmid R30217, complete sequence.	Homo sapiens	37,788	29-Jan-98
		GB_PL2:SPAC926	23193	AL110469	S.pombe chromosome I cosmid c926.	Schizosaccharomyces pombe	38,474	2-Sep-99
		GB_BA2:AE001081	11473	AE001081	Archaeoglobus fulgidus section 26 of 172 of the complete genome.	Archaeoglobus fulgidus	35,871	15-DEC-1997

Customer Number: 000959

Attorney's
Docket No. BGI-126CP

DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISMAND ENERGY PRODUCTION

X is attached hereto.

_ was filed on _____ as

Application Serial No. _____

and was amended on _____.
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

_ no such applications have been filed.

X such applications have been filed as follows

EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

Country	Application Number	Date of Filing (month,day,year)	Priority Claimed Under 35 USC 119
DE	19931412.8	07/08/99	X Yes No _
DE	19931413.6	07/08/99	X Yes No _
DE	19931419.5	07/08/99	X Yes No _
DE	19931420.9	07/08/99	X Yes No _
DE	19931424.1	07/08/99	X Yes No _
DE	19931428.4	07/08/99	X Yes No _
DE	19931431.4	07/08/99	X Yes No _
DE	19931433.0	07/08/99	X Yes No _
DE	19931434.9	07/08/99	X Yes No _
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DE	19942123.4	09/03/99	X Yes No _
DE	19942125.0	09/03/99	X Yes No _

ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

60/141,031	June 25, 1999
(Application Serial No.)	(Filing Date)
60/143,208	July 9, 1999
(Application Serial No.)	(Filing Date)
60/151,572	August 31, 1999
(Application Serial No.)	(Filing Date)

CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

(Application Serial No.)	(Filing Date)	(Status) (patented,pending,aband.)
(Application Serial No.)	(Filing Date)	(Status) (patented,pending,aband.)

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

James E. Cockfield	Reg. No. 19,162	Jeanne M. DiGiorgio	Reg. No. 41,710
Thomas V. Smurzynski	Reg. No. 24,798	Megan E. Williams	Reg. No. 43,270
Ralph A. Loren	Reg. No. 29,325	Nicholas P. Triano III	Reg. No. 36,397
Giulio A. DeConti, Jr.	Reg. No. 31,503	Peter C. Lauro	Reg. No. 32,360
Ann Lamport Hammitte	Reg. No. 34,858	Timothy J. Douros	Reg. No. 41,716
Elizabeth A. Hanley	Reg. No. 33,505	DeAnn F. Smith	Reg. No. 36,683
Amy E. Mandragouras	Reg. No. 36,207	William D. DeVaul	Reg. No. 42,483
Anthony A. Laurentano	Reg. No. 38,220	David J. Rikkers	Reg. No. 43,882
Jane E. Remillard	Reg. No. 38,872	Chi Suk Kim	Reg. No. 42,728
Jeremiah Lynch	Reg. No. 17,425	Maria Laccotripe Zacharakis	Limited Recognition Under 37 C.F.R. § 10.9(b)
Kevin J. Canning	Reg. No. 35,470		
David A. Lane, Jr.	Reg. No. 39,261	Debra J. Milasincic	Reg. No. P46,931
Catherine J. Kara	Reg. No. 41,106	David R. Burns	Reg. No. P46,590

Send Correspondence to Giulio A. DeConti, Jr., Esq. at **Customer Number: 000959** whose address is:

Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109

Direct Telephone Calls to: (name and telephone number)

Giulio A. DeConti, Jr., Esq., (617) 227-7400

Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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Inventor's signature Date
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Citizenship Germany
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Inventor's signature Date
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Citizenship Germany
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taaccacttg cagtataccc tag                                        468


<210> 4
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 4
Met Ser Lys Thr Ile Ile Val Arg Thr Glu Ile Glu Ile Pro Gly His
  1               5                  10                  15

Pro Thr Ala Ile His Ile Ala Glu Met Gln Glu Leu Pro Pro Ser Glu
             20                  25                  30

Ala Gln Gly Gly Val Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu
         35                  40                  45

Ala Gly Thr Ala Glu Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly
     50                  55                  60

Gly Ser Asn Phe Gln Leu Asn Asn Glu Pro Asn Glu Val Val Pro His
 65                  70                  75                  80

Pro Asp Thr Tyr Ala Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser
                 85                  90                  95

Ala Glu Thr Phe Glu Gly Leu Trp Leu Glu Ala Gly Ala Lys Phe Pro
            100                 105                 110

Gly Leu Asn
        115


<210> 5
<211> 780
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(757)
<223> RXA02245

<400> 5
gccacaccgc cacggcaccg atgcgatgtt tgtggcagtg ctgcgaaaga agtagacctg 60

tgagctaagt ggggtagaca agagggctat gatttagggc atg gca caa cgt act   115
                                            Met Ala Gln Arg Thr
                                              1               5

cca cta atc gcc cca tcc att ctt gct gct gat ttc tcc cgc tta ggg   163
Pro Leu Ile Ala Pro Ser Ile Leu Ala Ala Asp Phe Ser Arg Leu Gly
                 10                  15                  20
```

```
gag cag gtg ttg gct gtt cct gat gct gac tgg att cac gtc gac atc   211
Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp Ile His Val Asp Ile
            25                  30                  35

atg gac gga cac ttc gtt cca aac ttg agc ttt ggc gcg gat atc aca   259
Met Asp Gly His Phe Val Pro Asn Leu Ser Phe Gly Ala Asp Ile Thr
        40                  45                  50

gct gcg gtc aac cgc gtt acg gac aaa gaa cta gac gtc cac ctg atg   307
Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu Asp Val His Leu Met
    55                  60                  65

atc gaa aac cca gag aag tgg gtg gac aac tac atc gac gct ggc gcg   355
Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr Ile Asp Ala Gly Ala
70                  75                  80                  85

gac tgc att gtt ttc cac gtt gaa gcc acc gaa ggt cac gtt gag ttg   403
Asp Cys Ile Val Phe His Val Glu Ala Thr Glu Gly His Val Glu Leu
                90                  95                  100

gct aag tac atc cgt tcc aag ggt gtg cgt gca ggt ttc tcc ctg cgc   451
Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala Gly Phe Ser Leu Arg
            105                 110                 115

cct gga act ccc atc gag gat tac ttg gat gac ctc gag cac ttc gat   499
Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp Leu Glu His Phe Asp
        120                 125                 130

gaa gtc atc gtc atg agc gtc gag cct gga ttc ggt ggc caa agc ttc   547
Glu Val Ile Val Met Ser Val Glu Pro Gly Phe Gly Gly Gln Ser Phe
    135                 140                 145

atg cct gaa caa ctg gaa aag gtt cgt acc ctg cgc aag gtc atc gat   595
Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu Arg Lys Val Ile Asp
150                 155                 160                 165

gag cgc ggt ctg aac acc gtc atc gag atc gac ggc ggc att agc gcc   643
Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp Gly Gly Ile Ser Ala
                170                 175                 180

aag acc atc aag cag gct gcc gac gct ggc gtg gat gcc ttc gtt gca   691
Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val Asp Ala Phe Val Ala
            185                 190                 195

ggt tcc gct gtg tac ggc gct gag gat ccc aac aag gcg atc cag gag   739
Gly Ser Ala Val Tyr Gly Ala Glu Asp Pro Asn Lys Ala Ile Gln Glu
        200                 205                 210

ttg cga gca ctc gcg cag taaatggatg ttgcgcacgc gtt                 780
Leu Arg Ala Leu Ala Gln
    215
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<210> 6
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 6
Met Ala Gln Arg Thr Pro Leu Ile Ala Pro Ser Ile Leu Ala Ala Asp

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  1               5                  10                  15

Phe Ser Arg Leu Gly Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp
            20                  25                  30

Ile His Val Asp Ile Met Asp Gly His Phe Val Pro Asn Leu Ser Phe
        35                  40                  45

Gly Ala Asp Ile Thr Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu
    50                  55                  60

Asp Val His Leu Met Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr
65                  70                  75                  80

Ile Asp Ala Gly Ala Asp Cys Ile Val Phe His Val Glu Ala Thr Glu
                85                  90                  95

Gly His Val Glu Leu Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala
            100                 105                 110

Gly Phe Ser Leu Arg Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp
        115                 120                 125

Leu Glu His Phe Asp Glu Val Ile Val Met Ser Val Glu Pro Gly Phe
    130                 135                 140

Gly Gly Gln Ser Phe Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu
145                 150                 155                 160

Arg Lys Val Ile Asp Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp
                165                 170                 175

Gly Gly Ile Ser Ala Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val
            180                 185                 190

Asp Ala Phe Val Ala Gly Ser Ala Val Tyr Gly Ala Glu Asp Pro Asn
        195                 200                 205

Lys Ala Ile Gln Glu Leu Arg Ala Leu Ala Gln
    210                 215
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<210> 7
<211> 442
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA01015

<400> 7
ccaagattga gtcgagctat tttgcgattt gtgaaccccc aaatagggga aaagtccggg 60

tatccgccgt tgtgaaaatg cctgcagtaa actgacttcc atg cgc gta tac ctt 115
                                                Met Arg Val Tyr Leu
                                                  1   5

gga gca gac cac gct ggt ttc gaa act aaa aat gca atc gca gaa cac 163
Gly Ala Asp His Ala Gly Phe Glu Thr Lys Asn Ala Ile Ala Glu His

```
                10                  15                  20

ctt aag gcc cac ggc cac gaa gtg atc gac tgc gga gcc cac acc tat   211
Leu Lys Ala His Gly His Glu Val Ile Asp Cys Gly Ala His Thr Tyr
            25                  30                  35

gat gca gaa gat gac tac cca gcc ttc tgc atc gaa gca gct agc cgc   259
Asp Ala Glu Asp Asp Tyr Pro Ala Phe Cys Ile Glu Ala Ala Ser Arg
        40                  45                  50

aca gta aac gac cca ggc tca ctc ggc atc gtc ctg ggt gga tcc gga   307
Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val Leu Gly Gly Ser Gly
    55                  60                  65

aac ggc gag cag atc gcc gcc aac aag gtc aag ggt gca cgt tgt gca   355
Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys Gly Ala Arg Cys Ala
70                  75                  80                  85

ctt gct tgg tct gtt gaa act gca cgc ctc gcc cgc gag cac aac aat   403
Leu Ala Trp Ser Val Glu Thr Ala Arg Leu Ala Arg Glu His Asn Asn
                90                  95                  100

gcg aac ctc atc ggc atc ggc ggc cgc atg cac tca gag               442
Ala Asn Leu Ile Gly Ile Gly Gly Arg Met His Ser Glu
            105                 110
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<210> 8
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 8

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Met Arg Val Tyr Leu Gly Ala Asp His Ala Gly Phe Glu Thr Lys Asn
  1               5                  10                  15

Ala Ile Ala Glu His Leu Lys Ala His Gly His Glu Val Ile Asp Cys
            20                  25                  30

Gly Ala His Thr Tyr Asp Ala Glu Asp Asp Tyr Pro Ala Phe Cys Ile
        35                  40                  45

Glu Ala Ala Ser Arg Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val
    50                  55                  60

Leu Gly Gly Ser Gly Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys
65                  70                  75                  80

Gly Ala Arg Cys Ala Leu Ala Trp Ser Val Glu Thr Ala Arg Leu Ala
                85                  90                  95

Arg Glu His Asn Asn Ala Asn Leu Ile Gly Ile Gly Gly Arg Met His
            100                 105                 110

Ser Glu
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<210> 9
<211> 2142
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2119)
<223> RXN01312

<400> 9
gcagttgcgt acatcgttcc tgcactggtc ctgatcggca acatcaccat tccgttcgcc 60

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atcgctgttg gttggattgc gtaaaggtta ggaagaattt atg agc act cac tct   115
                                              Met Ser Thr His Ser
                                                1               5

gaa acc acc cgc cca gag ttc atc cac cca gtc tca gtc ctc cca gag   163
Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val Ser Val Leu Pro Glu
                   10                  15                  20

gtc tca gct ggt acg gtc ctt gac gct gca gag cca gca ggc gtt ccc   211
Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu Pro Ala Gly Val Pro
               25                  30                  35

acc aaa gat atg tgg gaa tac caa aaa gac cac atg aac ctg gtc tcc   259
Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His Met Asn Leu Val Ser
           40                  45                  50

cca ctg aac cga cgc aag ttc cgt gtc ctc gtc gtt ggc acc ggc ctg   307
Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val Val Gly Thr Gly Leu
       55                  60                  65

tcc ggt ggt gct gca gca gca gcc ctc ggc gaa ctc gga tac gac gtc   355
Ser Gly Gly Ala Ala Ala Ala Ala Leu Gly Glu Leu Gly Tyr Asp Val
   70                  75                  80                  85

aag gcg ttc acc tac cac gac gca cct cgc cgt gcg cac tcc att gct   403
Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg Ala His Ser Ile Ala
                   90                  95                 100

gca cag ggt ggc gtt aac tcc gcc cgc ggc aag aag gta gac aac gac   451
Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys Lys Val Asp Asn Asp
               105                 110                 115

ggc gca tac cgc cac gtc aag gac acc gtc aag ggc ggc gac tac cgt   499
Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys Gly Gly Asp Tyr Arg
           120                 125                 130

ggt cgc gag tcc gac tgc tgg cgt ctc gcc gtc gag tcc gtc cgc gtc   547
Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val Glu Ser Val Arg Val
       135                 140                 145

atc gac cac atg aac gcc atc ggt gca cca ttc gcc cgc gaa tac ggt   595
Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe Ala Arg Glu Tyr Gly
   150                 155                 160                 165

ggc gcc ttg gca acc cgt tcc ttc ggt ggt gtg cag gtc tcc cgt acc   643
Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val Gln Val Ser Arg Thr
                   170                 175                 180

tac tac acc cgt gga caa acc gga cag cag ctg cag ttc tcc acc gca   691
Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu Gln Phe Ser Thr Ala
               185                 190                 195
```

```
tcc gca cta cag cgc cag atc cac ctc ggc tcc gta gaa atc ttc acc   739
Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser Val Glu Ile Phe Thr
        200                 205                 210

cat aac gaa atg gtt gac gtc att gtc acc gaa cgt aac ggt gaa aag   787
His Asn Glu Met Val Asp Val Ile Val Thr Glu Arg Asn Gly Glu Lys
    215                 220                 225

cgc tgc gaa ggc ctg atc atg cgc aac ctg atc acc ggc gag ctc acc   835
Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile Thr Gly Glu Leu Thr
230                 235                 240                 245

gca cac acc ggc cat gcc gtt atc ctg gca acc ggt ggc tac ggc aac   883
Ala His Thr Gly His Ala Val Ile Leu Ala Thr Gly Gly Tyr Gly Asn
                250                 255                 260

gtg tac cac atg tcc acc ctg gcc aag aac tcc aac gcc tcg gcc atc   931
Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser Asn Ala Ser Ala Ile
            265                 270                 275

atg cgt gca tac gaa gcc ggc gca tac ttc gcg tcc cca tcg ttc atc   979
Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala Ser Pro Ser Phe Ile
        280                 285                 290

cag ttc cac cca acc ggc ctg cct gtg aac tcc acc tgg cag tcc aag   1027
Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser Thr Trp Gln Ser Lys
    295                 300                 305

acc att ctg atg tcc gag tcg ctg cgt aac gac ggc cgc atc tgg tcc   1075
Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser
310                 315                 320                 325

cct aag gaa ccg aac gat aac cgc gat cca aac acc atc cct gag gat   1123
Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp
                330                 335                 340

gag cgc gac tac ttc ctg gag cgc cgc tac cca gca ttc ggt aac ctc   1171
Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu
            345                 350                 355

gtc cca cgt gac gtt gct tcc cgt gcg atc tcc cag cag atc aat gct   1219
Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala
        360                 365                 370

ggt ctc ggt gtt gga cct ctg aac aac gct gca tac ctg gac ttc cgc   1267
Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg
    375                 380                 385

gac gcc acc gag cgc ctc gga cag gac acc atc cgc gag cgt tac tcc   1315
Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser
390                 395                 400                 405

aac ctc ttc acc atg tac gaa gag gca att ggc gag gac cca tac tcc   1363
Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser
                410                 415                 420

agc cca atg cgt att gca ccg acc tgc cac ttc acc atg ggt ggc ctc   1411
Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu
            425                 430                 435
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tgg act gac ttc aac gaa atg acg tca ctc cca ggt ctg ttc tgc gca   1459
Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala
        440                 445                 450

ggc gaa gca tcc tgg acc tac cac ggt gca aac cgt ctg ggc gca aac   1507
Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn
    455                 460                 465

tcc ctg ctc tcc gct tcc gtc gat ggc tgg ttc acc ctg cca ttc acc   1555
Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr
470                 475                 480                 485

atc cct aac tac ctc ggc cca ttg ctt ggc tcc gag cgt ctg tca gag   1603
Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu
                490                 495                 500

gat gca cca gaa gca cag gca gcg att gcg cgt gca cag gct cgc att   1651
Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile
            505                 510                 515

gac cgc ctc atg ggc aac cgc cca gag tgg gtc ggt gac aac gtt cac   1699
Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val Gly Asp Asn Val His
        520                 525                 530

gga cct gag tac tac cac cgc cag ctt ggc gat atc ctg tac ttc tcc   1747
Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser
    535                 540                 545

tgt ggc gtt tcc cga aac gta gaa gac ctc cag gat ggc atc aac aag   1795
Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys
550                 555                 560                 565

atc cgt gcc ctc cgc gat gac ttc tgg aag aac atg cgc atc acc ggc   1843
Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly
                570                 575                 580

agc acc gat gag atg aac cag gtt ctc gaa tac gca gca cgc gta gcc   1891
Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala
            585                 590                 595

gac tac atc gac ctc ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc   1939
Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg
        600                 605                 610

gac gag tcc tgt ggc gct cac ttc cgc gac gac cac ctc tcc gaa gat   1987
Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp His Leu Ser Glu Asp
    615                 620                 625

ggc gaa gca caa cgt gac gac caa aac tgg tgc ttc gtc tcc gca tgg   2035
Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp
630                 635                 640                 645

gaa cca ggc gag aat gga acc ttc gtc tgc cac gca gaa cca ctg ttc   2083
Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe
                650                 655                 660

ttc gaa tct gtc cca ctg cag aca agg aac tac aag taatgaaact        2129
Phe Glu Ser Val Pro Leu Gln Thr Arg Asn Tyr Lys
            665                 670

tacacttgag atc                                                   2142
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09525760.090502

<210> 10
<211> 673
<212> PRT
<213> Corynebacterium glutamicum

<400> 10

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Met Ser Thr His Ser Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val
  1               5                  10                  15

Ser Val Leu Pro Glu Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu
             20                  25                  30

Pro Ala Gly Val Pro Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His
         35                  40                  45

Met Asn Leu Val Ser Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val
     50                  55                  60

Val Gly Thr Gly Leu Ser Gly Gly Ala Ala Ala Ala Ala Leu Gly Glu
 65                  70                  75                  80

Leu Gly Tyr Asp Val Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg
                 85                  90                  95

Ala His Ser Ile Ala Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys
            100                 105                 110

Lys Val Asp Asn Asp Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys
        115                 120                 125

Gly Gly Asp Tyr Arg Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val
    130                 135                 140

Glu Ser Val Arg Val Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe
145                 150                 155                 160

Ala Arg Glu Tyr Gly Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val
                165                 170                 175

Gln Val Ser Arg Thr Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu
            180                 185                 190

Gln Phe Ser Thr Ala Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser
        195                 200                 205

Val Glu Ile Phe Thr His Asn Glu Met Val Asp Val Ile Val Thr Glu
    210                 215                 220

Arg Asn Gly Glu Lys Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile
225                 230                 235                 240

Thr Gly Glu Leu Thr Ala His Thr Gly His Ala Val Ile Leu Ala Thr
                245                 250                 255

Gly Gly Tyr Gly Asn Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser
            260                 265                 270

Asn Ala Ser Ala Ile Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala
        275                 280                 285
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Ser Pro Ser Phe Ile Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser
    290                 295                 300

Thr Trp Gln Ser Lys Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp
305                 310                 315                 320

Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn
                325                 330                 335

Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro
            340                 345                 350

Ala Phe Gly Asn Leu Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser
        355                 360                 365

Gln Gln Ile Asn Ala Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala
    370                 375                 380

Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile
385                 390                 395                 400

Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly
                405                 410                 415

Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe
            420                 425                 430

Thr Met Gly Gly Leu Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro
        435                 440                 445

Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn
    450                 455                 460

Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe
465                 470                 475                 480

Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser
                485                 490                 495

Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg
            500                 505                 510

Ala Gln Ala Arg Ile Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val
        515                 520                 525

Gly Asp Asn Val His Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp
    530                 535                 540

Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln
545                 550                 555                 560

Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn
                565                 570                 575

Met Arg Ile Thr Gly Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr
            580                 585                 590

Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val
        595                 600                 605
```

Sequence Listing

```
Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp
    610                 615                 620

His Leu Ser Glu Asp Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys
625                 630                 635                 640

Phe Val Ser Ala Trp Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His
                645                 650                 655

Ala Glu Pro Leu Phe Phe Glu Ser Val Pro Leu Gln Thr Arg Asn Tyr
            660                 665                 670

Lys
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<210> 11
<211> 1100
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1077)
<223> FRXA01312

<400> 11

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gag tcg ctg cgt aac gac ggc cgc atc tgg tcc cct aag gaa ccg aac   48
Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn
  1               5                  10                  15

gat aac cgc gat cca aac acc atc cct gag gat gag cgc gac tac ttc   96
Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe
            20                  25                  30

ctg gag cgc cgc tac cca gca ttc ggt aac ctc gtc cca cgt gac gtt   144
Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val
        35                  40                  45

gct tcc cgt gcg atc tcc cag cag atc aat gct ggt ctc ggt gtt gga   192
Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly
    50                  55                  60

cct ctg aac aac gct gca tac ctg gac ttc cgc gac gcc acc gag cgc   240
Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg
65                  70                  75                  80

ctc gga cag gac acc atc cgc gag cgt tac tcc aac ctc ttc acc atg   288
Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met
                85                  90                  95

tac gaa gag gca att ggc gag gac cca tac tcc agc cca atg cgt att   336
Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile
            100                 105                 110

gca ccg acc tgc cac ttc acc atg ggt ggc ctc tgg act gac ttc aac   384
Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn
        115                 120                 125

gaa atg acg tca ctc cca ggt ctg ttc tgc gca ggc gaa gca tcc tgg   432
Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp
```

```
    130                 135                 140

acc tac cac ggt gca aac cgt ctg ggc gca aac tcc ctg ctc tcc gct   480
Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala
145                 150                 155                 160

tcc gtc gat ggc tgg ttc acc ctg cca ttc acc atc cct aac tac ctc   528
Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu
                165                 170                 175

ggc cca ttg ctt ggc tcc gag cgt ctg tca gag gat gca cca gaa gca   576
Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala
            180                 185                 190

cag gca gcg att gcg cgt gca cag gct cgc att gac cgc ctc atg ggc   624
Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly
        195                 200                 205

aac cgc cca gag tgg gtc ggt gac aac gtt cac gga cct gag tac tac   672
Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr
    210                 215                 220

cac cgc cag ctt ggc gat atc ctg tac ttc tcc tgt ggc gtt tcc cga   720
His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg
225                 230                 235                 240

aac gta gaa gac ctc cag gat ggc atc aac aag atc cgt gcc ctc cgc   768
Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg
                245                 250                 255

gat gac ttc tgg aag aac atg cgc atc acc ggc agc acc gat gag atg   816
Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met
            260                 265                 270

aac cag gtt ctc gaa tac gca gca cgc gta gcc gac tac atc gac ctc   864
Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu
        275                 280                 285

ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc gac gag tcc tgt ggc   912
Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly
    290                 295                 300

gct cac ttc cgc gac gac cac ctc tcc gaa gat ggc gaa gca caa cgt   960
Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg
305                 310                 315                 320

gac gac caa aac tgg tgc ttc gtc tcc gca tgg gaa cca ggc gag aat  1008
Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn
                325                 330                 335

gga acc ttc gtc tgc cac gca gaa cca ctg ttc ttc gaa tct gtc cca  1056
Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro
            340                 345                 350

ctg cag aca agg aac tac aag taatgaaact tacacttgag atc           1100
Leu Gln Thr Arg Asn Tyr Lys
        355
```

<210> 12
<211> 359

<212> PRT
<213> Corynebacterium glutamicum

<400> 12

```
Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn
 1               5                  10                  15

Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe
            20                  25                  30

Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val
        35                  40                  45

Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly
    50                  55                  60

Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg
65                  70                  75                  80

Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met
                85                  90                  95

Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile
            100                 105                 110

Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn
        115                 120                 125

Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp
    130                 135                 140

Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala
145                 150                 155                 160

Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu
                165                 170                 175

Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala
            180                 185                 190

Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly
        195                 200                 205

Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr
    210                 215                 220

His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg
225                 230                 235                 240

Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg
                245                 250                 255

Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met
            260                 265                 270

Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu
        275                 280                 285

Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly
    290                 295                 300
```

```
Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg
305                 310                 315                 320

Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn
                325                 330                 335

Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro
            340                 345                 350

Leu Gln Thr Arg Asn Tyr Lys
        355
```

<210> 13
<211> 1593
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1570)
<223> RXN00231

<400> 13

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caggactacc tcgacgccgg cgccaacttt gtccgagtcg gtgccgatgt ccagcaactc 60

aacgctgctg gatacgaaaa gtgaaggaaa ataacgcatc atg act att aat gtt   115
                                          Met Thr Ile Asn Val
                                            1               5

ttc gaa cta ctt gtc aaa agt ccc acg ggt cta ctg att ggt gat tcc   163
Phe Glu Leu Leu Val Lys Ser Pro Thr Gly Leu Leu Ile Gly Asp Ser
                10                  15                  20

tgg gtg gaa gca tcc gac ggc ggt act ttc gat gtg gaa aac cca gcg   211
Trp Val Glu Ala Ser Asp Gly Gly Thr Phe Asp Val Glu Asn Pro Ala
            25                  30                  35

acg ggt gaa aca atc gca acg ctc gcg tct gct act tcc gag gat gca   259
Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala Thr Ser Glu Asp Ala
        40                  45                  50

ctg gct gct ctt gat gct gca tgc gct gtt cag gcc gag tgg gct agg   307
Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln Ala Glu Trp Ala Arg
    55                  60                  65

atg cca gcg cgc gag cgt tct aat att tta cgc cgc ggt ttt gag ctc   355
Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg Arg Gly Phe Glu Leu
70                  75                  80                  85

gta gca gaa cgt gca gaa gag ttc gcc acc ctc atg acc ttg gaa atg   403
Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu Met Thr Leu Glu Met
                90                  95                  100

ggc aag cct ttg gct gaa gct cgc ggc gaa gtc acc tac ggc aac gaa   451
Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val Thr Tyr Gly Asn Glu
            105                 110                 115

ttc ctg cgc tgg ttc tct gag gaa gca gtt cgt ctg tat ggc cgt tac   499
Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg Leu Tyr Gly Arg Tyr
        120                 125                 130
```

```
gga acc aca cca gaa ggc aac ttg cgg atg ctg acc gcc ctc aag cca   547
Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu Thr Ala Leu Lys Pro
    135                 140                 145

gtt ggc ccg tgc ctc ctg atc acc cca tgg aac ttc cca cta gca atg   595
Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn Phe Pro Leu Ala Met
150                 155                 160                 165

gct acc cgc aag gtc gca cct gcg atc gct gca ggt tgt gtc atg gtg   643
Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala Gly Cys Val Met Val
                170                 175                 180

ctc aag cca gct cga ctt acc ccg ctg acc tcc cag tat ttt gct cag   691
Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser Gln Tyr Phe Ala Gln
            185                 190                 195

acc atg ctt gat gcc ggt ctt cca gca ggt gtc ctc aat gtg gtc tcc   739
Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val Leu Asn Val Val Ser
        200                 205                 210

ggt gct tcc gcc tct gcg att tcc aac ccg att atg gaa gac gat cgc   787
Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile Met Glu Asp Asp Arg
    215                 220                 225

ctt cgt aaa gtc tcc ttc acc ggc tcc acc cca gtt ggc cag cag ctg   835
Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro Val Gly Gln Gln Leu
230                 235                 240                 245

ctc aaa aag gct gcc gat aaa gtt ctg cgc acc tcc atg gaa ctt ggt   883
Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr Ser Met Glu Leu Gly
                250                 255                 260

ggc aac gca cct ttc att gtc ttc gag gac gcc gac cta gat ctc gcg   931
Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala Asp Leu Asp Leu Ala
            265                 270                 275

atc gaa ggt gcc atg ggt gcc aaa atg cgc aac atc ggc gaa gct tgc   979
Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn Ile Gly Glu Ala Cys
        280                 285                 290

acc gca gcc aac cgt ttc tta gtc cac gaa tcc gtc gcc gat gaa ttc   1027
Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser Val Ala Asp Glu Phe
    295                 300                 305

ggc cgt cgc ttc gct gcc cgc ctt gaa gag caa gtc cta ggc aac ggc   1075
Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln Val Leu Gly Asn Gly
310                 315                 320                 325

ctc gac gaa ggc gtc acc gtg ggc ccc ctg gtt gag gaa aaa gca cga   1123
Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val Glu Glu Lys Ala Arg
                330                 335                 340

gac agc gtt gca tcg ctt gtc gac gcc gcc gtc gcc gaa ggt gcc acc   1171
Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val Ala Glu Gly Ala Thr
            345                 350                 355

gtc ctc acc ggc ggc aag gcc ggc aca ggt gca ggc tac ttc tac gaa   1219
Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala Gly Tyr Phe Tyr Glu
        360                 365                 370
```

Sequence Listing

```
cca acg gtg ctc acg gga gtt tca aca gat gcg gct atc ctg aac gaa   1267
Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala Ala Ile Leu Asn Glu
    375                 380                 385

gag atc ttc ggt ccc gtc gca ccg atc gtc acc ttc caa acc gag gaa   1315
Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr Phe Gln Thr Glu Glu
390                 395                 400                 405

gaa gcc ctg cgt cta gcc aac tcc acc gaa tac gga ctg gcc tcc tat   1363
Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr Gly Leu Ala Ser Tyr
                410                 415                 420

gtg ttc acc cag gac acc tca cgt att ttc cgc gtc tcc gat ggt ctc   1411
Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg Val Ser Asp Gly Leu
            425                 430                 435

gag ttc ggc cta gtg ggc gtc aat tcc ggt gtc atc tct aac gct gct   1459
Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val Ile Ser Asn Ala Ala
        440                 445                 450

gca cct ttt ggt ggc gta aaa caa tcc gga atg ggc cgc gaa ggt ggt   1507
Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met Gly Arg Glu Gly Gly
    455                 460                 465

ctc gaa gga atc gag gag tac acc tcc gtg cag tac atc ggt atc cgg   1555
Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln Tyr Ile Gly Ile Arg
470                 475                 480                 485

gat cct tac gcc ggc tagcatctgc ccctttacaa atc                    1593
Asp Pro Tyr Ala Gly
                490
```

09605460.060202

<210> 14
<211> 490
<212> PRT
<213> Corynebacterium glutamicum

<400> 14

```
Met Thr Ile Asn Val Phe Glu Leu Leu Val Lys Ser Pro Thr Gly Leu
  1               5                  10                  15

Leu Ile Gly Asp Ser Trp Val Glu Ala Ser Asp Gly Gly Thr Phe Asp
             20                  25                  30

Val Glu Asn Pro Ala Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala
         35                  40                  45

Thr Ser Glu Asp Ala Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln
     50                  55                  60

Ala Glu Trp Ala Arg Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg
 65                  70                  75                  80

Arg Gly Phe Glu Leu Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu
                 85                  90                  95

Met Thr Leu Glu Met Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val
            100                 105                 110

Thr Tyr Gly Asn Glu Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg
```

```
        115                 120                 125

Leu Tyr Gly Arg Tyr Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu
    130                 135                 140

Thr Ala Leu Lys Pro Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn
145                 150                 155                 160

Phe Pro Leu Ala Met Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala
                165                 170                 175

Gly Cys Val Met Val Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser
            180                 185                 190

Gln Tyr Phe Ala Gln Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val
        195                 200                 205

Leu Asn Val Val Ser Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile
    210                 215                 220

Met Glu Asp Asp Arg Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro
225                 230                 235                 240

Val Gly Gln Gln Leu Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr
                245                 250                 255

Ser Met Glu Leu Gly Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala
            260                 265                 270

Asp Leu Asp Leu Ala Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn
        275                 280                 285

Ile Gly Glu Ala Cys Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser
    290                 295                 300

Val Ala Asp Glu Phe Gly Arg Arg Phe Ala Ala Arg Leu Glu Glu Gln
305                 310                 315                 320

Val Leu Gly Asn Gly Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val
                325                 330                 335

Glu Glu Lys Ala Arg Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val
            340                 345                 350

Ala Glu Gly Ala Thr Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala
        355                 360                 365

Gly Tyr Phe Tyr Glu Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala
    370                 375                 380

Ala Ile Leu Asn Glu Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr
385                 390                 395                 400

Phe Gln Thr Glu Glu Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr
                405                 410                 415

Gly Leu Ala Ser Tyr Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg
            420                 425                 430

Val Ser Asp Gly Leu Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val
        435                 440                 445
```

```
Ile Ser Asn Ala Ala Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met
    450                 455                 460

Gly Arg Glu Gly Gly Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln
465                 470                 475                 480

Tyr Ile Gly Ile Arg Asp Pro Tyr Ala Gly
                485                 490
```

<210> 15
<211> 870
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(847)
<223> RXA01311

<400> 15

```
tcgtctccgc atgggaacca ggcgagaatg gaaccttcgt ctgccacgca gaaccactgt 60

tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt   115
                                            Met Lys Leu Thr Leu
                                              1               5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc   163
Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
                 10                  15                  20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt   211
Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
             25                  30                  35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg   259
Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
         40                  45                  50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc   307
Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
     55                  60                  65

gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg   355
Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala
 70                  75                  80                  85

cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca   403
Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro
                 90                  95                 100

ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc   451
Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg
            105                 110                 115

tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac   499
Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn
        120                 125                 130

gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc   547
```

```
Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr
    135                 140                 145

gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt   595
Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys
150                 155                 160                 165

gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag   643
Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys
                170                 175                 180

ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg   691
Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu
            185                 190                 195

cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc   739
Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys
        200                 205                 210

tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg   787
Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu
    215                 220                 225

acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga   835
Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg
230                 235                 240                 245

ggc aaa gac gac tagtctttaa tccaagtaag tac                        870
Gly Lys Asp Asp
```

<210> 16
<211> 249
<212> PRT
<213> Corynebacterium glutamicum

<400> 16

```
Met Lys Leu Thr Leu Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu
  1               5                  10                  15

Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser
             20                  25                  30

Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly
         35                  40                  45

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
     50                  55                  60

Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
 65                  70                  75                  80

Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
                 85                  90                  95

Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
            100                 105                 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
        115                 120                 125
```

```
Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
    130                 135                 140

Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
145                 150                 155                 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
                165                 170                 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
            180                 185                 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
        195                 200                 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
    210                 215                 220

Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
225                 230                 235                 240

Arg Ala Ala Phe Arg Gly Lys Asp Asp
                245
```

Substitute Sheet (Rule 26)

<210> 17
<211> 1530
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1507)
<223> RXA01535

<400> 17

```
acccacctca ctctaggggt ggactccagt gtttcgcgac aacacaatga gtaagcttgt 60

gacagccgta tttaattctc agtaagaaat gagtgatttc atg acc gag cag gaa   115
                                            Met Thr Glu Gln Glu
                                              1               5

ttc cgt att gag cac gac acc atg ggt gaa gtg aag gtt cca gca aag   163
Phe Arg Ile Glu His Asp Thr Met Gly Glu Val Lys Val Pro Ala Lys
                 10                  15                  20

gct ctg tgg cag gca cag acc cag cgc gct gtt gag aac ttc cct atc   211
Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val Glu Asn Phe Pro Ile
             25                  30                  35

tct ggt cgt ggt ctg gaa tcc gca cag atc cgc gca atg ggt ctg ctg   259
Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg Ala Met Gly Leu Leu
         40                  45                  50

aag gca gct tgt gcg cag gta aac aag gac tcc ggt gcg ctg gat gca   307
Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser Gly Ala Leu Asp Ala
     55                  60                  65

gag aag gca gat gcc atc att gca gct ggt aag gag atc gcg tcc ggt   355
Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys Glu Ile Ala Ser Gly
```

```
 70                  75                  80                  85

aag cat gac gct gag ttc cca att gat gtg ttc cag act ggt tcc ggt   403
Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe Gln Thr Gly Ser Gly
                90                  95                 100

act tcc tcc aac atg aac acc aat gag gtt atc gct tcc atc gcg aag   451
Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile Ala Ser Ile Ala Lys
            105                 110                 115

gct aac ggc gtt gag gtt cac cca aat gac cac gtc aac atg ggt cag   499
Ala Asn Gly Val Glu Val His Pro Asn Asp His Val Asn Met Gly Gln
        120                 125                 130

tcc tcc aat gac acc ttc cct act gca act cac gtt gct gca acc gaa   547
Ser Ser Asn Asp Thr Phe Pro Thr Ala Thr His Val Ala Ala Thr Glu
    135                 140                 145

gct gct gtc aat gac ctc atc cca ggc ctg aag gtt ctg cac gag tct   595
Ala Ala Val Asn Asp Leu Ile Pro Gly Leu Lys Val Leu His Glu Ser
150                 155                 160                 165

ttg gcg aag aag gct aac gag tgg tct gag gtt gtt aag tcc ggc cgc   643
Leu Ala Lys Lys Ala Asn Glu Trp Ser Glu Val Val Lys Ser Gly Arg
                170                 175                 180

acc cac ctg atg gac gct gtt cca gta acc ctg ggc cag gag ttc ggt   691
Thr His Leu Met Asp Ala Val Pro Val Thr Leu Gly Gln Glu Phe Gly
            185                 190                 195

ggc tac gct cgc cag atc cag ctc ggc atc gag cgc gtt gag gct act   739
Gly Tyr Ala Arg Gln Ile Gln Leu Gly Ile Glu Arg Val Glu Ala Thr
        200                 205                 210

ctt cct cgc ctt ggt gag ctg gct att ggt ggc acc gct gct ggt acc   787
Leu Pro Arg Leu Gly Glu Leu Ala Ile Gly Gly Thr Ala Ala Gly Thr
    215                 220                 225

ggt atc aac acc tcc gct gat ttc ggc ggc aag gtt gtt gct gaa ctg   835
Gly Ile Asn Thr Ser Ala Asp Phe Gly Gly Lys Val Val Ala Glu Leu
230                 235                 240                 245

atc aac ttg acc gac gtc aag gag ctc aag gaa gct gag aac cac ttc   883
Ile Asn Leu Thr Asp Val Lys Glu Leu Lys Glu Ala Glu Asn His Phe
                250                 255                 260

gag gct cag gct gca cgc gac gct ctt gtt gag ttc tcc ggc gca atg   931
Glu Ala Gln Ala Ala Arg Asp Ala Leu Val Glu Phe Ser Gly Ala Met
            265                 270                 275

cgc gtt atc gct gtc tcc ttg tac aag atc gct aac gat atc cgc ctc   979
Arg Val Ile Ala Val Ser Leu Tyr Lys Ile Ala Asn Asp Ile Arg Leu
        280                 285                 290

atg ggc tcc ggc cca ctg acc ggt ctt ggc gag atc cgt ctc cca gac   1027
Met Gly Ser Gly Pro Leu Thr Gly Leu Gly Glu Ile Arg Leu Pro Asp
    295                 300                 305

ctg cag cca ggt tcc tcc atc atg cca ggc aag gtc aac cca gtt ctc   1075
Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Leu
310                 315                 320                 325
```

Sequence Listing

```
tgt gag acc gct acc cag gtt tcc gct cag gtt atc ggc aat gac gca   1123
Cys Glu Thr Ala Thr Gln Val Ser Ala Gln Val Ile Gly Asn Asp Ala
                330                 335                 340

gct gtt gcg ttc tcc ggc acc cag ggc cag ttc gag ctc aac gtg ttc   1171
Ala Val Ala Phe Ser Gly Thr Gln Gly Gln Phe Glu Leu Asn Val Phe
            345                 350                 355

atc cca gtg atg gct cgc aac gtg ctt gag tcc gct cgc ctg ctg gct   1219
Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser Ala Arg Leu Leu Ala
        360                 365                 370

aac act tcc cgc gtg ttc gca acc cgt ctc gtt gat ggc att gag cca   1267
Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val Asp Gly Ile Glu Pro
    375                 380                 385

aac gag gca cac atg aag gag ctc gct gag tct tca cct tcc atc gtt   1315
Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser Ser Pro Ser Ile Val
390                 395                 400                 405

acc cca ctg aac tct gca atc ggc tac gaa gct gct gca aag gtg gct   1363
Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala Ala Ala Lys Val Ala
                410                 415                 420

aag act gct ttg gct gag ggc aag acc atc cgc cag act gtc atc gat   1411
Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg Gln Thr Val Ile Asp
            425                 430                 435

ttg ggc ttg gtt gat ggc gag aag ctc acc gag gaa gag ctg gac aag   1459
Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu Glu Glu Leu Asp Lys
        440                 445                 450

cgc ctc gac gtt ctt gct atg gct cac acc gag cgc gag aac aag ttc   1507
Arg Leu Asp Val Leu Ala Met Ala His Thr Glu Arg Glu Asn Lys Phe
    455                 460                 465

taaaactaga acccgataaa taa                                        1530
```

<210> 18
<211> 469
<212> PRT
<213> Corynebacterium glutamicum

<400> 18

```
Met Thr Glu Gln Glu Phe Arg Ile Glu His Asp Thr Met Gly Glu Val
  1               5                  10                  15

Lys Val Pro Ala Lys Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val
            20                  25                  30

Glu Asn Phe Pro Ile Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg
        35                  40                  45

Ala Met Gly Leu Leu Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser
    50                  55                  60

Gly Ala Leu Asp Ala Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys
65                  70                  75                  80
```

```
Glu Ile Ala Ser Gly Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe
                 85                  90                  95

Gln Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile
            100                 105                 110

Ala Ser Ile Ala Lys Ala Asn Gly Val Glu Val His Pro Asn Asp His
        115                 120                 125

Val Asn Met Gly Gln Ser Ser Asn Asp Thr Phe Pro Thr Ala Thr His
    130                 135                 140

Val Ala Ala Thr Glu Ala Ala Val Asn Asp Leu Ile Pro Gly Leu Lys
145                 150                 155                 160

Val Leu His Glu Ser Leu Ala Lys Lys Ala Asn Glu Trp Ser Glu Val
                165                 170                 175

Val Lys Ser Gly Arg Thr His Leu Met Asp Ala Val Pro Val Thr Leu
            180                 185                 190

Gly Gln Glu Phe Gly Gly Tyr Ala Arg Gln Ile Gln Leu Gly Ile Glu
        195                 200                 205

Arg Val Glu Ala Thr Leu Pro Arg Leu Gly Glu Leu Ala Ile Gly Gly
    210                 215                 220

Thr Ala Ala Gly Thr Gly Ile Asn Thr Ser Ala Asp Phe Gly Gly Lys
225                 230                 235                 240

Val Val Ala Glu Leu Ile Asn Leu Thr Asp Val Lys Glu Leu Lys Glu
                245                 250                 255

Ala Glu Asn His Phe Glu Ala Gln Ala Ala Arg Asp Ala Leu Val Glu
            260                 265                 270

Phe Ser Gly Ala Met Arg Val Ile Ala Val Ser Leu Tyr Lys Ile Ala
        275                 280                 285

Asn Asp Ile Arg Leu Met Gly Ser Gly Pro Leu Thr Gly Leu Gly Glu
    290                 295                 300

Ile Arg Leu Pro Asp Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys
305                 310                 315                 320

Val Asn Pro Val Leu Cys Glu Thr Ala Thr Gln Val Ser Ala Gln Val
                325                 330                 335

Ile Gly Asn Asp Ala Ala Val Ala Phe Ser Gly Thr Gln Gly Gln Phe
            340                 345                 350

Glu Leu Asn Val Phe Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser
        355                 360                 365

Ala Arg Leu Leu Ala Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val
    370                 375                 380

Asp Gly Ile Glu Pro Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser
385                 390                 395                 400

Ser Pro Ser Ile Val Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala
```

```
                405                 410                 415

Ala Ala Lys Val Ala Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg
            420                 425                 430

Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu
        435                 440                 445

Glu Glu Leu Asp Lys Arg Leu Asp Val Leu Ala Met Ala His Thr Glu
    450                 455                 460

Arg Glu Asn Lys Phe
465
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<210> 19
<211> 1164
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1141)
<223> RXA00517

<400> 19

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ggtcttagaa ccagcgtgca ctgatggcga ttaaaggggg ttgcgcctat acctattgct 60

ggtatacatt tcggtatacc taaaccgaat tgagggattc atg cca gaa gtc act   115
                                            Met Pro Glu Val Thr
                                              1               5

gtc aac gcc caa caa ctc act gtt ctc tgc aca gac atc ctc acc aaa   163
Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr Asp Ile Leu Thr Lys
                10                  15                  20

act gga gta cct gca gca gac gcc cat ctt gtc ggt gat agt ttg gtg   211
Thr Gly Val Pro Ala Ala Asp Ala His Leu Val Gly Asp Ser Leu Val
            25                  30                  35

cag gct gat ctt tgg ggt cac ccc tcc cac ggt gtg ctt cga ctg cct   259
Gln Ala Asp Leu Trp Gly His Pro Ser His Gly Val Leu Arg Leu Pro
        40                  45                  50

tgg tat gtg cgc aga ctc cac agt ggc gcg atg act aca cat gca cac   307
Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met Thr Thr His Ala His
    55                  60                  65

gtg gag gtt ctc aat gat ttg ggt gcc gtg ttg gcg ttg gat gga cac   355
Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu Ala Leu Asp Gly His
70                  75                  80                  85

aat gga atc ggc caa gtt tta gct gat cat gct cgt aaa gaa gca gtg   403
Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala Arg Lys Glu Ala Val
                90                  95                  100

act agg gca atg atg ttc ggc atc ggt gcg gtg tcg gtg cgc aac tcc   451
Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val Ser Val Arg Asn Ser
            105                 110                 115

aat cat ttt gga act gcc atg tac tac acc cgg aaa gcg gca gcg caa   499
```

```
Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg Lys Ala Ala Ala Gln
        120                 125                 130

gga tgt gtt tcc att ctc acc acc aat gca tct ccg gcg atg gcg ccc   547
Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser Pro Ala Met Ala Pro
    135                 140                 145

tgg ggt ggc aga gaa aaa cgg atc ggt acc aac cca tgg tct att gcg   595
Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn Pro Trp Ser Ile Ala
150                 155                 160                 165

gca cct ttt gga gaa acg gct acg gta gtc gat ata gcc aat act gcg   643
Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp Ile Ala Asn Thr Ala
                170                 175                 180

gtt gcg cgc gga aag atc tac cac gca cga cag aca aac atg ccc att   691
Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln Thr Asn Met Pro Ile
            185                 190                 195

cct gag act tgg gcg atc acg agt gag ggc gca ccc acc acg gat cct   739
Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala Pro Thr Thr Asp Pro
        200                 205                 210

gct gag gca atc aac ggt gtc gtc ctt ccc atg gct ggt cac aaa ggt   787
Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met Ala Gly His Lys Gly
    215                 220                 225

tat gcg att agc ttc atg atg gat gtg ctt tct gga gtt ctc act ggt   835
Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser Gly Val Leu Thr Gly
230                 235                 240                 245

tcc cag cac agc acc aag gta cat ggt ccg tat gat ccc act ccc cca   883
Ser Gln His Ser Thr Lys Val His Gly Pro Tyr Asp Pro Thr Pro Pro
                250                 255                 260

ggt gga gct ggc cac ttg ttc atc gcg ttg gat gtt gca gcg ttt cgc   931
Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp Val Ala Ala Phe Arg
            265                 270                 275

gat cca caa gat ttc gat gac gca ctc agc gat ctg gtt ggg gaa gtt   979
Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp Leu Val Gly Glu Val
        280                 285                 290

aaa tcc act ccg aaa gca caa aac acc gag gag att ttc tac ccc ggt  1027
Lys Ser Thr Pro Lys Ala Gln Asn Thr Glu Glu Ile Phe Tyr Pro Gly
    295                 300                 305

gaa tcg gaa gac cgt gcg cat cgg aaa aac tct gcg cac ggt att tca  1075
Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser Ala His Gly Ile Ser
310                 315                 320                 325

ttg cct gaa aaa acg tgg atg gaa ctg caa gaa ctg gca atc gag aac  1123
Leu Pro Glu Lys Thr Trp Met Glu Leu Gln Glu Leu Ala Ile Glu Asn
                330                 335                 340

cat gtt gta act cac cgt tgatctgcgc gttaaacctg gcc                1164
His Val Val Thr His Arg
            345
```

<210> 20

<211> 347
<212> PRT
<213> Corynebacterium glutamicum

<400> 20

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Met Pro Glu Val Thr Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr
  1               5                  10                  15

Asp Ile Leu Thr Lys Thr Gly Val Pro Ala Ala Asp Ala His Leu Val
             20                  25                  30

Gly Asp Ser Leu Val Gln Ala Asp Leu Trp Gly His Pro Ser His Gly
         35                  40                  45

Val Leu Arg Leu Pro Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met
     50                  55                  60

Thr Thr His Ala His Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu
 65                  70                  75                  80

Ala Leu Asp Gly His Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala
                 85                  90                  95

Arg Lys Glu Ala Val Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val
            100                 105                 110

Ser Val Arg Asn Ser Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg
        115                 120                 125

Lys Ala Ala Ala Gln Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser
    130                 135                 140

Pro Ala Met Ala Pro Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn
145                 150                 155                 160

Pro Trp Ser Ile Ala Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp
                165                 170                 175

Ile Ala Asn Thr Ala Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln
            180                 185                 190

Thr Asn Met Pro Ile Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala
        195                 200                 205

Pro Thr Thr Asp Pro Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met
    210                 215                 220

Ala Gly His Lys Gly Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser
225                 230                 235                 240

Gly Val Leu Thr Gly Ser Gln His Ser Thr Lys Val His Gly Pro Tyr
                245                 250                 255

Asp Pro Thr Pro Pro Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp
            260                 265                 270

Val Ala Ala Phe Arg Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp
        275                 280                 285

Leu Val Gly Glu Val Lys Ser Thr Pro Lys Ala Gln Asn Thr Glu Glu
    290                 295                 300
```

```
Ile Phe Tyr Pro Gly Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser
305                 310                 315                 320

Ala His Gly Ile Ser Leu Pro Glu Lys Thr Trp Met Glu Leu Gln Glu
                325                 330                 335

Leu Ala Ile Glu Asn His Val Val Thr His Arg
            340                 345
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<210> 21
<211> 1107
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1084)
<223> RXA01350

<400> 21

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tgcagtatcg tcaagatcac ccaaaactgg tggctgttct cttttaagcg ggatagcatg 60

ggttcttaga ggacccccta caaggattga ggattgttta atg aat tcc ccg cag   115
                                          Met Asn Ser Pro Gln
                                            1               5

aac gtc tcc acc aag aag gtc acc gtc acc ggc gca gct ggt caa atc   163
Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly Ala Ala Gly Gln Ile
                10                  15                  20

tct tat tca ctg ttg tgg cgc atc gcc aac ggt gaa gta ttc ggc acc   211
Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu Val Phe Gly Thr
            25                  30                  35

gac acc cct gta gaa ctg aaa ctt ctg gag atc cct cag gct ctt ggc   259
Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile Pro Gln Ala Leu Gly
        40                  45                  50

ggg gca gag ggt gtg gct atg gaa ctt ctg gat tct gcc ttc ccc ctc   307
Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser Ala Phe Pro Leu
    55                  60                  65

ctg cga aac atc acc atc acc gcg gat gcc aat gag gca ttc gac ggc   355
Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn Glu Ala Phe Asp Gly
70                  75                  80                  85

gct aat gcg gcg ttt ttg gtc ggt gcg aag cct cgc gga aaa ggc gaa   403
Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Lys Gly Glu
                90                  95                  100

gag cgc gca gat ttg ctg gct aac aac ggc aag att ttc gga cct caa   451
Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys Ile Phe Gly Pro Gln
            105                 110                 115

ggt aaa gct atc aat gac aac gcc gca gat gac att cgt gtc cta gtt   499
Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile Arg Val Leu Val
        120                 125                 130

gtt gga aac cca gcg aac acc aac gcg ttg att gct tca gct gcg gcc   547
```

```
Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Ser Ala Ala Ala
    135                 140                 145

cca gat gtt cca gca tcc cgc ttc aac gca atg atg cgc ctt gat cac   595
Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met Met Arg Leu Asp His
150                 155                 160                 165

aac cgt gcg atc tcc cag ctg gcc acc aag ctt ggc cgt gga tct gcg   643
Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu Gly Arg Gly Ser Ala
                170                 175                 180

gaa ttt aac aac att gtg gtc tgg gga aat cac tcc gca acc cag ttc   691
Glu Phe Asn Asn Ile Val Val Trp Gly Asn His Ser Ala Thr Gln Phe
            185                 190                 195

cca gac atc acc tac gca acc gtt ggt gga gaa aag gtc act gac ctg   739
Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu Lys Val Thr Asp Leu
        200                 205                 210

gtt gat cac gat tgg tat gtg gag gag ttc att cct cgc gtg gct aac   787
Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile Pro Arg Val Ala Asn
    215                 220                 225

cgt ggc gct gaa atc att gag gtc cgt gga aag tct tct gca gct tct   835
Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala Ser
230                 235                 240                 245

gca gca tcc tct gcg att gat cac atg cgc gat tgg gta cag ggc acc   883
Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp Trp Val Gln Gly Thr
                250                 255                 260

gag gcg tgg tcc tct gcg gca att cct tcc acc ggt gca tac ggc att   931
Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr Gly Ala Tyr Gly Ile
            265                 270                 275

cct gag ggc att ttt gtc ggt ctg cca acc gta tcc cgc aac ggt gag   979
Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val Ser Arg Asn Gly Glu
        280                 285                 290

tgg gaa atc gtt gaa ggc ctg gag att tcc gat ttc cag cgc gcc cgc   1027
Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp Phe Gln Arg Ala Arg
    295                 300                 305

atc gac gcg aat gct cag gaa ttg cag gcc gag cgc gag gca gtg cgc   1075
Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu Arg Glu Ala Val Arg
310                 315                 320                 325

gac ttg ctc taatctttaa cgcatgactt cgc                            1107
Asp Leu Leu
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<210> 22
<211> 328
<212> PRT
<213> Corynebacterium glutamicum

<400> 22

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Met Asn Ser Pro Gln Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly
  1               5                  10                  15
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Ala Ala Gly Gln Ile Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly
            20                  25                  30

Glu Val Phe Gly Thr Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile
        35                  40                  45

Pro Gln Ala Leu Gly Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp
    50                  55                  60

Ser Ala Phe Pro Leu Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn
65                  70                  75                  80

Glu Ala Phe Asp Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro
                85                  90                  95

Arg Gly Lys Gly Glu Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys
            100                 105                 110

Ile Phe Gly Pro Gln Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp
        115                 120                 125

Ile Arg Val Leu Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile
    130                 135                 140

Ala Ser Ala Ala Ala Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met
145                 150                 155                 160

Met Arg Leu Asp His Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu
                165                 170                 175

Gly Arg Gly Ser Ala Glu Phe Asn Asn Ile Val Val Trp Gly Asn His
            180                 185                 190

Ser Ala Thr Gln Phe Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu
        195                 200                 205

Lys Val Thr Asp Leu Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile
    210                 215                 220

Pro Arg Val Ala Asn Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys
225                 230                 235                 240

Ser Ser Ala Ala Ser Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp
                245                 250                 255

Trp Val Gln Gly Thr Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr
            260                 265                 270

Gly Ala Tyr Gly Ile Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val
        275                 280                 285

Ser Arg Asn Gly Glu Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp
    290                 295                 300

Phe Gln Arg Ala Arg Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu
305                 310                 315                 320

Arg Glu Ala Val Arg Asp Leu Leu
                325
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<210> 23
<211> 1092
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1069)
<223> RXA02149

<400> 23
ttgcagagtg aaccacgatg atggttggac agctgttgat agctaatctt tgaaagatta 60

aattcaccta atcctgtgt agaacgcgag gggcactctt atg cca caa aaa ccg 115
Met Pro Gln Lys Pro
1 5

gcc agt ttc gcg gtg ggc ttt gac atc ggc ggc acc aac atg cga gcc 163
Ala Ser Phe Ala Val Gly Phe Asp Ile Gly Gly Thr Asn Met Arg Ala
10 15 20

ggg ctt gtc gac gaa tcc ggg cgc atc gtg acc agt ttg tcg gcg ccg 211
Gly Leu Val Asp Glu Ser Gly Arg Ile Val Thr Ser Leu Ser Ala Pro
25 30 35

tcg ccg cgc acg acg cag gca atg gaa cag ggg att ttt gat cta gtc 259
Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly Ile Phe Asp Leu Val
40 45 50

gaa cag ctc aag gcc gaa tac ccg gtt ggt gct gtg gga ctt gcc gtc 307
Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala Val Gly Leu Ala Val
55 60 65

gcg gga ttt ttg gat cct gag tgc gag gtt gtt cga ttt gcc ccg cac 355
Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val Arg Phe Ala Pro His
70 75 80 85

ctt cct tgg cgc gat gag cca gtg cgt gaa aag ttg gaa aac ctt ttg 403
Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys Leu Glu Asn Leu Leu
90 95 100

ggc ctg cct gtt cgt ttg gaa cat gat gcc aac tca gca gcg tgg ggt 451
Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn Ser Ala Ala Trp Gly
105 110 115

gag cat cgt ttt ggt gca gct caa ggc gct gac aac tgg gtt ttg ttg 499
Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp Asn Trp Val Leu Leu
120 125 130

gca ctc ggc act gga att ggt gca gcg ctg att gaa aaa ggc gaa att 547
Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile Glu Lys Gly Glu Ile
135 140 145

tac cgt ggt gca tat ggc acg gca cca gaa ttt ggt cat ttg cgt gtt 595
Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe Gly His Leu Arg Val
150 155 160 165

gtt cgt ggc gga cgc gca tgt gcg tgt ggc aaa gaa ggc tgc ctg gag 643
Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys Glu Gly Cys Leu Glu
170 175 180

```
cgt tac tgt tcc ggt act gcc ttg gtt tac act gcg cgt gaa ttg gct   691
Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr Ala Arg Glu Leu Ala
            185                 190                 195

tcg cat ggc tca ttc cgc aac agc ggg ctg ttt gac aag atc aaa gcc   739
Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe Asp Lys Ile Lys Ala
        200                 205                 210

gat ccg aat tcc atc aat gga aaa acg atc act gcg gca gcg cgc caa   787
Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr Ala Ala Ala Arg Gln
    215                 220                 225

gaa gac cca ctt gct ctc gcc gtt ctg gaa gat ttc agc gag tgg ctg   835
Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp Phe Ser Glu Trp Leu
230                 235                 240                 245

ggc gaa act ttg gcg atc att gct gat gtc ctt gac cca ggc atg atc   883
Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu Asp Pro Gly Met Ile
                250                 255                 260

atc att ggt ggc gga ctg tcc aat gct gcc gac ctt tat ttg gat cgc   931
Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp Leu Tyr Leu Asp Arg
            265                 270                 275

tcg gtc aac cac tat tcc acc cgc atc gtc ggc gca gga tat cgc cct   979
Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly Ala Gly Tyr Arg Pro
        280                 285                 290

ttg gca cgc gtt gcc aca gct cag ttg ggt gcg gat gct ggc atg atc   1027
Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala Asp Ala Gly Met Ile
    295                 300                 305

ggt gtc gct gat cta gct cga cgc tct gta gtg gaa gcc aac           1069
Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val Glu Ala Asn
310                 315                 320

taggtgtttt tcggtgggct gcg                                        1092
```

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<210> 24
<211> 323
<212> PRT
<213> Corynebacterium glutamicum

<400> 24

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Met Pro Gln Lys Pro Ala Ser Phe Ala Val Gly Phe Asp Ile Gly Gly
  1               5                  10                  15

Thr Asn Met Arg Ala Gly Leu Val Asp Glu Ser Gly Arg Ile Val Thr
             20                  25                  30

Ser Leu Ser Ala Pro Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly
         35                  40                  45

Ile Phe Asp Leu Val Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala
     50                  55                  60

Val Gly Leu Ala Val Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val
 65                  70                  75                  80

Arg Phe Ala Pro His Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys
```

```
                85                  90                  95

Leu Glu Asn Leu Leu Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn
            100                 105                 110

Ser Ala Ala Trp Gly Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp
        115                 120                 125

Asn Trp Val Leu Leu Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile
    130                 135                 140

Glu Lys Gly Glu Ile Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe
145                 150                 155                 160

Gly His Leu Arg Val Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys
                165                 170                 175

Glu Gly Cys Leu Glu Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr
            180                 185                 190

Ala Arg Glu Leu Ala Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe
        195                 200                 205

Asp Lys Ile Lys Ala Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr
    210                 215                 220

Ala Ala Ala Arg Gln Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp
225                 230                 235                 240

Phe Ser Glu Trp Leu Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu
                245                 250                 255

Asp Pro Gly Met Ile Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp
            260                 265                 270

Leu Tyr Leu Asp Arg Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly
        275                 280                 285

Ala Gly Tyr Arg Pro Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala
    290                 295                 300

Asp Ala Gly Met Ile Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val
305                 310                 315                 320

Glu Ala Asn
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<210> 25
<211> 1785
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1762)
<223> RXA01814

<400> 25
tgttaagcca ccctactccg tgaattttgc cgtatctcgt gcgcacaatt gcttttgagg 60

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ggaagatgaa gagaaagtat tggtgtttta aggagcaaac atg gca cat gaa cgc   115
                                            Met Ala His Glu Arg
                                              1               5

gcc ggg caa ctc gcc caa cca gaa gat ctc atc gat gtt gcg gaa ctg   163
Ala Gly Gln Leu Ala Gln Pro Glu Asp Leu Ile Asp Val Ala Glu Leu
                 10                  15                  20

gtc acc gca tat ttc acc cgc aag ccg gac gtg aac aac cct gat cag   211
Val Thr Ala Tyr Phe Thr Arg Lys Pro Asp Val Asn Asn Pro Asp Gln
             25                  30                  35

cag gtc gct ttc ggc acc tcc gga cac cgt ggc ttc gcg ctg gac agc   259
Gln Val Ala Phe Gly Thr Ser Gly His Arg Gly Phe Ala Leu Asp Ser
         40                  45                  50

gct ttc aac gag gac cac atc ctg gca acc acc cag gcg atc gtc gac   307
Ala Phe Asn Glu Asp His Ile Leu Ala Thr Thr Gln Ala Ile Val Asp
     55                  60                  65

tac cgc aac cag cag cca aaa aac tgg gtc ggc ccg ctg ttt atc ggc   355
Tyr Arg Asn Gln Gln Pro Lys Asn Trp Val Gly Pro Leu Phe Ile Gly
 70                  75                  80                  85

cgc gat acg cac gcg ctg tcc gaa cca gcg atg atc agc gcg ctt gag   403
Arg Asp Thr His Ala Leu Ser Glu Pro Ala Met Ile Ser Ala Leu Glu
                 90                  95                 100

gtc ctc att gcc aac gac gtc gaa gtg ctt gtc gac gcc gac ggc cgc   451
Val Leu Ile Ala Asn Asp Val Glu Val Leu Val Asp Ala Asp Gly Arg
             105                 110                 115

tac acc ccg acg ccc gca gtg tcc cac gcg atc cta cga cac aac gat   499
Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile Leu Arg His Asn Asp
         120                 125                 130

ggc atc atc ctt ggc acc gca gga ccc tcc cgc ccc tac gcc gac ggc   547
Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg Pro Tyr Ala Asp Gly
     135                 140                 145

atc gtg atc acc cca tcc cac aac cct cct cgt gat ggc gga ttc aaa   595
Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg Asp Gly Gly Phe Lys
150                 155                 160                 165

tac aac cca gcc aac ggt ggc cct gca gat acc gac gcc acc gac tgg   643
Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr Asp Ala Thr Asp Trp
                 170                 175                 180

atc gcc aac cgc gcc aac gat att ctg cgc ggc gac ctt gca gac gtg   691
Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly Asp Leu Ala Asp Val
             185                 190                 195

aag cga gtt cca gtt tcc ggt gtc ctc gac gag cgc acc act gcc tac   739
Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu Arg Thr Thr Ala Tyr
         200                 205                 210

gac ttc aag ggc att tac atc gct gac ctg cca aac gtg gtc aac atc   787
Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro Asn Val Val Asn Ile
     215                 220                 225

gat gcc atc cgc gaa gct ggt gtt cga atc ggc gca gac cca atg ggt   835
```

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Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly Ala Asp Pro Met Gly
230                 235                 240                 245

ggc gca tcc gtg gat tac tgg ggt gcc atc gca gaa acc cat ggc ctc   883
Gly Ala Ser Val Asp Tyr Trp Gly Ala Ile Ala Glu Thr His Gly Leu
                250                 255                 260

aac ctc acc gtg gtc aac cca cac gtt gat tcc acc ttc cgc ttc atg   931
Asn Leu Thr Val Val Asn Pro His Val Asp Ser Thr Phe Arg Phe Met
            265                 270                 275

aca ttg gac acc gac ggc aag atc cgc atg gac tgc tcc agc cca cac   979
Thr Leu Asp Thr Asp Gly Lys Ile Arg Met Asp Cys Ser Ser Pro His
        280                 285                 290

gca atg gca tcg ctg att gac aac cga gac aag ttc gat gtg gca acc   1027
Ala Met Ala Ser Leu Ile Asp Asn Arg Asp Lys Phe Asp Val Ala Thr
    295                 300                 305

ggc aac gac gcc gac gcc gac cgc cac ggc atc gtc acc cca gac gct   1075
Gly Asn Asp Ala Asp Ala Asp Arg His Gly Ile Val Thr Pro Asp Ala
310                 315                 320                 325

ggc ttg atg aac ccc aac cac tac ctc gca gta gca att gag tac ctc   1123
Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val Ala Ile Glu Tyr Leu
                330                 335                 340

ttt gct cac cgc cca ggt tgg tcc gca gat acc gca gtg ggc aaa acc   1171
Phe Ala His Arg Pro Gly Trp Ser Ala Asp Thr Ala Val Gly Lys Thr
            345                 350                 355

ctg gtc agc tcc tcc atg atc gac cgc gtt gtg gcg cag ctt ggc cgc   1219
Leu Val Ser Ser Ser Met Ile Asp Arg Val Val Ala Gln Leu Gly Arg
        360                 365                 370

acc ctc gtt gag gtt cca gtc gga ttc aag tgg ttt gtc cca ggt ttg   1267
Thr Leu Val Glu Val Pro Val Gly Phe Lys Trp Phe Val Pro Gly Leu
    375                 380                 385

atc tcc ggc gaa atc gga ttc ggt ggt gaa gaa tcc gca ggt gca tcc   1315
Ile Ser Gly Glu Ile Gly Phe Gly Gly Glu Glu Ser Ala Gly Ala Ser
390                 395                 400                 405

ttc ctc cgc atg gac ggc acc acc tgg tcc acc gac aag gac ggc ctc   1363
Phe Leu Arg Met Asp Gly Thr Thr Trp Ser Thr Asp Lys Asp Gly Leu
                410                 415                 420

atc ctt gac ctc ctg gca gct gag atc att gca gta acc ggc aag acc   1411
Ile Leu Asp Leu Leu Ala Ala Glu Ile Ile Ala Val Thr Gly Lys Thr
            425                 430                 435

cca tca cag cgc tac gca gaa ctc gcc gaa gaa ttc ggt gca cct gcc   1459
Pro Ser Gln Arg Tyr Ala Glu Leu Ala Glu Glu Phe Gly Ala Pro Ala
        440                 445                 450

tac gcc cgc acc gat gca gaa gcc aac cga gaa caa aag gcc atc ctg   1507
Tyr Ala Arg Thr Asp Ala Glu Ala Asn Arg Glu Gln Lys Ala Ile Leu
    455                 460                 465

aag gca ctg tcc cca gaa cag gtc acc gcc acc gaa cta gcc ggc gaa   1555
Lys Ala Leu Ser Pro Glu Gln Val Thr Ala Thr Glu Leu Ala Gly Glu
```

```
470                 475                 480                 485

gca atc acc gct aag ctc acc gaa gct ccc ggc aat ggc gca gcc atc   1603
Ala Ile Thr Ala Lys Leu Thr Glu Ala Pro Gly Asn Gly Ala Ala Ile
                490                 495                 500

gga gga cta aaa gtg acc acc gaa aac gcc tgg ttc gca gca cgc cca   1651
Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp Phe Ala Ala Arg Pro
            505                 510                 515

tcc ggc acc gaa gac aag tac aag atc tac gca gaa tcc ttc aag ggc   1699
Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala Glu Ser Phe Lys Gly
        520                 525                 530

gaa gag cac ctc gcc cag gtt cag aag gaa gcc caa gcg ttg gtc agc   1747
Glu Glu His Leu Ala Gln Val Gln Lys Glu Ala Gln Ala Leu Val Ser
    535                 540                 545

gaa gta ctc gga cag taaaactgcg gacttgctga caa                    1785
Glu Val Leu Gly Gln
550
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<210> 26
<211> 554
<212> PRT
<213> Corynebacterium glutamicum

<400> 26

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Met Ala His Glu Arg Ala Gly Gln Leu Ala Gln Pro Glu Asp Leu Ile
  1               5                  10                  15

Asp Val Ala Glu Leu Val Thr Ala Tyr Phe Thr Arg Lys Pro Asp Val
             20                  25                  30

Asn Asn Pro Asp Gln Gln Val Ala Phe Gly Thr Ser Gly His Arg Gly
         35                  40                  45

Phe Ala Leu Asp Ser Ala Phe Asn Glu Asp His Ile Leu Ala Thr Thr
     50                  55                  60

Gln Ala Ile Val Asp Tyr Arg Asn Gln Gln Pro Lys Asn Trp Val Gly
 65                  70                  75                  80

Pro Leu Phe Ile Gly Arg Asp Thr His Ala Leu Ser Glu Pro Ala Met
                 85                  90                  95

Ile Ser Ala Leu Glu Val Leu Ile Ala Asn Asp Val Glu Val Leu Val
            100                 105                 110

Asp Ala Asp Gly Arg Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile
        115                 120                 125

Leu Arg His Asn Asp Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg
    130                 135                 140

Pro Tyr Ala Asp Gly Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg
145                 150                 155                 160

Asp Gly Gly Phe Lys Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr
                165                 170                 175
```

Asp Ala Thr Asp Trp Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly
180 185 190

Asp Leu Ala Asp Val Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu
195 200 205

Arg Thr Thr Ala Tyr Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro
210 215 220

Asn Val Val Asn Ile Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly
225 230 235 240

Ala Asp Pro Met Gly Gly Ala Ser Val Asp Tyr Trp Gly Ala Ile Ala
245 250 255

Glu Thr His Gly Leu Asn Leu Thr Val Val Asn Pro His Val Asp Ser
260 265 270

Thr Phe Arg Phe Met Thr Leu Asp Thr Asp Gly Lys Ile Arg Met Asp
275 280 285

Cys Ser Ser Pro His Ala Met Ala Ser Leu Ile Asp Asn Arg Asp Lys
290 295 300

Phe Asp Val Ala Thr Gly Asn Asp Ala Asp Ala Asp Arg His Gly Ile
305 310 315 320

Val Thr Pro Asp Ala Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val
325 330 335

Ala Ile Glu Tyr Leu Phe Ala His Arg Pro Gly Trp Ser Ala Asp Thr
340 345 350

Ala Val Gly Lys Thr Leu Val Ser Ser Ser Met Ile Asp Arg Val Val
355 360 365

Ala Gln Leu Gly Arg Thr Leu Val Glu Val Pro Val Gly Phe Lys Trp
370 375 380

Phe Val Pro Gly Leu Ile Ser Gly Glu Ile Gly Phe Gly Gly Glu Glu
385 390 395 400

Ser Ala Gly Ala Ser Phe Leu Arg Met Asp Gly Thr Thr Trp Ser Thr
405 410 415

Asp Lys Asp Gly Leu Ile Leu Asp Leu Leu Ala Ala Glu Ile Ile Ala
420 425 430

Val Thr Gly Lys Thr Pro Ser Gln Arg Tyr Ala Glu Leu Ala Glu Glu
435 440 445

Phe Gly Ala Pro Ala Tyr Ala Arg Thr Asp Ala Glu Ala Asn Arg Glu
450 455 460

Gln Lys Ala Ile Leu Lys Ala Leu Ser Pro Glu Gln Val Thr Ala Thr
465 470 475 480

Glu Leu Ala Gly Glu Ala Ile Thr Ala Lys Leu Thr Glu Ala Pro Gly
485 490 495

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```
Asn Gly Ala Ala Ile Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp
            500                 505                 510

Phe Ala Ala Arg Pro Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala
        515                 520                 525

Glu Ser Phe Lys Gly Glu Glu His Leu Ala Gln Val Gln Lys Glu Ala
    530                 535                 540

Gln Ala Leu Val Ser Glu Val Leu Gly Gln
545                 550
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<210> 27
<211> 680
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(657)
<223> RXN02803

<400> 27

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gtc tct gga gag atg ctc gcg gca gca ctt tca gca ggc atg gcc agc   48
Val Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser
  1               5                  10                  15

cag ggt gtt gat gtc att cgt gtt ggt gtc atc cca acc cca gct gtt   96
Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val
             20                  25                  30

gca ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct  144
Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser
         35                  40                  45

gca tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca  192
Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala
     50                  55                  60

ggt gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt  240
Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val
 65                  70                  75                  80

atg gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt  288
Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg
                 85                  90                  95

gtc atc gaa gaa gca acc gat gca cag gac cgt tac cta gag cac ctg  336
Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu
            100                 105                 110

aag gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat  384
Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp
        115                 120                 125

gca gcc aat ggt gcg gca agt gtt gta gct cca acg gct tat gag gct  432
Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala
    130                 135                 140

gcg ggt gca act gta att gct att cat aac aag cca gac tca tac aac  480
```

```
Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn
145                 150                 155                 160

atc aac atg gac tgc ggt tcc acc cac att gat cag gcg cag ccg cca   528
Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro
                165                 170                 175

gtc ttg aag cac ggt gct gac ctt gga ctc gcg cat gac ggt gat gct   576
Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
            180                 185                 190

gac cgt tgt ttg gct gtg aac aag gat gcc aac ctt gtt gat ggt gac   624
Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp
        195                 200                 205

caa atc atg gcg ctg tta gcc att gcg atg aaa taaaacggcg agctgcgcaa 677
Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys
    210                 215

gaa                                                               680
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<210> 28
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 28

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Val Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser
  1               5                  10                  15

Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val
             20                  25                  30

Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser
         35                  40                  45

Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala
     50                  55                  60

Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val
 65                  70                  75                  80

Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg
                 85                  90                  95

Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu
            100                 105                 110

Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp
        115                 120                 125

Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala
    130                 135                 140

Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn
145                 150                 155                 160

Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro
                165                 170                 175
```

```
Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
            180                 185                 190

Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp
        195                 200                 205

Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys
    210                 215


<210> 29
<211> 399
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(399)
<223> FRXA02803

<400> 29
tct gga gag atg ctc gcg gca gca ctt tca gca ggc atg gcc agc cag   48
Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser Gln
  1               5                  10                  15

ggt gtt gat gtc att cgt gtt ggt gtc atc cca acc cca gct gtt gca   96
Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala
             20                  25                  30

ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct gca   144
Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala
         35                  40                  45

tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca ggt   192
Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly
     50                  55                  60

gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt atg   240
Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met
 65                  70                  75                  80

gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt gtc   288
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val
                 85                  90                  95

atc gaa gaa gca acc gat gca cag gac cgc tac cta gag cac ctg aag   336
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys
            100                 105                 110

gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat gca   384
Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala
        115                 120                 125

gcc aat ggt gcg gca                                              399
Ala Asn Gly Ala Ala
    130


<210> 30
<211> 133
<212> PRT
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<213> Corynebacterium glutamicum

<400> 30
Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser Gln
1 5 10 15

Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala
20 25 30

Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala
35 40 45

Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly
50 55 60

Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met
65 70 75 80

Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val
85 90 95

Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys
100 105 110

Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala
115 120 125

Ala Asn Gly Ala Ala
130

<210> 31
<211> 1713
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1690)
<223> RXN03076

<400> 31
aataccttte tgttttgtcc gcaggcgtat caggaaaacc tgcagcgcgg tagagtcgag 60

tctaatagtg atcccacgaa aacaaaggat cggggtgttc atg gac gag tct cgt 115
Met Asp Glu Ser Arg
1 5

cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg 163
Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala
10 15 20

cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt 211
Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val
25 30 35

gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg 259
Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu
40 45 50

gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat 307

```
Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp
     55                  60                  65

ggt ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat   355
Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His
 70                  75                  80                  85

act ttt gct gca acc act gcg gag gtg ttc gcg ggt gct ggt ttt gag   403
Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu
                 90                  95                 100

gtg acg ttg ctc ccc acg cct agc cct acg ccg ttg att ccg tgg ttg   451
Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro Leu Ile Pro Trp Leu
            105                 110                 115

gtg aac aag cat ggg ttg gat gcg ggc gtt cag atc acg gct tcg cat   499
Val Asn Lys His Gly Leu Asp Ala Gly Val Gln Ile Thr Ala Ser His
        120                 125                 130

aat ggt gcg gcg gac aat ggc tac aag gtg ttt ttg tct aat ggt cgc   547
Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe Leu Ser Asn Gly Arg
    135                 140                 145

cag ctt tat tct gaa ctg gag cct gag ctt gag gcg cat atc aat gct   595
Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu Ala His Ile Asn Ala
150                 155                 160                 165

gtg gaa gat ccg att cgg gtt cct cgg gtg acg gtg cgc ccc act gct   643
Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr Val Arg Pro Thr Ala
                170                 175                 180

gat cag ctg cgt cga tat gtt gat gag atg gtg tcg ttg gtg act cct   691
Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val Ser Leu Val Thr Pro
            185                 190                 195

gat cag gct gat ttg ttg cgg gtg aat tct gag cgg ggc aat ctt cgc   739
Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu Arg Gly Asn Leu Arg
        200                 205                 210

gtg gtg tat acc gct ctg cat ggt gtg ggt ggc cgc gcg atg gcc aat   787
Val Val Tyr Thr Ala Leu His Gly Val Gly Gly Arg Ala Met Ala Asn
    215                 220                 225

gct ttc caa ttt gct ggt ttt ccc cat act cat ggc gtg aag gct cag   835
Ala Phe Gln Phe Ala Gly Phe Pro His Thr His Gly Val Lys Ala Gln
230                 235                 240                 245

cag tat cct gat ccc acc ttc ccc act gtg gcg ttc ccc aat ccg gaa   883
Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala Phe Pro Asn Pro Glu
                250                 255                 260

gag cct tct gcg att gag ttg ttg ttg gaa cgc gca aag gaa aag aac   931
Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg Ala Lys Glu Lys Asn
            265                 270                 275

gct gac att ttg ttt gcg ctt gat cct gat gcc gat cgt tgt gct gtg   979
Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala Asp Arg Cys Ala Val
        280                 285                 290

ggt att cgt acc gct gat ggc ggc cac cga atg ctc tct ggc gat gag   1027
Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met Leu Ser Gly Asp Glu
```

Doc. Ref. 9595/2

```
    295                 300                 305

gtg ggc aca ctt ttg gct act cgt ttg gtt ccg gag tat tcc ggt gaa   1075
Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro Glu Tyr Ser Gly Glu
310                 315                 320                 325

ggc cca cgt ccc gtg gtt gcc acc acg gtg gtg tct tcg cag ctt ctg   1123
Gly Pro Arg Pro Val Val Ala Thr Thr Val Val Ser Ser Gln Leu Leu
                330                 335                 340

ggt atc atc gcc gag gat aaa ggg tgg gat tat tcc gag aca ctg acg   1171
Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr
            345                 350                 355

gga ttc aaa aat ctg tcg agg gct gcc gat ggt ctc gac gga ccg ctt   1219
Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly Leu Asp Gly Pro Leu
        360                 365                 370

gct ttc gct tat gag gaa gct gtg ggc acc tgc ccg gtt cca gat gtc   1267
Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val
    375                 380                 385

gtg ccg gat aag gac ggc atc tct aca gcg ttg ttc atg gcg tcg tgg   1315
Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp
390                 395                 400                 405

gct gcc gaa ctg aag gct cag ggc gca agc ctg cag caa aaa ctc aat   1363
Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn
                410                 415                 420

gag ttg tat cgc cga tat ggg tat ttt gcg tcc tcg caa att gct gtg   1411
Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val
            425                 430                 435

cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct   1459
Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro
        440                 445                 450

cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa   1507
Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu
    455                 460                 465

aaa cag ggc att gct ttg cat ggc cag gtg ggg cat gtg cat atc cgt   1555
Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg
470                 475                 480                 485

gct att ggt cga gtc tct gga act gag gcg aaa gcc aag ctc tat ttg   1603
Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu
                490                 495                 500

gaa gtt ggt cag gcc agc tcc cat gat gaa gca gct cag ttg ttg cat   1651
Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His
            505                 510                 515

cag ctg gag gat gaa gtc caa agc tgg ttg agc aag ctt tagtttcctg   1700
Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser Lys Leu
        520                 525                 530

gctgctcccg gtt                                                  1713
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<210> 32
<211> 530
<212> PRT
<213> Corynebacterium glutamicum

<400> 32

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Met Asp Glu Ser Arg Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala
 1               5                  10                  15

Pro Val Gly Pro Ala Arg His Gln Met Asn Val Leu Gln Val Thr Arg
            20                  25                  30

Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn
        35                  40                  45

Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala
    50                  55                  60

Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala
65                  70                  75                  80

Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala
                85                  90                  95

Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro
            100                 105                 110

Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
        115                 120                 125

Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe
    130                 135                 140

Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu
145                 150                 155                 160

Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr
                165                 170                 175

Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val
            180                 185                 190

Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu
        195                 200                 205

Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly
    210                 215                 220

Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His
225                 230                 235                 240

Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
                245                 250                 255

Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
            260                 265                 270

Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
        275                 280                 285

Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
```

```
    290                 295                 300

Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
305                 310                 315                 320

Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val
                325                 330                 335

Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr
            340                 345                 350

Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly
        355                 360                 365

Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys
    370                 375                 380

Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu
385                 390                 395                 400

Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu
                405                 410                 415

Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser
            420                 425                 430

Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His
        435                 440                 445

Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
    450                 455                 460

His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly
465                 470                 475                 480

His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
                485                 490                 495

Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
            500                 505                 510

Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
        515                 520                 525

Lys Leu
    530
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<210> 33
<211> 1684
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1684)
<223> FRXA02854

<400> 33
aataccttc tgttttgtcc gcaggcgtat caggaaaacc tgcagcgcgg tagagtcgag 60

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tctaatagtg atcccacgaa aacaaaggat cggggtgttc atg gac gag tct cgt   115
                                            Met Asp Glu Ser Arg
                                              1               5

cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg   163
Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala
                 10                  15                  20

cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt   211
Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val
             25                  30                  35

gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg   259
Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu
         40                  45                  50

gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat   307
Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp
     55                  60                  65

ggt ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat   355
Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His
 70                  75                  80                  85

act ttt gct gca acc act gcg gag gtg ttc gcg ggt gct ggt ttt gag   403
Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu
                 90                  95                 100

gtg acg ttg ctc ccc acg cct agc cct acg ccg ttg att ccg tgg ttg   451
Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro Leu Ile Pro Trp Leu
             105                 110                 115

gtg aac aag cat ggg ttg gat gcg ggc gtt cag atc acg gct tcg cat   499
Val Asn Lys His Gly Leu Asp Ala Gly Val Gln Ile Thr Ala Ser His
         120                 125                 130

aat ggt gcg gcg gac aat ggc tac aag gtg ttt ttg tct aat ggt cgc   547
Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe Leu Ser Asn Gly Arg
     135                 140                 145

cag ctt tat tct gaa ctg gag cct gag ctt gag gcg cat atc aat gct   595
Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu Ala His Ile Asn Ala
150                 155                 160                 165

gtg gaa gat ccg att cgg gtt cct cgg gtg acg gtg cgc ccc act gct   643
Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr Val Arg Pro Thr Ala
                170                 175                 180

gat cag ctg cgt cga tat gtt gat gag atg gtg tcg ttg gtg act cct   691
Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val Ser Leu Val Thr Pro
            185                 190                 195

gat cag gct gat ttg ttg cgg gtg aat tct gag cgg ggc aat ctt cgc   739
Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu Arg Gly Asn Leu Arg
        200                 205                 210

gtg gtg tat acc gct ctg cat ggt gtg ggt ggc cgc gcg atg gcc aat   787
Val Val Tyr Thr Ala Leu His Gly Val Gly Gly Arg Ala Met Ala Asn
    215                 220                 225

gct ttc caa ttt gct ggt ttt ccc cat act cat ggc gtg aag gct cag   835
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```
Ala Phe Gln Phe Ala Gly Phe Pro His Thr His Gly Val Lys Ala Gln
230                 235                 240                 245

cag tat cct gat ccc acc ttc ccc act gtg gcg ttc ccc aat ccg gaa   883
Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala Phe Pro Asn Pro Glu
                250                 255                 260

gag cct tct gcg att gag ttg ttg ttg gaa cgc gca aag gaa aag aac   931
Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg Ala Lys Glu Lys Asn
            265                 270                 275

gct gac att ttg ttt gcg ctt gat cct gat gcc gat cgt tgt gct gtg   979
Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala Asp Arg Cys Ala Val
        280                 285                 290

ggt att cgt acc gct gat ggc ggc cac cga atg ctc tct ggc gat gag   1027
Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met Leu Ser Gly Asp Glu
    295                 300                 305

gtg ggc aca ctt ttg gct act cgt ttg gtt ccg gag tat tcc ggt gaa   1075
Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro Glu Tyr Ser Gly Glu
310                 315                 320                 325

ggc cca cgt ccc gtg gtt gcc acc acg gtg gtg tct tcg cag ctt ctg   1123
Gly Pro Arg Pro Val Val Ala Thr Thr Val Val Ser Ser Gln Leu Leu
                330                 335                 340

ggt atc atc gcc gag gat aaa ggg tgg gat tat tcc gag aca ctg acg   1171
Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr
            345                 350                 355

gga ttc aaa aat ctg tcg agg gct gcc gat ggt ctc gac gga ccg ctt   1219
Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly Leu Asp Gly Pro Leu
        360                 365                 370

gct ttc gct tat gag gaa gct gtg ggc acc tgc ccg gtt cca gat gtc   1267
Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val
    375                 380                 385

gtg ccg gat aag gac ggc atc tct aca gcg ttg ttc atg gcg tcg tgg   1315
Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp
390                 395                 400                 405

gct gcc gaa ctg aag gct cag ggc gca agc ctg cag caa aaa ctc aat   1363
Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn
                410                 415                 420

gag ttg tat cgc cga tat ggg tat ttt gcg tcc tcg caa att gct gtg   1411
Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val
            425                 430                 435

cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct   1459
Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro
        440                 445                 450

cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa   1507
Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu
    455                 460                 465

aaa cag ggc att gct ttg cat ggc cag gtg ggg cat gtg cat atc cgt   1555
Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg
```

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470                 475                 480                 485

gct att ggt cga gtc tct gga act gag gcg aaa gcc aag ctc tat ttg   1603
Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu
                490                 495                 500

gaa gtt ggt cag gcc agc tcc cat gat gaa gca gct cag ttg ttg cat   1651
Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His
            505                 510                 515

cag ctg gag gat gaa gtc caa agc tgg ttg agc                       1684
Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
        520                 525
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<210> 34
<211> 528
<212> PRT
<213> Corynebacterium glutamicum

<400> 34

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Met Asp Glu Ser Arg Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala
  1               5                  10                  15

Pro Val Gly Pro Ala Arg His Gln Met Asn Val Leu Gln Val Thr Arg
             20                  25                  30

Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn
         35                  40                  45

Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala
     50                  55                  60

Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala
 65                  70                  75                  80

Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala
                 85                  90                  95

Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro
            100                 105                 110

Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
        115                 120                 125

Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe
    130                 135                 140

Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu
145                 150                 155                 160

Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr
                165                 170                 175

Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val
            180                 185                 190

Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu
        195                 200                 205

Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly Gly
```

09253-0020US

```
    210                 215                 220

Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His
225                 230                 235                 240

Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala
                245                 250                 255

Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Leu Glu Arg
            260                 265                 270

Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala
        275                 280                 285

Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met
    290                 295                 300

Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro
305                 310                 315                 320

Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val
                325                 330                 335

Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr
            340                 345                 350

Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly
        355                 360                 365

Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys
    370                 375                 380

Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu
385                 390                 395                 400

Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu
                405                 410                 415

Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser
            420                 425                 430

Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His
        435                 440                 445

Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
    450                 455                 460

His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly
465                 470                 475                 480

His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
                485                 490                 495

Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
            500                 505                 510

Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
        515                 520                 525
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Doc No. 1-0000000

<210> 35
<211> 536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(513)
<223> RXA00511

<400> 35
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gag ctg cgc aag aac acc ctc gtg ggc act gtc atg agc aac ctg gga   48
Glu Leu Arg Lys Asn Thr Leu Val Gly Thr Val Met Ser Asn Leu Gly
  1               5                  10                  15

ttg aag att gct atg gat gaa gcc gga att aca ctg cgt acc acc aag   96
Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys
            20                  25                  30

gta gga gac cgc tac gtg ctg gaa gac ctc aat gca ggt gga ttc agc   144
Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
        35                  40                  45

ctg ggc ggc gag caa tct ggc cac att gtt ctt cca gat cat ggc acc   192
Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
    50                  55                  60

act ggc gat gga act ttg act ggt ctt tcc atc atg gcg cgc atg gct   240
Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
65                  70                  75                  80

gaa acc gga aag tcc ttg ggc gag ttg gca caa gct atg acg gtg ctg   288
Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
                85                  90                  95

cca cag gtt ctg atc aat gtg cca gtt tcg gat aag tcc acc atc gtg   336
Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
            100                 105                 110

agc cac cca agc gtt gtg gct gcg atc gcg gaa gca gaa gct gag ttg   384
Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
        115                 120                 125

ggc gcc acc ggt cgc gtt ctt ctt cgt gct tct ggc acc gaa gag ctt   432
Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
    130                 135                 140

ttc cgc gtg atg gtt gag gct gga gac aag gaa caa gct cgt cgt atc   480
Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
145                 150                 155                 160

gcg gga cgt ctt gct gca gtg gtt gca gaa gtc taattcactt cagtcacagc 533
Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
                165                 170

gca                                                               536
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<210> 36

<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 36
Glu Leu Arg Lys Asn Thr Leu Val Gly Thr Val Met Ser Asn Leu Gly
1 5 10 15

Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys
20 25 30

Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
35 40 45

Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
50 55 60

Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
65 70 75 80

Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
85 90 95

Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
100 105 110

Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
115 120 125

Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
130 135 140

Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
145 150 155 160

Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
165 170

<210> 37
<211> 1497
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1474)
<223> RXN01365

<400> 37
cctgatcagg acgaatcata aggtttgcta ttcggattgg atcctttggc aggggtagga 60

ttgcaagcgt tattttgttc cctaacccct tcgaggattt atg cgt acc cgt gaa 115
Met Arg Thr Arg Glu
1 5

tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
10 15 20

gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211

```
Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
            25                  30                  35

cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac   259
Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
        40                  45                  50

atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg   307
Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
    55                  60                  65

act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat   355
Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
70                  75                  80                  85

gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt   403
Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
                90                  95                  100

act gcg tcg cat aac ccc gct gag tac aac ggc atc aag ttg tgt cgt   451
Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly Ile Lys Leu Cys Arg
            105                 110                 115

gcg ggt gct cgt ccg gtc ggt cag gat tct ggt ttg gcc aac atc att   499
Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly Leu Ala Asn Ile Ile
        120                 125                 130

gat gat ctg gtt gag ggt gtt cca gcg ttt gat ggt gag tca ggt tcg   547
Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp Gly Glu Ser Gly Ser
    135                 140                 145

gtt tct gag cag gat ttg ctg agc gca tat gcc gag tac ctc aat gag   595
Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala Glu Tyr Leu Asn Glu
150                 155                 160                 165

ctt gtt gat ctg aag aac atc cgc ccg atg aag gtt gct gtg gat gcg   643
Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys Val Ala Val Asp Ala
                170                 175                 180

gca aac ggc atg ggt ggg ttc act gtc cct gag gta ttc aag ggt ctg   691
Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu Val Phe Lys Gly Leu
            185                 190                 195

cca ctt gat gtt gcg cca ctg tat ttt gag ctt gac ggc aat ttc ccc   739
Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu Asp Gly Asn Phe Pro
        200                 205                 210

aac cat gag gcc aat cct ctg gag cct gcc aac ctg gtt gat ttg cag   787
Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn Leu Val Asp Leu Gln
    215                 220                 225

aag ttt acc gta gag acc gga tct gat atc ggt ttg gcg ttc gac ggc   835
Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly Leu Ala Phe Asp Gly
230                 235                 240                 245

gat gcg gat cgt tgc ttc gtg gtc gat gag aag ggc cag cca gtc agc   883
Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys Gly Gln Pro Val Ser
                250                 255                 260

cct tcg gcg atc tgt gcg atc gta gcg gag cgt tac ttg gag aag ctt   931
Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg Tyr Leu Glu Lys Leu
```

```
            265                 270                 275

ccg ggt tcc acc atc atc cac aac ctg att acc tct aag gct gtg cct   979
Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr Ser Lys Ala Val Pro
        280                 285                 290

gag gtg att gct gaa aac ggt ggc act gcg gtg cgt act cgc gtg ggt   1027
Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val Arg Thr Arg Val Gly
    295                 300                 305

cac tcc ttc atc aag gcg aag atg gca gag acc ggt gcg gcc ttt ggt   1075
His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr Gly Ala Ala Phe Gly
310                 315                 320                 325

ggc gag cac tct gcg cac tac tac ttc act gag ttc ttc aat gcg gac   1123
Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu Phe Phe Asn Ala Asp
                330                 335                 340

tcc ggc att ttg gct gcg atg cac gtg ctg gct gcg ctg gga agc cag   1171
Ser Gly Ile Leu Ala Ala Met His Val Leu Ala Ala Leu Gly Ser Gln
            345                 350                 355

gac cag cca ctc agt gag atg atg gct agg tat aac cgg tac gtt gct   1219
Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr Asn Arg Tyr Val Ala
        360                 365                 370

tca ggc gag ttg aac tcc cgt ttg gct aat gca gag gcg cag caa gag   1267
Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala Glu Ala Gln Gln Glu
    375                 380                 385

cgc acc cag gct gtg ctc gat gcg ttc gct gat cgc acc gag tcc gtg   1315
Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp Arg Thr Glu Ser Val
390                 395                 400                 405

gac acc ctt gac ggc gtg act gtg gaa ctc aag gac acc tcc gcg tgg   1363
Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys Asp Thr Ser Ala Trp
                410                 415                 420

ttc aac gtg cgt gcg tcc aac acc gag ccg ctg ctt cgc ctc aat gtt   1411
Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu Leu Arg Leu Asn Val
            425                 430                 435

gaa gct gca tcg aag gaa gaa gtc gat gcg ttg gta gcg gag att cta   1459
Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu Val Ala Glu Ile Leu
        440                 445                 450

ggg att atc cgc gca taatcccatt ttccggcggg cat                    1497
Gly Ile Ile Arg Ala
    455
```

Sequence Listing

<210> 38
<211> 458
<212> PRT
<213> Corynebacterium glutamicum

<400> 38

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Met Arg Thr Arg Glu Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val
  1               5                  10                  15

Arg Gly Val Val Gly Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr
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            20                  25                  30

Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
        35                  40                  45

Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
    50                  55                  60

Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
65                  70                  75                  80

Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
                85                  90                  95

Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
            100                 105                 110

Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
        115                 120                 125

Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
    130                 135                 140

Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
145                 150                 155                 160

Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
                165                 170                 175

Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
            180                 185                 190

Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
        195                 200                 205

Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
    210                 215                 220

Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
225                 230                 235                 240

Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
                245                 250                 255

Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
            260                 265                 270

Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
        275                 280                 285

Ser Lys Ala Val Pro Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val
    290                 295                 300

Arg Thr Arg Val Gly His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr
305                 310                 315                 320

Gly Ala Ala Phe Gly Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu
                325                 330                 335

Phe Phe Asn Ala Asp Ser Gly Ile Leu Ala Ala Met His Val Leu Ala
            340                 345                 350
```

```
Ala Leu Gly Ser Gln Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr
        355                 360                 365

Asn Arg Tyr Val Ala Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala
    370                 375                 380

Glu Ala Gln Gln Glu Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp
385                 390                 395                 400

Arg Thr Glu Ser Val Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys
                405                 410                 415

Asp Thr Ser Ala Trp Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu
            420                 425                 430

Leu Arg Leu Asn Val Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu
        435                 440                 445

Val Ala Glu Ile Leu Gly Ile Ile Arg Ala
    450                 455
```

<210> 39
<211> 994
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(994)
<223> FRXA01365

<400> 39

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cctgatcagg acgaatcata aggtttgcta ttcggattgg atcctttggc aggggtagga 60

ttgcaagcgt tattttgttc cctaacccct tcgaggattt atg cgt acc cgt gaa   115
                                              Met Arg Thr Arg Glu
                                                1               5

tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt   163
Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
                10                  15                  20

gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt   211
Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
            25                  30                  35

cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac   259
Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
        40                  45                  50

atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg   307
Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
    55                  60                  65

act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat   355
Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
70                  75                  80                  85

gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt   403
```

```
Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
                 90                  95                 100

act gcg tcg cat aac ccc gct gag tac aac ggc atc aag ttg tgt cgt   451
Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly Ile Lys Leu Cys Arg
            105                 110                 115

gcg ggt gct cgt ccg gtc ggt cag gat tct ggt ttg gcc aac atc att   499
Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly Leu Ala Asn Ile Ile
        120                 125                 130

gat gat ctg gtt gag ggt gtt cca gcg ttt gat ggt gag tca ggt tcg   547
Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp Gly Glu Ser Gly Ser
    135                 140                 145

gtt tct gag cag gat ttg ctg agc gca tat gcc gag tac ctc aat gag   595
Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala Glu Tyr Leu Asn Glu
150                 155                 160                 165

ctt gtt gat ctg aag aac atc cgc ccg atg aag gtt gct gtg gat gcg   643
Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys Val Ala Val Asp Ala
                170                 175                 180

gca aac ggc atg ggt ggg ttc act gtc cct gag gta ttc aag ggt ctg   691
Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu Val Phe Lys Gly Leu
            185                 190                 195

cca ctt gat gtt gcg cca ctg tat ttt gag ctt gac ggc aat ttc ccc   739
Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu Asp Gly Asn Phe Pro
        200                 205                 210

aac cat gag gcc aat cct ctg gag cct gcc aac ctg gtt gat ttg cag   787
Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn Leu Val Asp Leu Gln
    215                 220                 225

aag ttt acc gta gag acc gga tct gat atc ggt ttg gcg ttc gac ggc   835
Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly Leu Ala Phe Asp Gly
230                 235                 240                 245

gat gcg gat cgt tgc ttc gtg gtc gat gag aag ggc cag cca gtc agc   883
Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys Gly Gln Pro Val Ser
                250                 255                 260

cct tcg gcg atc tgt gcg atc gta gcg gag cgt tac ttg gag aag ctt   931
Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg Tyr Leu Glu Lys Leu
            265                 270                 275

ccg ggt tcc acc atc atc cac aac ctg att acc tct aag gct gtg cct   979
Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr Ser Lys Ala Val Pro
        280                 285                 290

gag gtg att gct gaa                                              994
Glu Val Ile Ala Glu
    295
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<210> 40
<211> 298
<212> PRT
<213> Corynebacterium glutamicum

<400> 40

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Met Arg Thr Arg Glu Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val
 1               5                  10                  15

Arg Gly Val Val Gly Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr
            20                  25                  30

Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
        35                  40                  45

Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
    50                  55                  60

Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
65                  70                  75                  80

Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
                85                  90                  95

Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
            100                 105                 110

Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
        115                 120                 125

Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
    130                 135                 140

Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
145                 150                 155                 160

Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
                165                 170                 175

Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
            180                 185                 190

Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
        195                 200                 205

Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
    210                 215                 220

Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
225                 230                 235                 240

Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
                245                 250                 255

Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
            260                 265                 270

Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
        275                 280                 285

Ser Lys Ala Val Pro Glu Val Ile Ala Glu
    290                 295
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<210> 41
<211> 1743

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1720)
<223> RXA00098

<400> 41
taaatttgtc gtgtttccca ctttgaacac tcttcgatgc gcttggccac aaaagcaagc 60

taacctgaag atgttattta acgacaataa aggagttttc atg gcg gac att tcg 115
Met Ala Asp Ile Ser
1 5

acc acc cag gtt tgg caa gac ctg acc gat cat tac tca aac ttc cag 163
Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His Tyr Ser Asn Phe Gln
10 15 20

gca acc act ctg cgt gaa ctt ttc aag gaa gaa aac cgc gcc gag aag 211
Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu Asn Arg Ala Glu Lys
25 30 35

tac acc ttc tcc gcg gct ggc ctc cac gtc gac ctg tcg aag aat ctg 259
Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp Leu Ser Lys Asn Leu
40 45 50

ctt gac gac gcc acc ctc acc aag ctc ctt gca ctg acc gaa gaa tct 307
Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala Leu Thr Glu Glu Ser
55 60 65

ggc ctt cgc gaa cgc att gac gcg atg ttt gcc ggt gaa cac ctc aac 355
Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala Gly Glu His Leu Asn
70 75 80 85

aac acc gaa gac cgc gct gtc ctc cac acc gcg ctg cgc ctt cct gcc 403
Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala Leu Arg Leu Pro Ala
90 95 100

gaa gct gat ctg tca gta gat ggc caa gat gtt gct gct gat gtc cac 451
Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val Ala Ala Asp Val His
105 110 115

gaa gtt ttg gga cgc atg cgt gac ttc gct act gcg ctg cgc tca ggc 499
Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr Ala Leu Arg Ser Gly
120 125 130

aac tgg ttg gga cac acc ggc cac acg atc aag aag atc gtc aac att 547
Asn Trp Leu Gly His Thr Gly His Thr Ile Lys Lys Ile Val Asn Ile
135 140 145

ggt atc ggt ggc tct gac ctc gga cca gcc atg gct acg aag gct ctg 595
Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met Ala Thr Lys Ala Leu
150 155 160 165

cgt gca tac gcg acc gct ggt atc tca gca gaa ttc gtc tcc aac gtc 643
Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu Phe Val Ser Asn Val
170 175 180

gac cca gca gac ctc gtt tct gtg ttg gaa gac ctc gat gca gaa tcc 691
Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp Leu Asp Ala Glu Ser

```
            185                 190                 195

aca ttg ttc gtg atc gct tcg aaa act ttc acc acc cag gag acg ctg   739
Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr Thr Gln Glu Thr Leu
        200                 205                 210

tcc aac gct cgt gca gct cgt gct tgg ctg gta gag aag ctc ggt gaa   787
Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val Glu Lys Leu Gly Glu
    215                 220                 225

gag gct gtc gcg aag cac ttc gtc gca gtg tcc acc aat gct gaa aag   835
Glu Ala Val Ala Lys His Phe Val Ala Val Ser Thr Asn Ala Glu Lys
230                 235                 240                 245

gtc gca gag ttc ggt atc gac acg gac aac atg ttc ggc ttc tgg gac   883
Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met Phe Gly Phe Trp Asp
                250                 255                 260

tgg gtc gga ggt cgt tac tcc gtg gac tcc gca gtt ggt ctt tcc ctc   931
Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala Val Gly Leu Ser Leu
            265                 270                 275

atg gca gtg atc ggc cct cgc gac ttc atg cgt ttc ctc ggt gga ttc   979
Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg Phe Leu Gly Gly Phe
        280                 285                 290

cac gcg atg gat gaa cac ttc cgc acc acc aag ttc gaa gag aac gtt   1027
His Ala Met Asp Glu His Phe Arg Thr Thr Lys Phe Glu Glu Asn Val
    295                 300                 305

cca atc ttg atg gct ctg ctc ggt gtc tgg tac tcc gat ttc tat ggt   1075
Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr Ser Asp Phe Tyr Gly
310                 315                 320                 325

gca gaa acc cac gct gtc cta cct tat tcc gag gat ctc agc cgt ttt   1123
Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu Asp Leu Ser Arg Phe
                330                 335                 340

gct gct tac ctc cag cag ctg acc atg gaa tca aat ggc aag tca gtc   1171
Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser Asn Gly Lys Ser Val
            345                 350                 355

cac cgc gac ggc tcc cct gtt tcc act ggc act ggc gaa att tac tgg   1219
His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr Gly Glu Ile Tyr Trp
        360                 365                 370

ggt gag cct ggc aca aat ggc cag cac gct ttc ttc cag ctg atc cac   1267
Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe Phe Gln Leu Ile His
    375                 380                 385

cag ggc act cgc ctt gtt cca gct gat ttc att ggt ttc gct cgt cca   1315
Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile Gly Phe Ala Arg Pro
390                 395                 400                 405

aag cag gat ctt cct gcc ggt gag cgc acc atg cat gac ctt ttg atg   1363
Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met His Asp Leu Leu Met
                410                 415                 420

agc aac ttc ttc gca cag acc aag gtt ttg gct ttc ggt aag aac gct   1411
Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala Phe Gly Lys Asn Ala
            425                 430                 435
```

CN 102965360 A 20130313

```
gaa gag atc gct gcg gaa ggt gtc gca cct gag ctg gtc aac cac aag   1459
Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu Leu Val Asn His Lys
        440                 445                 450

gtc atg cca ggt aat cgc cca acc acc acc att ttg gcg gag gaa ctt   1507
Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu Glu Leu
    455                 460                 465

acc cct tct att ctc ggt gcg ttg atc gct ttg tac gaa cac atc gtg   1555
Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Ile Val
470                 475                 480                 485

atg gtt cag ggc gtg att tgg gac atc aac tcc ttc gac caa tgg ggt   1603
Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly
                490                 495                 500

gtt gaa ctg ggc aaa cag cag gca aat gac ctc gct ccg gct gtc tct   1651
Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala Val Ser
            505                 510                 515

ggt gaa gag gat gtt gac tcg gga gat tct tcc act gat tca ctg att   1699
Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile
        520                 525                 530

aag tgg tac cgc gca aat agg tagtcgcttg cttatagggt cag             1743
Lys Trp Tyr Arg Ala Asn Arg
    535                 540
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<210> 42
<211> 540
<212> PRT
<213> Corynebacterium glutamicum

<400> 42

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Met Ala Asp Ile Ser Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His
  1               5                  10                  15

Tyr Ser Asn Phe Gln Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu
             20                  25                  30

Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp
         35                  40                  45

Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
     50                  55                  60

Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
 65                  70                  75                  80

Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
                 85                  90                  95

Leu Arg Leu Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
            100                 105                 110

Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr
        115                 120                 125

Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys
```

```
    130                 135                 140

Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met
145                 150                 155                 160

Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu
                165                 170                 175

Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp
            180                 185                 190

Leu Asp Ala Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr
        195                 200                 205

Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val
    210                 215                 220

Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser
225                 230                 235                 240

Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met
                245                 250                 255

Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala
            260                 265                 270

Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg
        275                 280                 285

Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys
    290                 295                 300

Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr
305                 310                 315                 320

Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu
                325                 330                 335

Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser
            340                 345                 350

Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr
        355                 360                 365

Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe
    370                 375                 380

Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile
385                 390                 395                 400

Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met
                405                 410                 415

His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala
            420                 425                 430

Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu
        435                 440                 445

Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile
    450                 455                 460
```

```
Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu
465                 470                 475                 480

Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser
                485                 490                 495

Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu
            500                 505                 510

Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser
        515                 520                 525

Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg
    530                 535                 540


<210> 43
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(630)
<223> RXA01989

<400> 43
gtt aaa tca att cac aaa aca att cat gaa ggt act ggt gca ggt agt   48
Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser
  1               5                  10                  15

gac ttc tta ggc tgg gtt gat tta cca gtt gat tac gac aaa gaa gaa   96
Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu
             20                  25                  30

ttt tca aga att gtt gaa gca tca aaa cgc att aaa gaa aat tct gat   144
Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
         35                  40                  45

gtt tta gta gtc atc ggt att ggt ggt tct tac tta ggt gca cgt gca   192
Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
     50                  55                  60

gca atc gaa atg tta acg tca tca ttt aga aac agc aat gaa tac cct   240
Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65                  70                  75                  80

gaa att gta ttt gtt ggt aat cac tta tca tca aca tat acg aaa gag   288
Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
                 85                  90                  95

tta gtt gat tat tta gca gac aaa gat ttc tct gta aac gtt att tct   336
Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
            100                 105                 110

aaa tct ggt aca act aca gaa cca gca gtt gca ttt aga ttg ttc aaa   384
Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
        115                 120                 125

caa tta gtt gaa gaa aga tac ggt aaa gaa gaa gca caa aaa cgt ata   432
```

```
Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
    130                 135                 140

ttt gca aca acg gat aaa gaa aaa ggt gct tta aaa cag ttg gct aca   480
Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
145                 150                 155                 160

aac gaa ggt tat gaa acg ttt atc gta cct gat gat gta ggt gga aga   528
Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
                165                 170                 175

tat tct gtt tta aca gca gta gga tta tta cca att gca aca gct gga   576
Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
            180                 185                 190

att aac atc gaa gct atg atg att ggt gct gca aaa gca cgt gaa gaa   624
Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
        195                 200                 205

tta tct                                                          630
Leu Ser
    210
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Sequence Listing

<210> 44
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 44

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Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser
  1               5                  10                  15

Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu
             20                  25                  30

Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
         35                  40                  45

Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
     50                  55                  60

Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65                  70                  75                  80

Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
                 85                  90                  95

Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
            100                 105                 110

Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
        115                 120                 125

Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
    130                 135                 140

Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
145                 150                 155                 160

Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
```

```
                165                 170                 175

Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
            180                 185                 190

Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
        195                 200                 205

Leu Ser
    210


<210> 45
<211> 1269
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1246)
<223> RXA00340

<400> 45
cggtatctcc gacatccgca acacccccaa agatgaggtt ccacagtgcc cagaatgtgg 60

ctcttacctc atcactgaca tctcttagaa agaccaccca gtg aaa tta gtc atc   115
                                            Val Lys Leu Val Ile
                                              1               5

gag gcc gac ggc ggc tcc cgc gga aac ccc ggc gtc gcc ggc tcc ggc   163
Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly Val Ala Gly Ser Gly
                  10                  15                  20

acc gtg gtg tac tcc gac aac aaa gca gaa gtt ctc aaa gaa atc gcc   211
Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val Leu Lys Glu Ile Ala
              25                  30                  35

tat gtt gtc gga aca aaa gcc acc aac aac gtc gcc gaa tac cgc gga   259
Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val Ala Glu Tyr Arg Gly
          40                  45                  50

cta ctc gaa ggc ctc aaa gca gcc cgc gag ctc ggc gct acc tcc gtg   307
Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu Gly Ala Thr Ser Val
      55                  60                  65

gat gtc tac atg gac tcc aaa ctt gtc gtt gaa caa atg tcc ggc cgg   355
Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu Gln Met Ser Gly Arg
  70                  75                  80                  85

tgg aaa atc aaa cac ccc gac atg aaa gtt cta gcg atc gaa gcc aag   403
Trp Lys Ile Lys His Pro Asp Met Lys Val Leu Ala Ile Glu Ala Lys
                  90                  95                 100

gag att gct tcc gaa atc ggg tcc gtt tct tat acg tgg att ccg cgt   451
Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr Thr Trp Ile Pro Arg
              105                 110                 115

gag aaa aac aaa cga gct gac gca ttg tcc aac gtg gcg atg gat gct   499
Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn Val Ala Met Asp Ala
          120                 125                 130
```

```
gca gcg gca ggt aag ccg gta ggt gtt gta ggg gat tct gct tct gta   547
Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly Asp Ser Ala Ser Val
    135                 140                 145

tct tct gct tct tcg gtt gcg ggc tca gag aaa gaa gac ctc aac tgc   595
Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys Glu Asp Leu Asn Cys
150                 155                 160                 165

acc gaa acc aaa ccc acc aac tgg aac ggc gca acc aca gat ccc act   643
Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala Thr Thr Asp Pro Thr
                170                 175                 180

cgt ttc ttg ttg ctt cgc cac ggc caa act gct atg tca gtg gca cgc   691
Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala Met Ser Val Ala Arg
            185                 190                 195

ctt tac tcc ggt agg tcc aac cca gag ctg tct gaa ctt ggt gaa aaa   739
Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser Glu Leu Gly Glu Lys
        200                 205                 210

caa gca gca gcg gca gca cga cga ctc gct caa acc ggt ggc atc gac   787
Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln Thr Gly Gly Ile Asp
    215                 220                 225

gct att gtg agt tct ccg ctc acc cgc acg atg caa acc gca gaa gca   835
Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met Gln Thr Ala Glu Ala
230                 235                 240                 245

gca gcg gcc gca ctg gga atg aaa gta cgt gtt atc gat gat ctc atc   883
Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val Ile Asp Asp Leu Ile
                250                 255                 260

gaa act gac ttt gga ctg tgg gat gga aaa tca ttt tca gaa gcc cac   931
Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser Phe Ser Glu Ala His
            265                 270                 275

gaa caa gat cca gaa ctg cac acc aag tgg ctc act gac tca tct gta   979
Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu Thr Asp Ser Ser Val
        280                 285                 290

gcc cca ccc ggt ggt gag tcc ctg cag acg gtt aat cga cgt gtg aaa   1027
Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val Asn Arg Arg Val Lys
    295                 300                 305

aag gct cgt gaa agc ctc caa cgc gaa tac ggt gca gcg aat gtt ttg   1075
Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly Ala Ala Asn Val Leu
310                 315                 320                 325

gtg gtc agc cac gtc acc cca atc aaa gcc atc atg agg caa gca ttg   1123
Val Val Ser His Val Thr Pro Ile Lys Ala Ile Met Arg Gln Ala Leu
                330                 335                 340

gac gca ggc cca tcc ttc ttt cag aag gca cac ctt gac ttg gcg tcg   1171
Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His Leu Asp Leu Ala Ser
            345                 350                 355

ctg tcg atc gca gag ttt tac gaa gac ggc cca acc tgc gta aga ctg   1219
Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro Thr Cys Val Arg Leu
        360                 365                 370

ttc aac gac acc tca cac ctg gaa gcg tgacgacagt ctgacggaag         1266
```

CN 102286294 A 2011.12.21

Phe Asn Asp Thr Ser His Leu Glu Ala
375 380

ctc 1269

<210> 46
<211> 382
<212> PRT
<213> Corynebacterium glutamicum

<400> 46
Val Lys Leu Val Ile Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly
1 5 10 15

Val Ala Gly Ser Gly Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val
20 25 30

Leu Lys Glu Ile Ala Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val
35 40 45

Ala Glu Tyr Arg Gly Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu
50 55 60

Gly Ala Thr Ser Val Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu
65 70 75 80

Gln Met Ser Gly Arg Trp Lys Ile Lys His Pro Asp Met Lys Val Leu
85 90 95

Ala Ile Glu Ala Lys Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr
100 105 110

Thr Trp Ile Pro Arg Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn
115 120 125

Val Ala Met Asp Ala Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly
130 135 140

Asp Ser Ala Ser Val Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys
145 150 155 160

Glu Asp Leu Asn Cys Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala
165 170 175

Thr Thr Asp Pro Thr Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala
180 185 190

Met Ser Val Ala Arg Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser
195 200 205

Glu Leu Gly Glu Lys Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln
210 215 220

Thr Gly Gly Ile Asp Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met
225 230 235 240

Gln Thr Ala Glu Ala Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val
245 250 255

Ile Asp Asp Leu Ile Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser

```
            260                 265                 270

Phe Ser Glu Ala His Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu
        275                 280                 285

Thr Asp Ser Ser Val Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val
    290                 295                 300

Asn Arg Arg Val Lys Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly
305                 310                 315                 320

Ala Ala Asn Val Leu Val Val Ser His Val Thr Pro Ile Lys Ala Ile
                325                 330                 335

Met Arg Gln Ala Leu Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His
            340                 345                 350

Leu Asp Leu Ala Ser Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro
        355                 360                 365

Thr Cys Val Arg Leu Phe Asn Asp Thr Ser His Leu Glu Ala
    370                 375                 380


<210> 47
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> RXA02492

<400> 47
gctgtacaac gacgctattg ccaacgaaaa tgtcgacggt gaaacgcatc acggctaagt 60

aaacgcgcgt cgtggaacat aaagtggcaa actagtacct atg act aac gga aaa   115
                                        Met Thr Asn Gly Lys
                                          1               5

ttg att ctt ctt cgt cac ggt cag agc gaa tgg aac gca tcc aac cag   163
Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp Asn Ala Ser Asn Gln
                10                  15                  20

ttc act gga tgg gtc gac gtc aat ctg acc gaa cag ggt gag gct gag   211
Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu Gln Gly Glu Ala Glu
            25                  30                  35

gcc aaa ggc gtc ctc cca ggc gtt gta tac acc tcc ttg ctg cgt cgc   259
Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr Ser Leu Leu Arg Arg
        40                  45                  50

gcg atc cgc act gca aac atc gca ctg aac gct gca gac cgc cac tgg   307
Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp
    55                  60                  65

atc cca gtg atc cgc gac tgg cgc ctc aac gag cgt cac tac ggc gca   355
Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala
70                  75                  80                  85
```

```
ctg cag ggc ctt gac aag gct gca acc aag gaa aaa tac ggc gac gac   403
Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu Lys Tyr Gly Asp Asp
                 90                  95                 100

cag ttc atg gaa tgg cgc cgc tcc tac gac acc cca cca cca gag ctc   451
Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu
            105                 110                 115

gcg gat gac gca gag tac tcc cag gca aat gac cct cgt tac gcg gac   499
Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp Pro Arg Tyr Ala Asp
        120                 125                 130

ctc gac gta gtt cca cgc acc gaa tgc ctc aag gac gtt gtg gtt cgt   547
Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys Asp Val Val Val Arg
    135                 140                 145

ttt gtt cct tac ttc gag gaa gaa atc ctg cca cgc gca aag aag ggc   595
Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro Arg Ala Lys Lys Gly
150                 155                 160                 165

gaa acc gtc ctc atc gca gca cac ggc aac tcc ctg cgt gcg ctg gtt   643
Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val
                170                 175                 180

aag cac ctt gac ggc atc tcc gat gct gat atc gca gag ctc aac atc   691
Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile
            185                 190                 195

cca acc ggc atc cca ctg gtc tac gaa atc gcc gaa gac ggt tcc gta   739
Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala Glu Asp Gly Ser Val
        200                 205                 210

gta aac cca ggc ggc acc tac ctc gat cct gag gca gca gca gcc ggc   787
Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly
    215                 220                 225

gca gca gca gta gca aac cag ggt aat aag tagctatttg taggtgagca     837
Ala Ala Ala Val Ala Asn Gln Gly Asn Lys
230                 235

ctc                                                               840
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<210> 48
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 48

```
Met Thr Asn Gly Lys Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp
  1               5                  10                  15

Asn Ala Ser Asn Gln Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu
             20                  25                  30

Gln Gly Glu Ala Glu Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr
         35                  40                  45

Ser Leu Leu Arg Arg Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala
     50                  55                  60
```

```
Ala Asp Arg His Trp Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu
 65                  70                  75                  80

Arg His Tyr Gly Ala Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu
                85                  90                  95

Lys Tyr Gly Asp Asp Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr
            100                 105                 110

Pro Pro Pro Glu Leu Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp
        115                 120                 125

Pro Arg Tyr Ala Asp Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys
    130                 135                 140

Asp Val Val Val Arg Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro
145                 150                 155                 160

Arg Ala Lys Lys Gly Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser
                165                 170                 175

Leu Arg Ala Leu Val Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile
            180                 185                 190

Ala Glu Leu Asn Ile Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala
        195                 200                 205

Glu Asp Gly Ser Val Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu
    210                 215                 220

Ala Ala Ala Ala Gly Ala Ala Ala Val Ala Asn Gln Gly Asn Lys
225                 230                 235


<210> 49
<211> 729
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)
<223> RXA00381

<400> 49
aaacctggtt tgtgtcttcc gctctcacgg acgatgattt ctccaagatc gagcaggcac 60

tcaagcccgc cgcacgtgca gcagcagaag cgaaggcatc atg acg caa acc att   115
                                              Met Thr Gln Thr Ile
                                                1               5

gtc cat cta gtt cgc cac ggc gaa gtc cac aac cca gag aaa atc ctg   163
Val His Leu Val Arg His Gly Glu Val His Asn Pro Glu Lys Ile Leu
                10                  15                  20

tac gga cgc atg ccc gga tac agg ttg tct tcc cgt gga cgc agc caa   211
Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser Arg Gly Arg Ser Gln
            25                  30                  35

gcc gcc cgc act gca gct tct ttt gaa ggc cac gat gtc acc tac att   259
Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His Asp Val Thr Tyr Ile
```

```
         40                  45                  50

gcg gcc tcc cca ttg cag cgt gtg cag gaa acc tcc gaa ccg ttc atc   307
Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr Ser Glu Pro Phe Ile
     55                  60                  65

aag gtc aca ggc cta gaa ctg atc acc gac gag gat ctt ctg gaa gca   355
Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu Asp Leu Leu Glu Ala
 70                  75                  80                  85

ggc aac cgt ttc gaa ggc ctg cgc acc aaa ggt tgg cgt tcc cag ttg   403
Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly Trp Arg Ser Gln Leu
                 90                  95                 100

tgg aac ccc gtg cgt tgg cct ttg atg tac aac ccc acg ctt ccc agc   451
Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn Pro Thr Leu Pro Ser
            105                 110                 115

tgg ggc gaa cac tac acc gac att ttg gaa aga atg atg gcg gct gtg   499
Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg Met Met Ala Ala Val
        120                 125                 130

gaa cga gct cgg gtg gca gcg gaa gga cac gaa gca atc ctg gtg acc   547
Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu Ala Ile Leu Val Thr
    135                 140                 145

cac cag ttg ccg atc gtg tgc gtg caa cgc cac gcc cgc gga caa agc   595
His Gln Leu Pro Ile Val Cys Val Gln Arg His Ala Arg Gly Gln Ser
150                 155                 160                 165

ctg tcc cat aac cca gcg acc agg caa tgc gac ctc gcc tca gtg aca   643
Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp Leu Ala Ser Val Thr
                170                 175                 180

tcc ttg gtg ttc caa gac gat caa att gtc ggc gtg cat tac aac gaa   691
Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly Val His Tyr Asn Glu
            185                 190                 195

cca gct cag gag att tgatcactcg tgcgtttgac caa                    729
Pro Ala Gln Glu Ile
        200
```

<210> 50
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 50

```
Met Thr Gln Thr Ile Val His Leu Val Arg His Gly Glu Val His Asn
  1               5                  10                  15

Pro Glu Lys Ile Leu Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser
             20                  25                  30

Arg Gly Arg Ser Gln Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His
         35                  40                  45

Asp Val Thr Tyr Ile Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr
     50                  55                  60
```

```
Ser Glu Pro Phe Ile Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu
 65                  70                  75                  80

Asp Leu Leu Glu Ala Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly
                85                  90                  95

Trp Arg Ser Gln Leu Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn
            100                 105                 110

Pro Thr Leu Pro Ser Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg
        115                 120                 125

Met Met Ala Ala Val Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu
    130                 135                 140

Ala Ile Leu Val Thr His Gln Leu Pro Ile Val Cys Val Gln Arg His
145                 150                 155                 160

Ala Arg Gly Gln Ser Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp
                165                 170                 175

Leu Ala Ser Val Thr Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly
            180                 185                 190

Val His Tyr Asn Glu Pro Ala Gln Glu Ile
        195                 200
```

<210> 51
<211> 822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(799)
<223> RXA02122

<400> 51
ggccttcagc tcaccgacag tttgtacatt tggtggaaga ctcacacccc acaccctaga 60

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ccttttttta agtgggcggt caggaatttt tcgcacaggt atg ctg cat gtc atg   115
                                                Met Leu His Val Met
                                                  1               5

aag ccg ggt tca cac gca gct gcc gaa aag act caa tcc act gtg gtt   163
Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr Gln Ser Thr Val Val
                 10                  15                  20

tta ctc att cgg cat ggg caa acc cca aca act ggt cag gtt ctg cct   211
Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr Gly Gln Val Leu Pro
             25                  30                  35

ggt cag acg ccg ggt tta cac ctg tct gat aag ggt gaa gag cag gcg   259
Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys Gly Glu Glu Gln Ala
         40                  45                  50

cgg gag gtg gca cag cgt ctg gcg gag gtg ccg att acc gct gtg tat   307
Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro Ile Thr Ala Val Tyr
     55                  60                  65
```

```
tca tcg ccg atg gag cgt gcg cag gaa aca gca gca ccg acg gtc agc   355
Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala Ala Pro Thr Val Ser
 70                  75                  80                  85

gct cat ggc ctc gag ttg acg gtg gaa cct ggg ctt att gaa tgc gat   403
Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly Leu Ile Glu Cys Asp
                90                  95                 100

ttc ggc gag tgg acg ggc cgg aaa cta act gag ctc aat gcc cta gag   451
Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu Leu Asn Ala Leu Glu
            105                 110                 115

gag tgg aaa gcg gtg cag aag aca ccg tct acc ttc agg ttt cca ggt   499
Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr Phe Arg Phe Pro Gly
        120                 125                 130

ggt gag agt ttc gtg gaa atg cag gat cgg atg gtg gag gct atc ggc   547
Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met Val Glu Ala Ile Gly
    135                 140                 145

aac att gcg cag cag cat ccg gga gaa atc gtt gct gcg ttt agt cat   595
Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val Ala Ala Phe Ser His
150                 155                 160                 165

gcc gac acg atc aag gct gcg gtg gct cat ttt gta ggc act cca ctg   643
Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe Val Gly Thr Pro Leu
                170                 175                 180

gat tct ttt cag cgc att ttc atc gac acg gcg tca att tcc gca gtg   691
Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala Ser Ile Ser Ala Val
            185                 190                 195

gaa ttt acc ggg aaa tct tca ggc gtc tcc tcc cat atg ctg ctg aca   739
Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser His Met Leu Leu Thr
        200                 205                 210

aat tcc aga aca gga tcg ttg gga tac ctt cga gac aaa ctt ccg aaa   787
Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg Asp Lys Leu Pro Lys
    215                 220                 225

gct ccg caa cca tgatcacctc accatttgag cgc                        822
Ala Pro Gln Pro
230
```

<210> 52
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 52

```
Met Leu His Val Met Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr
  1               5                  10                  15

Gln Ser Thr Val Val Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr
             20                  25                  30

Gly Gln Val Leu Pro Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys
         35                  40                  45

Gly Glu Glu Gln Ala Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro
```

```
     50                  55                  60

Ile Thr Ala Val Tyr Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala
 65                  70                  75                  80

Ala Pro Thr Val Ser Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly
                 85                  90                  95

Leu Ile Glu Cys Asp Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu
            100                 105                 110

Leu Asn Ala Leu Glu Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr
        115                 120                 125

Phe Arg Phe Pro Gly Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met
    130                 135                 140

Val Glu Ala Ile Gly Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val
145                 150                 155                 160

Ala Ala Phe Ser His Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe
                165                 170                 175

Val Gly Thr Pro Leu Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala
            180                 185                 190

Ser Ile Ser Ala Val Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser
        195                 200                 205

His Met Leu Leu Thr Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg
    210                 215                 220

Asp Lys Leu Pro Lys Ala Pro Gln Pro
225                 230
```

09625.0139

<210> 53
<211> 1161
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1138)
<223> RXA00206

<400> 53

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ttaaataaga tggtcagaga cagtttttg gcctgtcaac ccctgtgatt ctcttatttt 60

tgggtgattg ttccggcgcg ggtgttgtga tgggtttaat atg gaa gac atg cga   115
                                        Met Glu Asp Met Arg
                                          1               5

att gct act ctc acg tca ggc ggc gac tgc ccc gga cta aac gcc gtc   163
Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val
                 10                  15                  20

atc cga gga atc gtc cgc aca gcc agc aat gaa ttt ggc tcc acc gtc   211
Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val
             25                  30                  35
```

```
gtt ggt tat caa gac ggt tgg gaa gga ctg tta ggc gat cgt cgc gta   259
Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu Gly Asp Arg Arg Val
          40                  45                  50

cag ctg tat gac gat gaa gat att gac cga atc ctc ctt cga ggc ggc   307
Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly
     55                  60                  65

acc att ttg ggc act ggt cgc ctc cat ccg gac aag ttt aag gcc gga   355
Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys Ala Gly
 70                  75                  80                  85

att gat cag att aag gcc aac tta gaa gac gcc ggc atc gat gcc ctt   403
Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp Ala Leu
                 90                  95                 100

atc cca atc ggt ggc gaa gga acc ctg aag ggt gcc aag tgg ctg tct   451
Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ser
            105                 110                 115

gat aac ggt atc cct gtt gtc ggt gtc cca aag acc att gac aat gac   499
Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp
        120                 125                 130

gtg aat ggc act gac ttc acc ttc ggt ttc gat act gct gtg gca gtg   547
Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val Ala Val
    135                 140                 145

gct acc gac gct gtt gac cgc ctg cac acc acc gct gaa tct cac aac   595
Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser His Asn
150                 155                 160                 165

cgt gtg atg atc gtg gag gtc atg ggc cgc cac gtg ggt tgg att gct   643
Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala
                170                 175                 180

ctg cac gca ggt atg gcc ggc ggt gct cac tac acc gtt att cca gaa   691
Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu
            185                 190                 195

gta cct ttc gat att gca gag atc tgc aag gcg atg gaa cgt cgc ttc   739
Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg Arg Phe
        200                 205                 210

cag atg ggc gag aag tac ggc att atc gtc gtt gcg gaa ggt gcg ttg   787
Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu
    215                 220                 225

cca cgc gaa ggc acc atg gag ctt cgt gaa ggc cac att gac cag ttc   835
Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp Gln Phe
230                 235                 240                 245

ggt cac aag acc ttc acg gga att gga cag cag atc gct gat gag atc   883
Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Ile
                250                 255                 260

cac gtg cgc ctc ggc cac gat gtt cgt acg acc gtt ctt ggc cac att   931
His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile
            265                 270                 275

caa cgt ggt gga acc cca act gct ttc gac cgt gtt ctg gcc act cgt   979
```

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```
Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg
        280                 285                 290

tat ggt gtt cgt gca gct cgt gcg tgc cat gag gga agc ttt gac aag   1027
Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys
    295                 300                 305

gtt gtt gct ttg aag ggt gag agc att gag atg atc acc ttt gaa gaa   1075
Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu
310                 315                 320                 325

gca gtc gga acc ttg aag gaa gtt cca ttc gaa cgc tgg gtt act gcc   1123
Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val Thr Ala
                330                 335                 340

cag gca atg ttt gga tagtttttcg ggcttttatc aac                    1161
Gln Ala Met Phe Gly
            345
```

<210> 54
<211> 346
<212> PRT
<213> Corynebacterium glutamicum

<400> 54

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Met Glu Asp Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro
  1               5                  10                  15

Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu
             20                  25                  30

Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu
         35                  40                  45

Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
     50                  55                  60

Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
 65                  70                  75                  80

Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala
                 85                  90                  95

Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
            100                 105                 110

Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
        115                 120                 125

Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
    130                 135                 140

Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr
145                 150                 155                 160

Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
                165                 170                 175

Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
            180                 185                 190
```

```
Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala
        195                 200                 205

Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val
    210                 215                 220

Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly
225                 230                 235                 240

His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln
                245                 250                 255

Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr
            260                 265                 270

Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg
        275                 280                 285

Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu
    290                 295                 300

Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met
305                 310                 315                 320

Ile Thr Phe Glu Glu Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu
                325                 330                 335

Arg Trp Val Thr Ala Gln Ala Met Phe Gly
            340                 345
```

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<210> 55
<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> RXA01243

<400> 55
gcgcaatcag cgatatcgat gtggtggtca ccgatgcggg tgcaccagca agtttcgttg 60

agcagttgcg agaacgcgat gtagaagttg tgattgcaga atg att ctt aca gtc 115
Met Ile Leu Thr Val
1 5

act gca agt ccg tat ctg ttg agc acc aat gag ctt gac ggc acc atc 163
Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu Leu Asp Gly Thr Ile
10 15 20

gaa att ggc gaa gca aac aaa atc cgg cag gtt tcc act gtt gcc ggt 211
Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val Ser Thr Val Ala Gly
25 30 35

ggt ttt ggc acc ggt gtg gct gcc acc ttg ttt tat ggc ggc aat gaa 259
Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe Tyr Gly Gly Asn Glu
40 45 50

```
act ttt gca gtt ttt ccc gct cca gaa atc tct cat tac atg cgc ctg   307
Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser His Tyr Met Arg Leu
     55                  60                  65

gtg acg ttt gct ggg ttg cct cat gaa att att ccg gtg gca ggt ccc   355
Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile Pro Val Ala Gly Pro
 70                  75                  80                  85

atc ccc atg cat ttg acc atg cgt gat gca gag ggc aat gag act aag   403
Ile Pro Met His Leu Thr Met Arg Asp Ala Glu Gly Asn Glu Thr Lys
                 90                  95                 100

ttc aaa gac tcc ccc atg cct ttg gat gtg tcc cag ttg gca att ctt   451
Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser Gln Leu Ala Ile Leu
            105                 110                 115

cgt gat cta gtg gtg cgt cga gcc gaa gat gcc gcg tgg gtg ttg ttg   499
Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala Ala Trp Val Leu Leu
        120                 125                 130

ggt ggc aat ttg ccg tct atc gcg cct gct gcg tgg ttt gtg gat gtg   547
Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala Trp Phe Val Asp Val
    135                 140                 145

gtg aga tca ctt cgc ttg tac cac cct cat gtg aag gta gct atc gca   595
Val Arg Ser Leu Arg Leu Tyr His Pro His Val Lys Val Ala Ile Ala
150                 155                 160                 165

gca act ggt gct gcg ttg cgt gcg gtt att cga cag ctt gca gct acg   643
Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg Gln Leu Ala Ala Thr
                170                 175                 180

tcc ccg gat gcg ctg att gtg gct gcg gaa gaa atc gaa att gcc act   691
Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu Ile Glu Ile Ala Thr
            185                 190                 195

gga tta gaa ccc aaa acc ttg aga ggt cca tgg gta gag gga gat ctc   739
Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp Val Glu Gly Asp Leu
        200                 205                 210

tcc ccg act gtg gcg gca gcg cgc gct tta att gat agc ggt gtc acc   787
Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile Asp Ser Gly Val Thr
    215                 220                 225

gag gtg ttg gtt acc aac aag cgg acg gaa tct ttg tat gtt tcc gag   835
Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser Leu Tyr Val Ser Glu
230                 235                 240                 245

tct gaa tca ctg tta gcc agc tac gac agc acc cct ggt aag cag ggc   883
Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr Pro Gly Lys Gln Gly
                250                 255                 260

gtg aat tgg cgg gaa tct ttt act gca gga ttc ttg gca gca tcc aat   931
Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe Leu Ala Ala Ser Asn
            265                 270                 275

gat gga aaa tcc act gag gac agc gtg atc aac gcg gtt gct tac gcc   979
Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn Ala Val Ala Tyr Ala
        280                 285                 290

aac gct gaa ggc agt gag tgg gac aac tac att ccc aca ccc gat aag  1027
```

```
Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile Pro Thr Pro Asp Lys
    295                 300                 305

ctt cgg gcg gag cac gtg gtc atc aaa tcg ctt tagaccacgc aaaaagcctc 1080
Leu Arg Ala Glu His Val Val Ile Lys Ser Leu
310                 315                 320

aaa                                                               1083


<210> 56
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 56
Met Ile Leu Thr Val Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu
  1               5                  10                  15

Leu Asp Gly Thr Ile Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val
            20                  25                  30

Ser Thr Val Ala Gly Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe
        35                  40                  45

Tyr Gly Gly Asn Glu Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser
    50                  55                  60

His Tyr Met Arg Leu Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile
65                  70                  75                  80

Pro Val Ala Gly Pro Ile Pro Met His Leu Thr Met Arg Asp Ala Glu
                85                  90                  95

Gly Asn Glu Thr Lys Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser
            100                 105                 110

Gln Leu Ala Ile Leu Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala
        115                 120                 125

Ala Trp Val Leu Leu Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala
    130                 135                 140

Trp Phe Val Asp Val Val Arg Ser Leu Arg Leu Tyr His Pro His Val
145                 150                 155                 160

Lys Val Ala Ile Ala Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg
                165                 170                 175

Gln Leu Ala Ala Thr Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu
            180                 185                 190

Ile Glu Ile Ala Thr Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp
        195                 200                 205

Val Glu Gly Asp Leu Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile
    210                 215                 220

Asp Ser Gly Val Thr Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser
225                 230                 235                 240
```

Sequence Listing

```
Leu Tyr Val Ser Glu Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr
                245                 250                 255

Pro Gly Lys Gln Gly Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe
            260                 265                 270

Leu Ala Ala Ser Asn Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn
        275                 280                 285

Ala Val Ala Tyr Ala Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile
    290                 295                 300

Pro Thr Pro Asp Lys Leu Arg Ala Glu His Val Val Ile Lys Ser Leu
305                 310                 315                 320
```

<210> 57
<211> 1113
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1090)
<223> RXA01882

<400> 57

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acccttttttc caccttggct gattttgatg cccttgttac cgatgaccac acgctagatt 60

ttccagtttt gcccgaccac aactttcagg tggtaacccc atg atc atc aca ttc   115
                                            Met Ile Ile Thr Phe
                                              1               5

acc cca aac ccg agt att gat tcc acg ctg tcg ctc ggc gaa gag ctc   163
Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser Leu Gly Glu Glu Leu
                10                  15                  20

tcc cgt gga tcc gtc caa cga ctt gat tcc gtc acc gct gtc gca ggt   211
Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val Thr Ala Val Ala Gly
            25                  30                  35

ggt aaa ggc atc aat gtc gcc cac gct gtc ttg ctt gcg ggc ttt gaa   259
Gly Lys Gly Ile Asn Val Ala His Ala Val Leu Leu Ala Gly Phe Glu
        40                  45                  50

acc ttg gct gtg ttc cca gcc ggc aag ctc gac ccc ttc gtc cca ctg   307
Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp Pro Phe Val Pro Leu
    55                  60                  65

gtc cgc gac atc ggc ttg ccc gtg gaa act gtt gtg atc aac aag aac   355
Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val Val Ile Asn Lys Asn
70                  75                  80                  85

gtc cgc acc aac acc aca gtc acc gaa ccg gac ggc acc acc acc aag   403
Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp Gly Thr Thr Thr Lys
                90                  95                  100

ctc aac ggc ccc ggc gcg ccg ctc agc gag cag aag ctc cgt agc ttg   451
```

```
Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln Lys Leu Arg Ser Leu
            105                 110                 115

gaa aag gtg ctt atc gac gcg ctc cgc ccc gaa gtc acc tgg gtt gtc   499
Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu Val Thr Trp Val Val
        120                 125                 130

ctg gcg ggc tcg ctg cca cca ggg gca cca gtt gac tgg tac gcg cgt   547
Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val Asp Trp Tyr Ala Arg
    135                 140                 145

ctc acc gcg ttg atc cat tca gca cgc cct gac gtt cgc gtg gct gtc   595
Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp Val Arg Val Ala Val
150                 155                 160                 165

gat acc tca gac aag cca ctg atg gcg ttg ggc gag agc ttg gat aca   643
Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly Glu Ser Leu Asp Thr
                170                 175                 180

cct ggc gct gct ccg aac ctg att aag cca aat ggt ctg gaa ctg ggc   691
Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn Gly Leu Glu Leu Gly
            185                 190                 195

cag ctg gct aac act gat ggt gaa gag ctg gag gcg cgt gct gcg caa   739
Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu Ala Arg Ala Ala Gln
        200                 205                 210

ggc gat tac gac gcc atc atc gca gct gcg gac gta ctg gtt aac cgt   787
Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp Val Leu Val Asn Arg
    215                 220                 225

ggc atc gaa cag gtg ctt gtc acc ttg ggt gcc gca gga gcg gtg ttg   835
Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala Ala Gly Ala Val Leu
230                 235                 240                 245

gtc aac gca gaa ggt gcg tgg act gct act tct cca aag att gat gtt   883
Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser Pro Lys Ile Asp Val
                250                 255                 260

gta tcc acc gtt gga gct gga gac tgt gct ctt gca ggt ttt gtt atg   931
Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu Ala Gly Phe Val Met
            265                 270                 275

gca cgt tcc cag aag aaa aca ctg gag gaa tct ctg ctg aat gcc gtg   979
Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser Leu Leu Asn Ala Val
        280                 285                 290

tct tac ggc tcg act gcg gcg tct ctt cct ggc act acc att cct cgt  1027
Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly Thr Thr Ile Pro Arg
    295                 300                 305

cct gac caa ctc gcc aca gct ggt gca acg gtc acc caa gtc aaa gga  1075
Pro Asp Gln Leu Ala Thr Ala Gly Ala Thr Val Thr Gln Val Lys Gly
310                 315                 320                 325

ttg aaa gaa tca gca tgaatagcgt aaataattcc tcg                   1113
Leu Lys Glu Ser Ala
                330
```

<210> 58

<211> 330
<212> PRT
<213> Corynebacterium glutamicum

<400> 58

```
Met Ile Ile Thr Phe Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser
  1               5                  10                  15

Leu Gly Glu Glu Leu Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val
             20                  25                  30

Thr Ala Val Ala Gly Gly Lys Gly Ile Asn Val Ala His Ala Val Leu
         35                  40                  45

Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp
     50                  55                  60

Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val
 65                  70                  75                  80

Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp
                 85                  90                  95

Gly Thr Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln
            100                 105                 110

Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu
        115                 120                 125

Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val
    130                 135                 140

Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp
145                 150                 155                 160

Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly
                165                 170                 175

Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn
            180                 185                 190

Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu
        195                 200                 205

Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp
    210                 215                 220

Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala
225                 230                 235                 240

Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser
                245                 250                 255

Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu
            260                 265                 270

Ala Gly Phe Val Met Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser
        275                 280                 285

Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly
    290                 295                 300
```

```
Thr Thr Ile Pro Arg Pro Asp Gln Leu Ala Thr Ala Gly Ala Thr Val
305                 310                 315                 320

Thr Gln Val Lys Gly Leu Lys Glu Ser Ala
                325                 330
```

<210> 59
<211> 1155
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1132)
<223> RXA01702

<400> 59

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attgtgaatg tgggattatc ggttcgcgct tcaccatgtt tctgcatgat gaaattacat 60

acatagttca gtgacagtca ccttttggag gagacacctt atg cct atc gca act   115
                                            Met Pro Ile Ala Thr
                                              1               5

ccc gag gtc tat aac gag atg ctc gat cgt gct aag gaa ggc gga ttc   163
Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala Lys Glu Gly Gly Phe
                10                  15                  20

gcc ttc cca gcc atc aac tgc acc tcc tcg gaa acc atc aac gca gct   211
Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu Thr Ile Asn Ala Ala
            25                  30                  35

ctc aag ggc ttc gca gag gct gaa tct gac gga atc atc cag ttc tcc   259
Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly Ile Ile Gln Phe Ser
        40                  45                  50

acc ggt ggt gca gag ttc ggt tcc ggc ctg gca gta aag aac aag gtc   307
Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala Val Lys Asn Lys Val
    55                  60                  65

aag ggc gca gtt gcg ctt gca gcc ttc gcc cac gag gca gca aag agc   355
Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His Glu Ala Ala Lys Ser
70                  75                  80                  85

tac ggc atc aac gtt gct ctg cac act gac cac tgc cag aag gaa gtc   403
Tyr Gly Ile Asn Val Ala Leu His Thr Asp His Cys Gln Lys Glu Val
                90                  95                  100

ctg gac gag tac gtc cgc cca ctg ctg gct atc tcc cag gag cgc gtc   451
Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile Ser Gln Glu Arg Val
            105                 110                 115

gac cgc ggc gag ctt cca ctg ttc cag tcc cac atg tgg gat ggt tcc   499
Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His Met Trp Asp Gly Ser
        120                 125                 130

gct gtc cca atc gac gag aac ctc gaa atc gca cag gag ctg ctg gct   547
Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala Gln Glu Leu Leu Ala
    135                 140                 145
```

```
aag gcc aag gca gcg aac atc atc ttg gaa gtt gag atc ggt gtt gtc   595
Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val Glu Ile Gly Val Val
150                 155                 160                 165

ggt ggc gaa gaa gac ggc gtt gag gct aag gct ggc gca aac ctc tac   643
Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala Gly Ala Asn Leu Tyr
                170                 175                 180

acc tcc cca gaa gac ttt gag aag acc atc gat gca atc ggc acc ggt   691
Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp Ala Ile Gly Thr Gly
            185                 190                 195

gag aag ggc cgc tac ctg cta gca gct acc ttc ggt aac gtc cac ggc   739
Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe Gly Asn Val His Gly
        200                 205                 210

gtt tac aag cca ggc aac gtc aag ctg cgc cca gag gtc ctc ctt gag   787
Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro Glu Val Leu Leu Glu
    215                 220                 225

ggc cag cag gtt gca cgc aag aag ctt gga ctt gca gac gac gca ctt   835
Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu Ala Asp Asp Ala Leu
230                 235                 240                 245

cca ttc gac ttc gtc ttc cac ggt ggc tca ggc tcc gag aag gaa aag   883
Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly Ser Glu Lys Glu Lys
                250                 255                 260

atc gaa gag gcg ctg acc tac ggc gtc atc aag atg aac gtt gat act   931
Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys Met Asn Val Asp Thr
            265                 270                 275

gac acc cag tac gca ttc acc cgc cca atc gtc tcc cac atg ttt gag   979
Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val Ser His Met Phe Glu
        280                 285                 290

aac tac aac ggc gtt ctc aag atc gac ggc gag gtc gga aac aag aag   1027
Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu Val Gly Asn Lys Lys
    295                 300                 305

gct tac gac cca cgc tct tac atg aag aag gct gag cag agc atg tct   1075
Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala Glu Gln Ser Met Ser
310                 315                 320                 325

gag cgc att atc gag tct tgc cag gac ctc aag tct gtt gga aag acc   1123
Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys Ser Val Gly Lys Thr
                330                 335                 340

acc tct aag taatctcagc agttaaaaag ggc                            1155
Thr Ser Lys
```

<210> 60
<211> 344
<212> PRT
<213> Corynebacterium glutamicum

<400> 60

```
Met Pro Ile Ala Thr Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala
  1               5                  10                  15
```

Lys Glu Gly Gly Phe Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu
20 25 30

Thr Ile Asn Ala Ala Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly
35 40 45

Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala
50 55 60

Val Lys Asn Lys Val Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His
65 70 75 80

Glu Ala Ala Lys Ser Tyr Gly Ile Asn Val Ala Leu His Thr Asp His
85 90 95

Cys Gln Lys Glu Val Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile
100 105 110

Ser Gln Glu Arg Val Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His
115 120 125

Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala
130 135 140

Gln Glu Leu Leu Ala Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val
145 150 155 160

Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
165 170 175

Gly Ala Asn Leu Tyr Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp
180 185 190

Ala Ile Gly Thr Gly Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe
195 200 205

Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
210 215 220

Glu Val Leu Leu Glu Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu
225 230 235 240

Ala Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly
245 250 255

Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys
260 265 270

Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
275 280 285

Ser His Met Phe Glu Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu
290 295 300

Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala
305 310 315 320

Glu Gln Ser Met Ser Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys
325 330 335

```
Ser Val Gly Lys Thr Thr Ser Lys
            340


<210> 61
<211> 900
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(877)
<223> RXA02258

<400> 61
cgttgcaatt ctcgctcagt aaatccgaca cggccctttg ttagaaaaca aaacataaag 60

ggccaccggg aaacttttt aagaaaggtg tgtttcacac atg gca cgt aag cca   115
                                        Met Ala Arg Lys Pro
                                          1               5

ctt atc gct ggt aac tgg aag atg aac ctg gat cac cag cag gca atc   163
Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp His Gln Gln Ala Ile
                 10                  15                  20

ggc act gtt cag aag ctt gca ttc gcc ctt cca aag gaa tac ttc gag   211
Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro Lys Glu Tyr Phe Glu
             25                  30                  35

aag gtt gac gtt gca gtc acc gtt cct ttc act gac atc cgc tcc gtc   259
Lys Val Asp Val Ala Val Thr Val Pro Phe Thr Asp Ile Arg Ser Val
         40                  45                  50

cag act ctc gtt gag ggc gac aag ctt gag gtc act ttc ggt gct cag   307
Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val Thr Phe Gly Ala Gln
     55                  60                  65

gac gtc tcc cag cac gag tcc ggt gcg tac acc ggt gaa gtt tct gca   355
Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr Gly Glu Val Ser Ala
 70                  75                  80                  85

agc atg ctg gca aag ttg aac tgc tct tgg gtt gtc gtt gga cac tcc   403
Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val Val Val Gly His Ser
                 90                  95                 100

gag cgc cgc gag tac cac aac gag tct gat gag ttg gtt gct gcg aag   451
Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu Leu Val Ala Ala Lys
            105                 110                 115

gca aag gca gct ctg tcc aac ggc atc agc ccg atc gtc tgc gtt ggt   499
Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro Ile Val Cys Val Gly
        120                 125                 130

gag cca ctg gaa atc cgt gaa gct ggc acc cac gtt gag tac gtc gtc   547
Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His Val Glu Tyr Val Val
    135                 140                 145

gag cag acc cgt aag tcc ctt gct ggc ctg gat gct gct gag ctg gcc   595
Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp Ala Ala Glu Leu Ala
150                 155                 160                 165
```

```
aac acc gtt atc gcg tat gag cca gtg tgg gct atc ggc acc ggt aag   643
Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Lys
                170                 175                 180

gtt gct tcc gca gct gac gct cag gaa gtg tgc aag gct atc cgc ggt   691
Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys Lys Ala Ile Arg Gly
            185                 190                 195

ctg atc gtg gag ctt gca ggc gac gag gtc gct gag ggc ctg cgt att   739
Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala Glu Gly Leu Arg Ile
        200                 205                 210

ctt tac ggt ggt tct gtt aag gca gaa acc gtc gct gag atc gtc ggt   787
Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val Ala Glu Ile Val Gly
    215                 220                 225

cag cct gac gtc gac ggc gga ctt gtc ggt ggc gct tcc ctc gac ggt   835
Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly Ala Ser Leu Asp Gly
230                 235                 240                 245

gaa gca ttc gcc aag ctg gct gcc aac gct gcg agc gtt gct           877
Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala Ser Val Ala
                250                 255

taaagtacag agctttaaag cac                                        900
```

<210> 62
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 62

```
Met Ala Arg Lys Pro Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp
  1               5                  10                  15

His Gln Gln Ala Ile Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro
             20                  25                  30

Lys Glu Tyr Phe Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
         35                  40                  45

Asp Ile Arg Ser Val Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val
     50                  55                  60

Thr Phe Gly Ala Gln Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr
 65                  70                  75                  80

Gly Glu Val Ser Ala Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val
                 85                  90                  95

Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
            100                 105                 110

Leu Val Ala Ala Lys Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro
        115                 120                 125

Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
    130                 135                 140

Val Glu Tyr Val Val Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp
```

```
145                 150                 155                 160

Ala Ala Glu Leu Ala Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala
                165                 170                 175

Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys
            180                 185                 190

Lys Ala Ile Arg Gly Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala
        195                 200                 205

Glu Gly Leu Arg Ile Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val
    210                 215                 220

Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly
225                 230                 235                 240

Ala Ser Leu Asp Gly Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala
                245                 250                 255

Ser Val Ala
```

20050208

<210> 63
<211> 1563
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1540)
<223> RXN01225

<400> 63

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tttgggctaa tgttgggggg agtgctttca actatccacg agagctgccc agtgataaac 60

cccgggttaa ccccacgcct aagtcagtga aggacttttt atg acg cac aac cac   115
                                              Met Thr His Asn His
                                                1               5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg   163
Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
            10                  15                  20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt   211
Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
        25                  30                  35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc   259
Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
    40                  45                  50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg   307
Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
55                  60                  65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc   355
Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
70                  75                  80                  85
```

```
gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac   403
Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
                 90                  95                 100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa   451
Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
            105                 110                 115

acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc   499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile
        120                 125                 130

ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac   547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp
    135                 140                 145

ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac   595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp
150                 155                 160                 165

ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga   643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly
                170                 175                 180

ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc   691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala
            185                 190                 195

aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att   739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile
        200                 205                 210

gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc   787
Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr
    215                 220                 225

ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag   835
Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys
230                 235                 240                 245

ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag   883
Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys
                250                 255                 260

aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag   931
Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln
            265                 270                 275

atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc   979
Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu
        280                 285                 290

aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc   1027
Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr
    295                 300                 305

gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag   1075
Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys
310                 315                 320                 325

ggt tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa   1123
```

```
Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu
                330                 335                 340

acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc  1171
Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly
            345                 350                 355

aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg  1219
Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
        360                 365                 370

gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc  1267
Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
    375                 380                 385

aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa  1315
Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
390                 395                 400                 405

atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc  1363
Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
                410                 415                 420

acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt  1411
Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
            425                 430                 435

cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc  1459
Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
        440                 445                 450

aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc  1507
Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
    455                 460                 465

gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
470                 475                 480

cac                                                              1563
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<210> 64
<211> 480
<212> PRT
<213> Corynebacterium glutamicum

<400> 64

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Met Thr His Asn His Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu
  1               5                  10                  15

Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Asn Val Val
             20                  25                  30

Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
         35                  40                  45

Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
     50                  55                  60

Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
```

65 70 75 80

Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
85 90 95

Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
100 105 110

Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
115 120 125

Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
130 135 140

Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
145 150 155 160

Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
165 170 175

Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
180 185 190

Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
195 200 205

Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
210 215 220

Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
225 230 235 240

His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
245 250 255

Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
260 265 270

Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
275 280 285

Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
290 295 300

Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
305 310 315 320

Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
325 330 335

Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
340 345 350

Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
355 360 365

Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
370 375 380

Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
385 390 395 400

```
Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
                405                 410                 415

Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
            420                 425                 430

Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
        435                 440                 445

Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala
    450                 455                 460

Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
465                 470                 475                 480
```

09250200

<210> 65
<211> 1563
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1540)
<223> FRXA01225

<400> 65

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tttgggctaa tgttgggggg agtgctttca actatccacg agagctgccc agtgataaac 60

cccgggttaa ccccacgcct aagtcagtga aggacttttt atg acg cac aac cac   115
                                            Met Thr His Asn His
                                              1               5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg   163
Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
                  10                  15                  20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt   211
Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
              25                  30                  35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc   259
Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
          40                  45                  50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg   307
Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
      55                  60                  65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc   355
Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
  70                  75                  80                  85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac   403
Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
                  90                  95                 100
```

```
ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa   451
Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
            105                 110                 115

acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc   499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile
        120                 125                 130

ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac   547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp
    135                 140                 145

ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac   595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp
150                 155                 160                 165

ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga   643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly
                170                 175                 180

ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc   691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala
            185                 190                 195

aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att   739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile
        200                 205                 210

gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc   787
Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr
    215                 220                 225

ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag   835
Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys
230                 235                 240                 245

ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag   883
Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys
                250                 255                 260

aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag   931
Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln
            265                 270                 275

atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc   979
Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu
        280                 285                 290

aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc   1027
Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr
    295                 300                 305

gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag   1075
Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys
310                 315                 320                 325

ggt tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa   1123
Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu
                330                 335                 340

acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc   1171
```

```
Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly
            345                 350                 355

aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg   1219
Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met
        360                 365                 370

gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc   1267
Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val
    375                 380                 385

aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa   1315
Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln
390                 395                 400                 405

atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc   1363
Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly
                410                 415                 420

acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt   1411
Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly
            425                 430                 435

cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc   1459
Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
        440                 445                 450

aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc   1507
Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
    455                 460                 465

gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
470                 475                 480

cac                                                               1563


<210> 66
<211> 480
<212> PRT
<213> Corynebacterium glutamicum

<400> 66
Met Thr His Asn His Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu
  1               5                  10                  15

Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Asn Val Val
             20                  25                  30

Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
         35                  40                  45

Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
     50                  55                  60

Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65                  70                  75                  80

Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
                 85                  90                  95
```

```
Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
            100                 105                 110

Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
        115                 120                 125

Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
    130                 135                 140

Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
145                 150                 155                 160

Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
                165                 170                 175

Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
            180                 185                 190

Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
        195                 200                 205

Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
    210                 215                 220

Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
225                 230                 235                 240

His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
                245                 250                 255

Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
            260                 265                 270

Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
        275                 280                 285

Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
    290                 295                 300

Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
305                 310                 315                 320

Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
                325                 330                 335

Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
            340                 345                 350

Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
        355                 360                 365

Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
    370                 375                 380

Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
385                 390                 395                 400

Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
                405                 410                 415
```

```
Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
            420                 425                 430

Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
        435                 440                 445

Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala
    450                 455                 460

Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
465                 470                 475                 480
```

<210> 67
<211> 1125
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1102)
<223> RXA02256

<400> 67

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ttgggttctg tcagctcaag aattcttgag tgaccgatgc tctgattgac ctaactgctt 60

gacacattgc atttcctaca atctttagag gagacacaac atg acc att cgt gtt   115
                                            Met Thr Ile Arg Val
                                              1               5

ggt att aac gga ttt ggc cgt atc gga cgt aac ttc ttc cgc gca gtt   163
Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn Phe Phe Arg Ala Val
                  10                  15                  20

ctg gag cgc agc gac gat ctc gag gta gtt gca gtc aac gac ctc acc   211
Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala Val Asn Asp Leu Thr
              25                  30                  35

gac aac aag acc ctt tcc acc ctt ctc aag ttc gac tcc atc atg ggc   259
Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe Asp Ser Ile Met Gly
          40                  45                  50

cgc ctt ggc cag gaa gtt gaa tac gac gat gac tcc atc acc gtt ggt   307
Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp Ser Ile Thr Val Gly
      55                  60                  65

ggc aag cgc atc gct gtt tac gca gag cgc gat cca aag aac ctg gac   355
Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp Pro Lys Asn Leu Asp
  70                  75                  80                  85

tgg gct gca cac aac gtt gac atc gtg atc gag tcc acc ggc ttc ttc   403
Trp Ala Ala His Asn Val Asp Ile Val Ile Glu Ser Thr Gly Phe Phe
                  90                  95                 100

acc gat gca aac gcg gct aag gct cac atc gaa gca ggt gcc aag aag   451
Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu Ala Gly Ala Lys Lys
              105                 110                 115
```

```
gtc atc atc tcc gca cca gca agc aac gaa gac gca acc ttc gtt tac   499
Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp Ala Thr Phe Val Tyr
        120                 125                 130

ggt gtg aac cac gag tcc tac gat cct gag aac cac aac gtg atc tcc   547
Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn His Asn Val Ile Ser
    135                 140                 145

ggc gca tct tgc acc acc aac tgc ctc gca cca atg gca aag gtc cta   595
Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys Val Leu
150                 155                 160                 165

aac gac aag ttc ggc atc gag aac ggc ctc atg acc acc gtt cac gca   643
Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met Thr Thr Val His Ala
                170                 175                 180

tac act ggc gac cag cgc ctg cac gat gca cct cac cgc gac ctg cgt   691
Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro His Arg Asp Leu Arg
            185                 190                 195

cgt gca cgt gca gca gca gtc aac atc gtt cct acc tcc acc ggt gca   739
Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro Thr Ser Thr Gly Ala
        200                 205                 210

gct aag gct gtt gct ctg gtt ctc cca gag ctc aag ggc aag ctt gac   787
Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys Leu Asp
    215                 220                 225

ggc tac gca ctt cgc gtt cca gtt atc acc ggt tcc gca acc gac ctg   835
Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly Ser Ala Thr Asp Leu
230                 235                 240                 245

acc ttc aac acc aag tct gag gtc acc gtt gag tcc atc aac gct gca   883
Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu Ser Ile Asn Ala Ala
                250                 255                 260

atc aag gaa gct gca gtc ggc gag ttc ggc gag acc ctg gct tac tcc   931
Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu Thr Leu Ala Tyr Ser
            265                 270                 275

gaa gag cca ctg gtt tcc acc gac atc gtc cac gat tcc cac ggc tcc   979
Glu Glu Pro Leu Val Ser Thr Asp Ile Val His Asp Ser His Gly Ser
        280                 285                 290

atc ttc gac gct ggc ctg acc aag gtc tcc ggc aac acc gtc aag gtt   1027
Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly Asn Thr Val Lys Val
    295                 300                 305

gtt tcc tgg tac gac aac gag tgg ggc tac acc tgc cag ctc ctg cgt   1075
Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr Cys Gln Leu Leu Arg
310                 315                 320                 325

ctg acc gag ctc gta gct tcc aag ctc taattagttc acatcgctaa         1122
Leu Thr Glu Leu Val Ala Ser Lys Leu
                330

cgt                                                               1125
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<210> 68
<211> 334

<212> PRT
<213> Corynebacterium glutamicum

<400> 68

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Met Thr Ile Arg Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn
 1               5                  10                  15

Phe Phe Arg Ala Val Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala
            20                  25                  30

Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe
        35                  40                  45

Asp Ser Ile Met Gly Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp
    50                  55                  60

Ser Ile Thr Val Gly Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp
65                  70                  75                  80

Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
                85                  90                  95

Ser Thr Gly Phe Phe Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu
            100                 105                 110

Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp
        115                 120                 125

Ala Thr Phe Val Tyr Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn
    130                 135                 140

His Asn Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
145                 150                 155                 160

Met Ala Lys Val Leu Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met
                165                 170                 175

Thr Thr Val His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro
            180                 185                 190

His Arg Asp Leu Arg Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro
        195                 200                 205

Thr Ser Thr Gly Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu
    210                 215                 220

Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly
225                 230                 235                 240

Ser Ala Thr Asp Leu Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu
                245                 250                 255

Ser Ile Asn Ala Ala Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu
            260                 265                 270

Thr Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Thr Asp Ile Val His
        275                 280                 285

Asp Ser His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly
    290                 295                 300
```

```
Asn Thr Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr
305                 310                 315                 320

Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu
                325                 330
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<210> 69
<211> 1338
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1315)
<223> RXA02257

<400> 69

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gaagaatttt ttaaacaatc aaatctccaa ggagtacggc atg gct gtt aag acc   115
                                            Met Ala Val Lys Thr
                                              1               5

ctc aag gac ttg ctc gac gaa ggc gta gac gga cgc cac gtc atc gtt   163
Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly Arg His Val Ile Val
                  10                  15                  20

cga tct gac ttc aat gtt ccc ctc aac gat gac cgc gag atc acc gat   211
Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp Arg Glu Ile Thr Asp
              25                  30                  35

aag ggc cga atc att gcc tcc cta cca acc ctt aaa gca ctg agc gaa   259
Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu Lys Ala Leu Ser Glu
          40                  45                  50

ggt ggc gca aag gtc atc gtc atg gct cac ctt ggc cgc cca aag ggc   307
Gly Gly Ala Lys Val Ile Val Met Ala His Leu Gly Arg Pro Lys Gly
      55                  60                  65

gag gtc aac gag aag tac tcc ctc gca cct gtc gct gag gca ctc tcc   355
Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val Ala Glu Ala Leu Ser
  70                  75                  80                  85

gat gag ctt ggc cag tac gtt gca ctt gcc gca gac gtt gtt ggc gaa   403
Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala Asp Val Val Gly Glu
                  90                  95                 100

gac gca cac gag cgc gca aac ggc ctg acc gag ggc gac atc ctg ctc   451
Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu Gly Asp Ile Leu Leu
             105                 110                 115

ctg gag aac gtg cgc ttc gac cca cgc gaa acc tcc aag gac gag gca   499
Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr Ser Lys Asp Glu Ala
         120                 125                 130

gag cgc acc gct ttc gct cag gag ctc gca gct ctt gca gca gac aac   547
Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala Leu Ala Ala Asp Asn
     135                 140                 145

ggc gca ttc gtt tct gac ggc ttc ggt gtt gtc cac cgc gca cag acc   595
```

```
Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val His Arg Ala Gln Thr
150                 155                 160                 165

tcc gtc tac gac att gca aag ttg ctg cca cac tac gct ggc gga ctg   643
Ser Val Tyr Asp Ile Ala Lys Leu Leu Pro His Tyr Ala Gly Gly Leu
                170                 175                 180

gta gag acc gag att tcc gtt ctg gaa aag atc gca gaa tca cca gag   691
Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile Ala Glu Ser Pro Glu
            185                 190                 195

gca cca tac gta gtg gtt ctc ggt gga tcc aag gtc tct gac aag atc   739
Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys Val Ser Asp Lys Ile
        200                 205                 210

ggt gtt att gag gcg ctg gct gcc aag gct gac aag atc atc gtc ggt   787
Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp Lys Ile Ile Val Gly
    215                 220                 225

ggc ggc atg tgc tac acc ttc ctc gca gct cag gga cac aac gtt cag   835
Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln Gly His Asn Val Gln
230                 235                 240                 245

cag tcc ctc ctg cag gaa gaa atg aag gct acc tgc acc gac ctg ctc   883
Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr Cys Thr Asp Leu Leu
                250                 255                 260

gca cgc ttc ggt gac aag atc gtt ctc cca gtt gac ctg gtt gca gca   931
Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val Asp Leu Val Ala Ala
            265                 270                 275

tcc gaa ttt aac aag gac gca gag aag cag atc gtt gac ctg gac tcc   979
Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile Val Asp Leu Asp Ser
        280                 285                 290

atc cca gaa ggc tgg atg tct ctt gac atc gga cca gag tcc gtc aag   1027
Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly Pro Glu Ser Val Lys
    295                 300                 305

aac ttc ggt gag gtt ctc agc acc gct aag acc atc ttc tgg aac ggc   1075
Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr Ile Phe Trp Asn Gly
310                 315                 320                 325

cca atg ggc gtg ttc gag ttc gca gca ttc tct gaa ggc acc cgc ggc   1123
Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser Glu Gly Thr Arg Gly
                330                 335                 340

atc gcc cag gcc atc atc gat gca act gca ggc aac gac gca ttc tcc   1171
Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly Asn Asp Ala Phe Ser
            345                 350                 355

gtt gtt ggc ggt ggc gac tcc gca gca tcc gtt cgc gtg ctc ggc ctg   1219
Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val Arg Val Leu Gly Leu
        360                 365                 370

aac gaa gac ggc ttc tcc cac atc tcc acc ggt ggt ggc gca tcc ctc   1267
Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly Gly Gly Ala Ser Leu
    375                 380                 385

gag tac ctt gaa ggc aag gaa ctc cca ggc gtt gca att ctc gct cag   1315
Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val Ala Ile Leu Ala Gln
```

```
390                 395                 400                 405

taaatccgac acggcccttt gtt                                       1338


<210> 70
<211> 405
<212> PRT
<213> Corynebacterium glutamicum

<400> 70
Met Ala Val Lys Thr Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly
  1               5                  10                  15

Arg His Val Ile Val Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp
             20                  25                  30

Arg Glu Ile Thr Asp Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu
         35                  40                  45

Lys Ala Leu Ser Glu Gly Gly Ala Lys Val Ile Val Met Ala His Leu
     50                  55                  60

Gly Arg Pro Lys Gly Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val
 65                  70                  75                  80

Ala Glu Ala Leu Ser Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala
                 85                  90                  95

Asp Val Val Gly Glu Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu
            100                 105                 110

Gly Asp Ile Leu Leu Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr
        115                 120                 125

Ser Lys Asp Glu Ala Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala
    130                 135                 140

Leu Ala Ala Asp Asn Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val
145                 150                 155                 160

His Arg Ala Gln Thr Ser Val Tyr Asp Ile Ala Lys Leu Leu Pro His
                165                 170                 175

Tyr Ala Gly Gly Leu Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile
            180                 185                 190

Ala Glu Ser Pro Glu Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys
        195                 200                 205

Val Ser Asp Lys Ile Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp
    210                 215                 220

Lys Ile Ile Val Gly Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln
225                 230                 235                 240

Gly His Asn Val Gln Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr
                245                 250                 255

Cys Thr Asp Leu Leu Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val
            260                 265                 270
```

```
Asp Leu Val Ala Ala Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile
        275                 280                 285

Val Asp Leu Asp Ser Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly
    290                 295                 300

Pro Glu Ser Val Lys Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr
305                 310                 315                 320

Ile Phe Trp Asn Gly Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser
                325                 330                 335

Glu Gly Thr Arg Gly Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly
            340                 345                 350

Asn Asp Ala Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val
        355                 360                 365

Arg Val Leu Gly Leu Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly
    370                 375                 380

Gly Gly Ala Ser Leu Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val
385                 390                 395                 400

Ala Ile Leu Ala Gln
                405
```

<210> 71
<211> 1398
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1375)
<223> RXA00235

<400> 71
cgaaacaaga ttcgtgcaac aattgggtgt agacgtgatt gaagacattt gatcacgtga 60

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ataattctag ttagctccca agttggcata ggaggccaca gtg gct gaa atc atg   115
                                            Val Ala Glu Ile Met
                                              1               5

cac gta ttc gct cgc gaa att ctc gac tcc cgc ggt aac cca acc gtc   163
His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg Gly Asn Pro Thr Val
                 10                  15                  20

gag gca gag gtt ttc ctg gat gac ggt tcc cac ggt gtc gca ggt gtt   211
Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His Gly Val Ala Gly Val
             25                  30                  35

cca tcc ggc gca tcc acc ggc gtc cac gag gct cat gag ctg cgt gac   259
Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala His Glu Leu Arg Asp
         40                  45                  50

ggt ggc gat cgc tac ctg ggc aag ggc gtt ttg aag gca gtt gaa aac   307
Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu Lys Ala Val Glu Asn
     55                  60                  65
```

```
gtc aac gaa gaa atc ggc gac gag ctc gct ggc cta gag gct gac gat   355
Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly Leu Glu Ala Asp Asp
 70                  75                  80                  85

cag cgc ctc atc gac gaa gca atg atc aag ctt gat ggc acc gcc aac   403
Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu Asp Gly Thr Ala Asn
                 90                  95                 100

aag tcc cgc ctg ggt gca aac gca atc ctt ggt gtt tcc atg gct gtt   451
Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly Val Ser Met Ala Val
            105                 110                 115

gca aag gct gct gct gat tcc gca ggc ctc cca ctg ttc cgc tac atc   499
Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro Leu Phe Arg Tyr Ile
        120                 125                 130

ggt gga cca aac gca cac gtt ctt cca gtt cca atg atg aac atc atc   547
Gly Gly Pro Asn Ala His Val Leu Pro Val Pro Met Met Asn Ile Ile
    135                 140                 145

acc ggt ggc gct cac gct gac tcc ggt gtt gac gtt cag gaa ttc atg   595
Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp Val Gln Glu Phe Met
150                 155                 160                 165

atc gct cca atc ggt gca gag acc ttc tct gag gct ctc cgc aac ggc   643
Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu Ala Leu Arg Asn Gly
                170                 175                 180

gcg gag gtc tac cac gca ctg aag tcc gtc atc aag gaa aag ggc ctg   691
Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile Lys Glu Lys Gly Leu
            185                 190                 195

tcc acc gga ctt ggc gat gag ggc ggc ttc gct cct tcc gtc ggc tcc   739
Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala Pro Ser Val Gly Ser
        200                 205                 210

acc cgt gag gct ctt gac ctt atc gtt gag gca atc gag aag gct ggc   787
Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala Ile Glu Lys Ala Gly
    215                 220                 225

ttc acc cca ggc aag gac atc gct ctt gct ctg gac gtt gct tcc tct   835
Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu Asp Val Ala Ser Ser
230                 235                 240                 245

gag ttc ttc aag gac ggc acc tac cac ttc gaa ggt ggc cag cac tcc   883
Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu Gly Gly Gln His Ser
                250                 255                 260

gca gct gag atg gca aac gtt tac gct gag ctc gtt gac gcg tac cca   931
Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu Val Asp Ala Tyr Pro
            265                 270                 275

atc gtc tcc atc gag gac cca ctg cag gaa gat gac tgg gag ggt tac   979
Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp Asp Trp Glu Gly Tyr
        280                 285                 290

acc aac ctc acc gca acc atc ggc gac aag gtt cag atc gtt ggc gac  1027
Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val Gln Ile Val Gly Asp
    295                 300                 305
```

Sequence Listing

```
gac ttc ttc gtc acc aac cct gag cgc ctg aag gag ggc atc gct aag   1075
Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys Glu Gly Ile Ala Lys
310                 315                 320                 325

aag gct gcc aac tcc atc ctg gtt aag gtg aac cag atc ggt acc ctc   1123
Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn Gln Ile Gly Thr Leu
                330                 335                 340

acc gag acc ttc gac gct gtc gac atg gct cac cgc gca ggc tac acc   1171
Thr Glu Thr Phe Asp Ala Val Asp Met Ala His Arg Ala Gly Tyr Thr
            345                 350                 355

tcc atg atg tcc cac cgt tcc ggt gag acc gag gac acc acc att gct   1219
Ser Met Met Ser His Arg Ser Gly Glu Thr Glu Asp Thr Thr Ile Ala
        360                 365                 370

gac ctc gca gtt gca ctc aac tgt ggc cag atc aag act ggt gct cca   1267
Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile Lys Thr Gly Ala Pro
    375                 380                 385

gca cgt tcc gac cgt gtc gca aag tac aac cag ctt ctc cgc atc gag   1315
Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu
390                 395                 400                 405

cag ctg ctt ggc gac gcc ggc gtc tac gca ggt cgc agc gca ttc cca   1363
Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly Arg Ser Ala Phe Pro
                410                 415                 420

cgc ttt cag ggc taaataaaag cgcttttcga cgc                        1398
Arg Phe Gln Gly
            425
```

09605368 - 060205

<210> 72
<211> 425
<212> PRT
<213> Corynebacterium glutamicum

<400> 72

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Val Ala Glu Ile Met His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg
  1               5                  10                  15

Gly Asn Pro Thr Val Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His
             20                  25                  30

Gly Val Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
         35                  40                  45

His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
     50                  55                  60

Lys Ala Val Glu Asn Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly
 65                  70                  75                  80

Leu Glu Ala Asp Asp Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu
                 85                  90                  95

Asp Gly Thr Ala Asn Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly
            100                 105                 110

Val Ser Met Ala Val Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro
```

```
        115                 120                 125

Leu Phe Arg Tyr Ile Gly Gly Pro Asn Ala His Val Leu Pro Val Pro
    130                 135                 140

Met Met Asn Ile Ile Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp
145                 150                 155                 160

Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
                165                 170                 175

Ala Leu Arg Asn Gly Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile
            180                 185                 190

Lys Glu Lys Gly Leu Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala
        195                 200                 205

Pro Ser Val Gly Ser Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala
    210                 215                 220

Ile Glu Lys Ala Gly Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu
225                 230                 235                 240

Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu
                245                 250                 255

Gly Gly Gln His Ser Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu
            260                 265                 270

Val Asp Ala Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
        275                 280                 285

Asp Trp Glu Gly Tyr Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val
    290                 295                 300

Gln Ile Val Gly Asp Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys
305                 310                 315                 320

Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn
                325                 330                 335

Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Asp Met Ala His
            340                 345                 350

Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu
        355                 360                 365

Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile
    370                 375                 380

Lys Thr Gly Ala Pro Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln
385                 390                 395                 400

Leu Leu Arg Ile Glu Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly
                405                 410                 415

Arg Ser Ala Phe Pro Arg Phe Gln Gly
            420                 425
```

<210> 73

<211> 1554
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1531)
<223> RXA01093

<400> 73
cagaggcgta gaacattgtc tgttcacact ctgggtcgca agattcatcg agaattaatg 60

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gtagtacctg tggcttgagg gggaatgacg tactaggctt atg ggc gtg gat aga   115
                                              Met Gly Val Asp Arg
                                                1               5

cga act aag att gta tgt acc cta ggc cca gcg gtg gct agt gca gat   163
Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Val Ala Ser Ala Asp
                  10                  15                  20

gga att ctg cgt ttg gta gaa gac ggc atg gat gtt gct cgc ctc aac   211
Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn
              25                  30                  35

ttc tcc cat ggt gac cac cca gat cat gag caa aac tac aag tgg gtc   259
Phe Ser His Gly Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val
          40                  45                  50

cgc gag gcg gcg gag aag act ggc cgt gca gtc ggt att ctc gca gac   307
Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val Gly Ile Leu Ala Asp
      55                  60                  65

ctc caa gga ccg aag atc cgt ctt ggc cgt ttc act gac ggc gca acc   355
Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe Thr Asp Gly Ala Thr
  70                  75                  80                  85

gtg tgg gaa aac ggc gag acc att cgg atc acc gtt gac gat gta gag   403
Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr Val Asp Asp Val Glu
                  90                  95                 100

gga acg cac gat cgt gtg tcc acc acc tac aag aat ctg gca aaa gac   451
Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Lys Asp
             105                 110                 115

gcg aag cca ggc gac cgc ctg ctc gtt gat gac ggc aag gtt ggc ctc   499
Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu
         120                 125                 130

gtc tgc gtt tcc gtc gaa ggt aac gac gtc atc tgt gag gtt gtt gag   547
Val Cys Val Ser Val Glu Gly Asn Asp Val Ile Cys Glu Val Val Glu
     135                 140                 145

ggc gga cca gtc tcc aac aac aag ggt gtt tcc ctg cca ggt atg gat   595
Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp
150                 155                 160                 165

att tcc gta cct gca ctg tcc gaa aag gat atc cgt gac ctg cgc ttc   643
Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile Arg Asp Leu Arg Phe
                 170                 175                 180

gcc ctg aag ctc ggc gtg gac ttt att gca ctg tcc ttc gta cgt tcc   691
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09356742.030502

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Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser
            185                 190                 195

cca gca gat gct gaa ctc gtt cac aag atc atg gac gaa gaa ggt cgt   739
Pro Ala Asp Ala Glu Leu Val His Lys Ile Met Asp Glu Glu Gly Arg
        200                 205                 210

cgt gtt cct gtg atc gcc aag ctg gaa aag cca gag gct gtc acc tcc   787
Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro Glu Ala Val Thr Ser
    215                 220                 225

ctc gag cca atc gtg ttg gca ttc gac gcc gtc atg gtt gct cgt ggt   835
Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val Met Val Ala Arg Gly
230                 235                 240                 245

gac ctc ggc gtt gag gtt cct ctg gag gag gtt cca ctg gtt cag aag   883
Asp Leu Gly Val Glu Val Pro Leu Glu Glu Val Pro Leu Val Gln Lys
                250                 255                 260

cgc gca atc cag att gcc cgt gag aac gca aag cca gtt atc gtg gca   931
Arg Ala Ile Gln Ile Ala Arg Glu Asn Ala Lys Pro Val Ile Val Ala
            265                 270                 275

acc cag atg ctg gat tcc atg att gag aac tcc cgc cca acc cgt gcg   979
Thr Gln Met Leu Asp Ser Met Ile Glu Asn Ser Arg Pro Thr Arg Ala
        280                 285                 290

gaa gct tct gac gtg gca aac gct gtg ctc gat ggc gca gat gct gtc   1027
Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp Gly Ala Asp Ala Val
    295                 300                 305

atg ctt tct ggt gaa act tca gtg ggc aaa gat ccg cac aac gtt gtg   1075
Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp Pro His Asn Val Val
310                 315                 320                 325

cgc acc atg tct cgc att gtt cgc ttc gct gaa acc gac ggt cgc gtc   1123
Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu Thr Asp Gly Arg Val
                330                 335                 340

cca gac ctg acc cac atc cct cgc act aag cgt ggc gtt att tcc tac   1171
Pro Asp Leu Thr His Ile Pro Arg Thr Lys Arg Gly Val Ile Ser Tyr
            345                 350                 355

tct gca cgt gat atc gcc gag cgc ctc aac gct cgt gca ttg gtt gcg   1219
Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala Arg Ala Leu Val Ala
        360                 365                 370

ttc acc acc tct ggt gat acc gca aag cgt gtg gct cgt ctg cac agc   1267
Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val Ala Arg Leu His Ser
    375                 380                 385

cac ctg cca ctg ctc gtg ttc act cca aat gag gca gtt cgc tct gag   1315
His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu Ala Val Arg Ser Glu
390                 395                 400                 405

ctg gcg ctg acc tgg ggt gca acc acc ttc ctg tgt cca cct gtc agc   1363
Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu Cys Pro Pro Val Ser
                410                 415                 420

gat acc gat gac atg atg cgc gaa gtc gac cgt gct ctt tta gca atg   1411
Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg Ala Leu Leu Ala Met
```

```
            425                 430                 435

cct gag tac aac aag ggt gac atg atg gtt gtt gtt gca ggt tcc cct   1459
Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val Val Ala Gly Ser Pro
        440                 445                 450

cct ggt gtt acc ggt aac acc aac atg att cac gtc cac ctt ctt ggt   1507
Pro Gly Val Thr Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly
    455                 460                 465

gac gac aca agg att gca aag ctc taatcgctta aatctttcaa aaa         1554
Asp Asp Thr Arg Ile Ala Lys Leu
470                 475
```

<210> 74
<211> 477
<212> PRT
<213> Corynebacterium glutamicum

<400> 74

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Met Gly Val Asp Arg Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala
  1               5                  10                  15

Val Ala Ser Ala Asp Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp
             20                  25                  30

Val Ala Arg Leu Asn Phe Ser His Gly Asp His Pro Asp His Glu Gln
         35                  40                  45

Asn Tyr Lys Trp Val Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val
     50                  55                  60

Gly Ile Leu Ala Asp Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe
 65                  70                  75                  80

Thr Asp Gly Ala Thr Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr
                 85                  90                  95

Val Asp Asp Val Glu Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys
            100                 105                 110

Asn Leu Ala Lys Asp Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp
        115                 120                 125

Gly Lys Val Gly Leu Val Cys Val Ser Val Glu Gly Asn Asp Val Ile
    130                 135                 140

Cys Glu Val Val Glu Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser
145                 150                 155                 160

Leu Pro Gly Met Asp Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile
                165                 170                 175

Arg Asp Leu Arg Phe Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu
            180                 185                 190

Ser Phe Val Arg Ser Pro Ala Asp Ala Glu Leu Val His Lys Ile Met
        195                 200                 205

Asp Glu Glu Gly Arg Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro
```

```
    210                 215                 220

Glu Ala Val Thr Ser Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val
225                 230                 235                 240

Met Val Ala Arg Gly Asp Leu Gly Val Glu Val Pro Leu Glu Glu Val
                245                 250                 255

Pro Leu Val Gln Lys Arg Ala Ile Gln Ile Ala Arg Glu Asn Ala Lys
            260                 265                 270

Pro Val Ile Val Ala Thr Gln Met Leu Asp Ser Met Ile Glu Asn Ser
        275                 280                 285

Arg Pro Thr Arg Ala Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp
    290                 295                 300

Gly Ala Asp Ala Val Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp
305                 310                 315                 320

Pro His Asn Val Val Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu
                325                 330                 335

Thr Asp Gly Arg Val Pro Asp Leu Thr His Ile Pro Arg Thr Lys Arg
            340                 345                 350

Gly Val Ile Ser Tyr Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala
        355                 360                 365

Arg Ala Leu Val Ala Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val
    370                 375                 380

Ala Arg Leu His Ser His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu
385                 390                 395                 400

Ala Val Arg Ser Glu Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu
                405                 410                 415

Cys Pro Pro Val Ser Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg
            420                 425                 430

Ala Leu Leu Ala Met Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val
        435                 440                 445

Val Ala Gly Ser Pro Pro Gly Val Thr Gly Asn Thr Asn Met Ile His
    450                 455                 460

Val His Leu Leu Gly Asp Asp Thr Arg Ile Ala Lys Leu
465                 470                 475


<210> 75
<211> 1980
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1957)
<223> RXN02675
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<400> 75
aagtgtttca ttggaacact tgcgctgcca acttttttggt ttacgggcac aatgaaactg 60

ttggatggaa tttagagtgt ttgtagctta aggagctcaa atg aat gag ttt gac 115
Met Asn Glu Phe Asp
1 5

cag gac att ctc cag gag atc aag act gaa ctc gac gag tta att cta 163
Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu
10 15 20

gaa ctt gat gag gtg aca caa act cac agc gag gcc atc ggg cag gtc 211
Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val
25 30 35

tcc cca acc cat tac gtt ggt gcc cgc aac ctc atg cat tac gcg cat 259
Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His
40 45 50

ctt cgc acc aaa gac ctc cgt ggc ctg cag caa cgc ctc tcc tct gtg 307
Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln Arg Leu Ser Ser Val
55 60 65

gga gct acc cgc ttg act acc acc gaa cca gca gtg cag gcc cgc ctc 355
Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala Val Gln Ala Arg Leu
70 75 80 85

aag gcc gcc cgc aat gtt atc gga gct ttc gca ggt gaa ggc cca ctt 403
Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala Gly Glu Gly Pro Leu
90 95 100

tat cca ccc tca gat gtc gtc gat gcc ttc gaa gat gcc gat gag att 451
Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu Asp Ala Asp Glu Ile
105 110 115

ctc gac gag cac gcc gaa att ctc ctt ggc gaa ccc cta ccg gat act 499
Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu Pro Leu Pro Asp Thr
120 125 130

cca tcc tgc atc atg gtc acc ctg ccc acc gaa gcc gcc acc gac att 547
Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu Ala Ala Thr Asp Ile
135 140 145

gaa ctt gtc cgt ggc ttc gcc aaa agc ggc atg aat cta gct cgc atc 595
Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met Asn Leu Ala Arg Ile
150 155 160 165

aac tgt gca cac gac gat gaa acc gtc tgg aag cag atg atc gac aac 643
Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys Gln Met Ile Asp Asn
170 175 180

gtc cac acc gtt gca gaa gaa gtt ggc cgg gaa atc cgc gtc agc atg 691
Val His Thr Val Ala Glu Glu Val Gly Arg Glu Ile Arg Val Ser Met
185 190 195

gac ctc gcc gga cca aaa gta cgc acc ggc gaa atc gcc cca ggc gca 739
Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu Ile Ala Pro Gly Ala
200 205 210

gaa gta ggt cgc gca cga gta acc cgc gac gaa acc gga aaa gta ctg 787
Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu Thr Gly Lys Val Leu

```
    215                 220                 225

acg ccc gca aaa ctg tgg atc acc gcc cac ggc tcc gaa cca gtc cca   835
Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly Ser Glu Pro Val Pro
230                 235                 240                 245

gcc ccc gaa agc ctg ccc ggt cgc ccc gct ctg ccg att gaa gtc acc   883
Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu Pro Ile Glu Val Thr
                250                 255                 260

cca gaa tgg ttc gac aaa cta gaa atc ggc agc gtc atc aac gtc cca   931
Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser Val Ile Asn Val Pro
            265                 270                 275

gac acc cgc gga tcc cgc cga gca ttc acc gtg acc agg gtt ttt gat   979
Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp
        280                 285                 290

ggc gcg gtc ctc gcc gaa ggc cca caa aaa gcc tac atc tcc aac ggc   1027
Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala Tyr Ile Ser Asn Gly
    295                 300                 305

acc ctc ctg gaa cac aac tac gac cgc tcc cgg gtc tac ggc atc ccc   1075
Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg Val Tyr Gly Ile Pro
310                 315                 320                 325

gcc gta gtt cag cgc atc aac ctc aaa gtc ggc gac cgc ctc atc ctt   1123
Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly Asp Arg Leu Ile Leu
                330                 335                 340

acc gac gaa gaa ctc acc tac gat cca tcc ctc gga tcc ggc cgc aca   1171
Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu Gly Ser Gly Arg Thr
            345                 350                 355

cca cgc atc agc tgc acc ctt cca caa gca gtc gat gca att aaa gtc   1219
Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val Asp Ala Ile Lys Val
        360                 365                 370

ggg cac cgc gtg ctt ttc gac gac gga gcc atc gcc gca gtc tgc atc   1267
Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile Ala Ala Val Cys Ile
    375                 380                 385

gac aag acc tcc act gcc gac ggc cac aac gac gta gaa ttg gaa gtc   1315
Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp Val Glu Leu Glu Val
390                 395                 400                 405

acc cac gcc cgc cca caa ggc gta aac ctg gcc gca tac aag gga atc   1363
Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala Ala Tyr Lys Gly Ile
                410                 415                 420

aac ctc cca gac tcc gaa ctt cca ctc cca agc ctc act gaa gaa gac   1411
Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser Leu Thr Glu Glu Asp
            425                 430                 435

ctc caa cac ctg cgc ttt gtc gtc aaa tac gcc gac atc gca gcc atc   1459
Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala Asp Ile Ala Ala Ile
        440                 445                 450

tcc ttc atc cga aac gtc gcc gac gtg gaa tac ctc ctc caa gca ctc   1507
Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu
    455                 460                 465
```

```
gcc gac atc gga gat cca gta gcc gtc gaa cgc ctt ggc ctc gtc ctt   1555
Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg Leu Gly Leu Val Leu
470                 475                 480                 485

aaa atc gag acc atc cca ggc tac gaa ggc ctc gcc caa atc ctc ctg   1603
Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu Ala Gln Ile Leu Leu
                490                 495                 500

acc ggc atg cgc cac gaa aac ttc ggc atc atg atc gcc cgc gga gac   1651
Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala Arg Gly Asp
            505                 510                 515

ctc gcc gtc gaa ctc ggc ttc gac cgc atg gca gaa gtc ccc caa ctg   1699
Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val Pro Gln Leu
        520                 525                 530

atc atg gcc ctt gcc gaa gcc gcc cac gtc cca acc atc ttg gcc acc   1747
Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile Leu Ala Thr
    535                 540                 545

caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct cgc gca gaa   1795
Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser Arg Ala Glu
550                 555                 560                 565

atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc atg ctg aac   1843
Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val Met Leu Asn
                570                 575                 580

aag gga cca cac atc aac gac gcc atc aag gtc ctc acc gaa atg agc   1891
Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr Glu Met Ser
            585                 590                 595

cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg ctg cgc aag   1939
Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu Leu Arg Lys
        600                 605                 610

gtg aag agc tgg gaa gag taactcacaa aggcgattgg cgt                 1980
Val Lys Ser Trp Glu Glu
    615
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<210> 76
<211> 619
<212> PRT
<213> Corynebacterium glutamicum

<400> 76

```
Met Asn Glu Phe Asp Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu
  1               5                  10                  15

Asp Glu Leu Ile Leu Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu
             20                  25                  30

Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
         35                  40                  45

Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
     50                  55                  60

Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
```

65 70 75 80

Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
85 90 95

Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
100 105 110

Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu
115 120 125

Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
130 135 140

Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met
145 150 155 160

Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys
165 170 175

Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
180 185 190

Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu
195 200 205

Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu
210 215 220

Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
225 230 235 240

Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu
245 250 255

Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser
260 265 270

Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val
275 280 285

Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala
290 295 300

Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg
305 310 315 320

Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly
325 330 335

Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu
340 345 350

Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val
355 360 365

Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile
370 375 380

Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
385 390 395 400

```
Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala
                405                 410                 415

Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
            420                 425                 430

Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
        435                 440                 445

Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
    450                 455                 460

Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg
465                 470                 475                 480

Leu Gly Leu Val Leu Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu
                485                 490                 495

Ala Gln Ile Leu Leu Thr Gly Met Arg His Glu Asn Phe Gly Ile Met
            500                 505                 510

Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala
        515                 520                 525

Glu Val Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro
    530                 535                 540

Thr Ile Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu
545                 550                 555                 560

Pro Ser Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu
                565                 570                 575

Cys Val Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val
            580                 585                 590

Leu Thr Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg
        595                 600                 605

Leu Leu Leu Arg Lys Val Lys Ser Trp Glu Glu
    610                 615
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<210> 77
<211> 386
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(363)
<223> FRXA02675

<400> 77

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atc ctc atg acc ggc atg cgc cac gaa aac ttc ggc atc atg atc gcc   48
Ile Leu Met Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala
  1               5                  10                  15

cgc gga gac ctc gcc gtc gaa ctc ggc ttc gac cgc atg gca gaa gtc   96
Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val
```

```
            20                  25                  30

ccc caa ctg atc atg gcc ctt gca gaa gcc gcc cac gtc cca acc atc   144
Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile
        35                  40                  45

ttg gcc acc caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct   192
Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser
    50                  55                  60

cgc gca gaa atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc   240
Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val
65                  70                  75                  80

atg ctg aac aag gga cca cac atc aac gac gcc atc aag gtc ctc acc   288
Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr
                85                  90                  95

gaa atg agc cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg   336
Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu
            100                 105                 110

ctg cgc aag gtg aag agc tgg gaa gag taactcacaa aggcgattgg        383
Leu Arg Lys Val Lys Ser Trp Glu Glu
        115                 120

cgt                                                              386
```

<210> 78
<211> 121
<212> PRT
<213> Corynebacterium glutamicum

<400> 78

```
Ile Leu Met Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala
  1               5                  10                  15

Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val
            20                  25                  30

Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile
        35                  40                  45

Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser
    50                  55                  60

Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val
65                  70                  75                  80

Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr
                85                  90                  95

Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu
            100                 105                 110

Leu Arg Lys Val Lys Ser Trp Glu Glu
        115                 120
```

<210> 79

<211> 1522
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1522)
<223> FRXA02695

<400> 79
aagtgtttca ttggaacact tgcgctgcca acttttttggt ttacgggcac aatgaaactg 60

ttggatggaa tttagagtgt ttgtagctta aggagctcaa atg aat gag ttt gac 115
Met Asn Glu Phe Asp
1 5

cag gac att ctc cag gag atc aag act gaa ctc gac gag tta att cta 163
Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu
10 15 20

gaa ctt gat gag gtg aca caa act cac agc gag gcc atc ggg cag gtc 211
Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val
25 30 35

tcc cca acc cat tac gtt ggt gcc cgc aac ctc atg cat tac gcg cat 259
Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His
40 45 50

ctt cgc acc aaa gac ctc cgt ggc ctg cag caa cgc ctc tcc tct gtg 307
Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln Arg Leu Ser Ser Val
55 60 65

gga gct acc cgc ttg act acc acc gaa cca gca gtg cag gcc cgc ctc 355
Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala Val Gln Ala Arg Leu
70 75 80 85

aag gcc gcc cgc aat gtt atc gga gct ttc gca ggt gaa ggc cca ctt 403
Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala Gly Glu Gly Pro Leu
90 95 100

tat cca ccc tca gat gtc gtc gat gcc ttc gaa gat gcc gat gag att 451
Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu Asp Ala Asp Glu Ile
105 110 115

ctc gac gag cac gcc gaa att ctc ctt ggc gaa ccc cta ccg gat act 499
Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu Pro Leu Pro Asp Thr
120 125 130

cca tcc tgc atc atg gtc acc ctg ccc acc gaa gcc gcc acc gac att 547
Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu Ala Ala Thr Asp Ile
135 140 145

gaa ctt gtc cgt ggc ttc gcc aaa agc ggc atg aat cta gct cgc atc 595
Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met Asn Leu Ala Arg Ile
150 155 160 165

aac tgt gca cac gac gat gaa acc gtc tgg aag cag atg atc gac aac 643
Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys Gln Met Ile Asp Asn
170 175 180

gtc cac acc gtt gca gaa gaa gtt ggc cgg gaa atc cgc gtc agc atg 691

```
Val His Thr Val Ala Glu Glu Val Gly Arg Glu Ile Arg Val Ser Met
            185                 190                 195

gac ctc gcc gga cca aaa gta cgc acc ggc gaa atc gcc cca ggc gca   739
Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu Ile Ala Pro Gly Ala
        200                 205                 210

gaa gta ggt cgc gca cga gta acc cgc gac gaa acc gga aaa gta ctg   787
Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu Thr Gly Lys Val Leu
    215                 220                 225

acg ccc gca aaa ctg tgg atc acc gcc cac ggc tcc gaa cca gtc cca   835
Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly Ser Glu Pro Val Pro
230                 235                 240                 245

gcc ccc gaa agc ctg ccc ggt cgc ccc gct ctg ccg att gaa gtc acc   883
Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu Pro Ile Glu Val Thr
                250                 255                 260

cca gaa tgg ttc gac aaa cta gaa atc ggc agc gtc atc aac gtc cca   931
Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser Val Ile Asn Val Pro
            265                 270                 275

gac acc cgc gga tcc cgc cga gca ttc acc gtg acc agg gtt ttt gat   979
Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp
        280                 285                 290

ggc gcg gtc ctc gcc gaa ggc cca caa aaa gcc tac atc tcc aac ggc   1027
Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala Tyr Ile Ser Asn Gly
    295                 300                 305

acc ctc ctg gaa cac aac tac gac cgc tcc cgg gtc tac ggc atc ccc   1075
Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg Val Tyr Gly Ile Pro
310                 315                 320                 325

gcc gta gtt cag cgc atc aac ctc aaa gtc ggc gac cgc ctc atc ctt   1123
Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly Asp Arg Leu Ile Leu
                330                 335                 340

acc gac gaa gaa ctc acc tac gat cca tcc ctc gga tcc ggc cgc aca   1171
Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu Gly Ser Gly Arg Thr
            345                 350                 355

cca cgc atc agc tgc acc ctt cca caa gca gtc gat gca att aaa gtc   1219
Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val Asp Ala Ile Lys Val
        360                 365                 370

ggg cac cgc gtg ctt ttc gac gac gga gcc atc gcc gca gtc tgc atc   1267
Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile Ala Ala Val Cys Ile
    375                 380                 385

gac aag acc tcc act gcc gac ggc cac aac gac gta gaa ttg gaa gtc   1315
Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp Val Glu Leu Glu Val
390                 395                 400                 405

acc cac gcc cgc cca caa ggc gta aac ctg gcc gca tac aag gga atc   1363
Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala Ala Tyr Lys Gly Ile
                410                 415                 420

aac ctc cca gac tcc gaa ctt cca ctc cca agc ctc act gaa gaa gac   1411
Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser Leu Thr Glu Glu Asp
```

```
            425                 430                 435

ctc caa cac ctg cgc ttt gtc gtc aaa tac gcc gac atc gca gcc atc   1459
Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala Asp Ile Ala Ala Ile
        440                 445                 450

tcc ttc atc cga aac gtc gcc gac gtg gaa tac ctc ctc caa gca ctc   1507
Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr Leu Leu Gln Ala Leu
    455                 460                 465

gcc gac atc gga gat                                               1522
Ala Asp Ile Gly Asp
470
```

<210> 80
<211> 474
<212> PRT
<213> Corynebacterium glutamicum

<400> 80

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Met Asn Glu Phe Asp Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu
  1               5                  10                  15

Asp Glu Leu Ile Leu Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu
             20                  25                  30

Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
         35                  40                  45

Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
     50                  55                  60

Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
 65                  70                  75                  80

Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
                 85                  90                  95

Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
            100                 105                 110

Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu
        115                 120                 125

Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
    130                 135                 140

Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met
145                 150                 155                 160

Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys
                165                 170                 175

Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
            180                 185                 190

Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu
        195                 200                 205

Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu
```

```
    210                 215                 220

Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
225                 230                 235                 240

Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu
                245                 250                 255

Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser
            260                 265                 270

Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val
        275                 280                 285

Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala
    290                 295                 300

Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg
305                 310                 315                 320

Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly
                325                 330                 335

Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu
            340                 345                 350

Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val
        355                 360                 365

Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile
    370                 375                 380

Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
385                 390                 395                 400

Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala
                405                 410                 415

Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
            420                 425                 430

Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
        435                 440                 445

Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr
    450                 455                 460

Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp
465                 470
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<210> 81
<211> 2022
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1999)
<223> RXA00682

<400> 81
ataggcacct tcgatttcag ctcaatcacc gtcgcaatga ccggcacgaa gtaaaaccac 60

cgcatctttt cgtcgaaaag catctaaaag gagtttgacc atg gct aat aaa tct 115
Met Ala Asn Lys Ser
1 5

ttc ccc aag ccc tcc gat ctt cca gtg ccc aag ggc gct gaa ggt tgg 163
Phe Pro Lys Pro Ser Asp Leu Pro Val Pro Lys Gly Ala Glu Gly Trp
10 15 20

gaa gat ctg tac ccg tac tac ctc gtt ttc caa gac aag ctc atg gat 211
Glu Asp Leu Tyr Pro Tyr Tyr Leu Val Phe Gln Asp Lys Leu Met Asp
25 30 35

caa gag aat gag aaa ttc tgg ttc tgc gat tca cag cac tgg cca act 259
Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser Gln His Trp Pro Thr
40 45 50

gtg ttc aag cct ttt gaa act atc ggt ggt gaa ttc gct gta aag tgc 307
Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu Phe Ala Val Lys Cys
55 60 65

ctc ggc caa tac aac gct cgg cat ttg atg atc ccg aat gcc aat ggc 355
Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile Pro Asn Ala Asn Gly
70 75 80 85

atc gag ttc cgc gtg cat ctg gga tac ctc tat atg tcc cct att cca 403
Ile Glu Phe Arg Val His Leu Gly Tyr Leu Tyr Met Ser Pro Ile Pro
90 95 100

gtg cct gaa gat cag att gcg gaa cgc gtc ccc atg ttc cag gaa cgc 451
Val Pro Glu Asp Gln Ile Ala Glu Arg Val Pro Met Phe Gln Glu Arg
105 110 115

atc acg cac tac ttc caa aac tgg gag cca atg ctg gca aat tgg aag 499
Ile Thr His Tyr Phe Gln Asn Trp Glu Pro Met Leu Ala Asn Trp Lys
120 125 130

gag cga gta tta gga acc atc aat gag ctg gaa tct cta gaa ttc aag 547
Glu Arg Val Leu Gly Thr Ile Asn Glu Leu Glu Ser Leu Glu Phe Lys
135 140 145

cca ctg cct gac tac gtg cct atc gat gat att gtc tcc gga aaa gcc 595
Pro Leu Pro Asp Tyr Val Pro Ile Asp Asp Ile Val Ser Gly Lys Ala
150 155 160 165

aaa gac ggc acc gaa gta ctc atg gaa aac ttc gat cgg ctc att cag 643
Lys Asp Gly Thr Glu Val Leu Met Glu Asn Phe Asp Arg Leu Ile Gln
170 175 180

ctc gcc tac caa aac tgg caa tac cac ttt gag ttc ctc aac ttg ggt 691
Leu Ala Tyr Gln Asn Trp Gln Tyr His Phe Glu Phe Leu Asn Leu Gly
185 190 195

tac atc gct tac cta gat ttc ttc aat ttc tgc aag gaa gtc ttc cca 739
Tyr Ile Ala Tyr Leu Asp Phe Phe Asn Phe Cys Lys Glu Val Phe Pro
200 205 210

gat atc cct gat caa tca att tcg atg atg gtt cag ggc gtg gat atg 787
Asp Ile Pro Asp Gln Ser Ile Ser Met Met Val Gln Gly Val Asp Met

```
    215                 220                 225

gag ctg ttc cgc ccc gat gat gaa cta aag att ctg gca cag cta gcg   835
Glu Leu Phe Arg Pro Asp Asp Glu Leu Lys Ile Leu Ala Gln Leu Ala
230                 235                 240                 245

gtc gac ctt ggc ctg caa act cac ttt gcc aac ccg gat gat ccg caa   883
Val Asp Leu Gly Leu Gln Thr His Phe Ala Asn Pro Asp Asp Pro Gln
                250                 255                 260

gct acc ttg gct gct atc gca aag gca gaa ggc ggc gcg aca tgg ata   931
Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly Gly Ala Thr Trp Ile
            265                 270                 275

gcg cgc tgg gaa gaa gca caa gat ccg tgg ttc aac ttc acc gtc ggt   979
Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe Asn Phe Thr Val Gly
        280                 285                 290

aat ggc ttc tac ggt cac gat aaa tac tgg atc gag cac ctg gaa ctt   1027
Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile Glu His Leu Glu Leu
    295                 300                 305

cca ctg ggg tac atc gcg gat tac atc cgc cgc cta gat gaa ggc caa   1075
Pro Leu Gly Tyr Ile Ala Asp Tyr Ile Arg Arg Leu Asp Glu Gly Gln
310                 315                 320                 325

acc atc tcc cgc ccg aaa gat gaa ctc atc gca gaa aag gaa cgc gtg   1123
Thr Ile Ser Arg Pro Lys Asp Glu Leu Ile Ala Glu Lys Glu Arg Val
                330                 335                 340

gtg gaa gaa tac cgc gac ctt ttg gat gga gaa caa ctc gcg cag ttt   1171
Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu Gln Leu Ala Gln Phe
            345                 350                 355

gat gct aaa tgc ggc ctc gct gct act gca tac ccc tat gtg gaa aac   1219
Asp Ala Lys Cys Gly Leu Ala Ala Thr Ala Tyr Pro Tyr Val Glu Asn
        360                 365                 370

cat aac ttc tac atc gag cac tgg acc atg tca gta ttt tgg cgc aaa   1267
His Asn Phe Tyr Ile Glu His Trp Thr Met Ser Val Phe Trp Arg Lys
    375                 380                 385

gta cgc gaa ctt tcc cgc act ctc cag ggc tac ggt ttc tgg gag aac   1315
Val Arg Glu Leu Ser Arg Thr Leu Gln Gly Tyr Gly Phe Trp Glu Asn
390                 395                 400                 405

gag gat gac atg ttg tac ctc aac cgc act gaa gtc cgc gat gtc ctc   1363
Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu Val Arg Asp Val Leu
                410                 415                 420

ttc gac ctg gct act gcg tgg ggt gtc ggc gca ccc ggt ggt cca att   1411
Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala Pro Gly Gly Pro Ile
            425                 430                 435

ggc acg atc att tgg ccg gaa gaa att gag cga aga aaa gca att gtc   1459
Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg Arg Lys Ala Ile Val
        440                 445                 450

acc gct ttg aaa act gcc cga cca gcg cca gct ctt aac act cct cca   1507
Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala Leu Asn Thr Pro Pro
    455                 460                 465
```

```
gag tcc atc acc gaa cct ttc acc cgc atg ctc tgg gga atc acc acc   1555
Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu Trp Gly Ile Thr Thr
470                 475                 480                 485

gaa cag gtg caa tca tgg ttg ggc aat gac gag gat gcc gaa gaa gga   1603
Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu Asp Ala Glu Glu Gly
                490                 495                 500

acc ctt aaa ggc atg gct gca tcc cct ggt gtg gtg gaa ggc tac gct   1651
Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val Val Glu Gly Tyr Ala
            505                 510                 515

cga gta att ctc agc gca gat gac ctt tca gaa atc cag cag gat gaa   1699
Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu Ile Gln Gln Asp Glu
        520                 525                 530

atc ctc gtt gcc cct gta aca gca cct tct tgg ggc cca atc ttt ggc   1747
Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp Gly Pro Ile Phe Gly
    535                 540                 545

aaa atc aag gca aca gtc act gat att ggt ggc atg atg agc cat gct   1795
Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly Met Met Ser His Ala
550                 555                 560                 565

gcg atc gtg tgc cgc gaa tac ggc ttg ccg gct gtt act gga act ggc   1843
Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala Val Thr Gly Thr Gly
                570                 575                 580

gct gca tcc acc acc atc aaa acc ggc gat tac ctc aag gtc gat gga   1891
Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr Leu Lys Val Asp Gly
            585                 590                 595

acc aag ggc aag gtt gtc att gtt gat cca gat gcg cca cgc atc gaa   1939
Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp Ala Pro Arg Ile Glu
        600                 605                 610

gga ccc ggc gcg cac agc cat gcg cac tca gta gca gca cat ggg gtg   1987
Gly Pro Gly Ala His Ser His Ala His Ser Val Ala Ala His Gly Val
    615                 620                 625

gat aca cat gcc tagtccacgc actgttctta tca                        2022
Asp Thr His Ala
630
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<210> 82
<211> 633
<212> PRT
<213> Corynebacterium glutamicum

<400> 82

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Met Ala Asn Lys Ser Phe Pro Lys Pro Ser Asp Leu Pro Val Pro Lys
  1               5                  10                  15

Gly Ala Glu Gly Trp Glu Asp Leu Tyr Pro Tyr Tyr Leu Val Phe Gln
             20                  25                  30

Asp Lys Leu Met Asp Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser
         35                  40                  45
```

```
Gln His Trp Pro Thr Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu
     50                  55                  60

Phe Ala Val Lys Cys Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile
 65                  70                  75                  80

Pro Asn Ala Asn Gly Ile Glu Phe Arg Val His Leu Gly Tyr Leu Tyr
                85                  90                  95

Met Ser Pro Ile Pro Val Pro Glu Asp Gln Ile Ala Glu Arg Val Pro
            100                 105                 110

Met Phe Gln Glu Arg Ile Thr His Tyr Phe Gln Asn Trp Glu Pro Met
        115                 120                 125

Leu Ala Asn Trp Lys Glu Arg Val Leu Gly Thr Ile Asn Glu Leu Glu
    130                 135                 140

Ser Leu Glu Phe Lys Pro Leu Pro Asp Tyr Val Pro Ile Asp Asp Ile
145                 150                 155                 160

Val Ser Gly Lys Ala Lys Asp Gly Thr Glu Val Leu Met Glu Asn Phe
                165                 170                 175

Asp Arg Leu Ile Gln Leu Ala Tyr Gln Asn Trp Gln Tyr His Phe Glu
            180                 185                 190

Phe Leu Asn Leu Gly Tyr Ile Ala Tyr Leu Asp Phe Phe Asn Phe Cys
        195                 200                 205

Lys Glu Val Phe Pro Asp Ile Pro Asp Gln Ser Ile Ser Met Met Val
    210                 215                 220

Gln Gly Val Asp Met Glu Leu Phe Arg Pro Asp Asp Glu Leu Lys Ile
225                 230                 235                 240

Leu Ala Gln Leu Ala Val Asp Leu Gly Leu Gln Thr His Phe Ala Asn
                245                 250                 255

Pro Asp Asp Pro Gln Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly
            260                 265                 270

Gly Ala Thr Trp Ile Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe
        275                 280                 285

Asn Phe Thr Val Gly Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile
    290                 295                 300

Glu His Leu Glu Leu Pro Leu Gly Tyr Ile Ala Asp Tyr Ile Arg Arg
305                 310                 315                 320

Leu Asp Glu Gly Gln Thr Ile Ser Arg Pro Lys Asp Glu Leu Ile Ala
                325                 330                 335

Glu Lys Glu Arg Val Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu
            340                 345                 350

Gln Leu Ala Gln Phe Asp Ala Lys Cys Gly Leu Ala Ala Thr Ala Tyr
        355                 360                 365

Pro Tyr Val Glu Asn His Asn Phe Tyr Ile Glu His Trp Thr Met Ser
```

370 375 380

Val Phe Trp Arg Lys Val Arg Glu Leu Ser Arg Thr Leu Gln Gly Tyr
385 390 395 400

Gly Phe Trp Glu Asn Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu
405 410 415

Val Arg Asp Val Leu Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala
420 425 430

Pro Gly Gly Pro Ile Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg
435 440 445

Arg Lys Ala Ile Val Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala
450 455 460

Leu Asn Thr Pro Pro Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu
465 470 475 480

Trp Gly Ile Thr Thr Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu
485 490 495

Asp Ala Glu Glu Gly Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val
500 505 510

Val Glu Gly Tyr Ala Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu
515 520 525

Ile Gln Gln Asp Glu Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp
530 535 540

Gly Pro Ile Phe Gly Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly
545 550 555 560

Met Met Ser His Ala Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala
565 570 575

Val Thr Gly Thr Gly Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr
580 585 590

Leu Lys Val Asp Gly Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp
595 600 605

Ala Pro Arg Ile Glu Gly Pro Gly Ala His Ser His Ala His Ser Val
610 615 620

Ala Ala His Gly Val Asp Thr His Ala
625 630

<210> 83
<211> 1215
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1192)
<223> RXA00683

<400> 83
ggacaaagct atcgggttcc gggagaacct ctccttccgc gtccccactt ctgttcccgt 60

gacttggaac gcttaacgct ttattaaata aggagacacc atg acc aac agt ttg 115
Met Thr Asn Ser Leu
1 5

aac atc ccg ttt gtc cag cgc ttc gat gaa ggc ctg gat cct gtt cta 163
Asn Ile Pro Phe Val Gln Arg Phe Asp Glu Gly Leu Asp Pro Val Leu
10 15 20

gaa gta ctc ggt ggc aag ggc gct tca cta gtc acc atg aca gat gct 211
Glu Val Leu Gly Gly Lys Gly Ala Ser Leu Val Thr Met Thr Asp Ala
25 30 35

gga atg ccc gtt cca cct gga ttt gtg gtc act act gcc agc ttt gat 259
Gly Met Pro Val Pro Pro Gly Phe Val Val Thr Thr Ala Ser Phe Asp
40 45 50

gaa ttc atc cgt gaa gca ggg gtt gct gaa cac atc gat aaa ttc cta 307
Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His Ile Asp Lys Phe Leu
55 60 65

aac gat ctc gat gca gaa gat gtt aag gaa gtg gat cga gtt tct gcg 355
Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val Asp Arg Val Ser Ala
70 75 80 85

atc atc cgc gat gag ctg tgc agt ctt gac gtt cca gag aat gct cgt 403
Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val Pro Glu Asn Ala Arg
90 95 100

ttc gca gtg cac cag gct tat cgc gat ctc atg gaa cga tgc ggt ggc 451
Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met Glu Arg Cys Gly Gly
105 110 115

gac gtc ccg gtt gct gtc cgg tca tcg gcc act gcc gaa gat ctg ccc 499
Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr Ala Glu Asp Leu Pro
120 125 130

gat gct tcc ttc gca ggg caa cag gac acc tat ctg tgg caa gtc ggt 547
Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr Leu Trp Gln Val Gly
135 140 145

ttg agc gct gtc act gaa cac atc cgt aaa tgc tgg gct tcg ctg ttc 595
Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys Trp Ala Ser Leu Phe
150 155 160 165

act tcc cgt gcc att atc tac cgt ctg aaa aac aac atc ccc aat gag 643
Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn Asn Ile Pro Asn Glu
170 175 180

ggc ctc tcc atg gcg gta gtt gtt caa aaa atg gtc aac tct cgt gtc 691
Gly Leu Ser Met Ala Val Val Val Gln Lys Met Val Asn Ser Arg Val
185 190 195

gca ggc gtg gca atc act atg aat cct tcc aac ggc gac cgc tcg aag 739
Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn Gly Asp Arg Ser Lys
200 205 210

atc acc atc gat tcc tca tgg ggt gtt ggt gaa atg gtg gtc tca ggt 787
Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu Met Val Val Ser Gly

```
    215                 220                 225

gaa gtg aca cca gac aat atc ttg ctg gac aag atc acg ctg cag gtt   835
Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys Ile Thr Leu Gln Val
230                 235                 240                 245

gtc tcc gaa cac att gga agc aaa cac gct gaa ctc atc ccc gat gcc   883
Val Ser Glu His Ile Gly Ser Lys His Ala Glu Leu Ile Pro Asp Ala
                250                 255                 260

acc agt gga agc ctc gtg gaa aag ccc gtt gat gaa gaa cgc gca aac   931
Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp Glu Glu Arg Ala Asn
            265                 270                 275

cgc cgc agt ctg act gat gag gaa atg ctc gct gtg gca caa atg gct   979
Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala Val Ala Gln Met Ala
        280                 285                 290

aag cgt gca gaa aaa cac tac aag tgc cca caa gat atc gaa tgg gcg   1027
Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln Asp Ile Glu Trp Ala
    295                 300                 305

ctg gac gct gat ctg cca gat gga gaa aac ctt ctg tta ttg caa tcc   1075
Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu Leu Leu Leu Gln Ser
310                 315                 320                 325

cgc ccg gaa act atc cac tcc aac ggt gtg aag aag gaa acc cca act   1123
Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys Lys Glu Thr Pro Thr
                330                 335                 340

ccg cag gct gcc aaa acc ata ggc acc ttc gat ttc agc tca atc acc   1171
Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp Phe Ser Ser Ile Thr
            345                 350                 355

gtc gca atg acc ggc acg aag taaaaccacc gcatcttttc gtc            1215
Val Ala Met Thr Gly Thr Lys
        360
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<210> 84
<211> 364
<212> PRT
<213> Corynebacterium glutamicum

<400> 84

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Met Thr Asn Ser Leu Asn Ile Pro Phe Val Gln Arg Phe Asp Glu Gly
  1               5                  10                  15

Leu Asp Pro Val Leu Glu Val Leu Gly Gly Lys Gly Ala Ser Leu Val
             20                  25                  30

Thr Met Thr Asp Ala Gly Met Pro Val Pro Pro Gly Phe Val Val Thr
         35                  40                  45

Thr Ala Ser Phe Asp Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His
     50                  55                  60

Ile Asp Lys Phe Leu Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val
 65                  70                  75                  80

Asp Arg Val Ser Ala Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val
```

```
                85                  90                  95

Pro Glu Asn Ala Arg Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met
            100                 105                 110

Glu Arg Cys Gly Gly Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr
        115                 120                 125

Ala Glu Asp Leu Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr
    130                 135                 140

Leu Trp Gln Val Gly Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys
145                 150                 155                 160

Trp Ala Ser Leu Phe Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn
                165                 170                 175

Asn Ile Pro Asn Glu Gly Leu Ser Met Ala Val Val Val Gln Lys Met
            180                 185                 190

Val Asn Ser Arg Val Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn
        195                 200                 205

Gly Asp Arg Ser Lys Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu
    210                 215                 220

Met Val Val Ser Gly Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys
225                 230                 235                 240

Ile Thr Leu Gln Val Val Ser Glu His Ile Gly Ser Lys His Ala Glu
                245                 250                 255

Leu Ile Pro Asp Ala Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp
            260                 265                 270

Glu Glu Arg Ala Asn Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala
        275                 280                 285

Val Ala Gln Met Ala Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln
    290                 295                 300

Asp Ile Glu Trp Ala Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu
305                 310                 315                 320

Leu Leu Leu Gln Ser Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys
                325                 330                 335

Lys Glu Thr Pro Thr Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp
            340                 345                 350

Phe Ser Ser Ile Thr Val Ala Met Thr Gly Thr Lys
        355                 360
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<210> 85
<211> 1860
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1837)
<223> RXN00635

<400> 85
ctggcaggcg ggcgaagcgt ggcaacaact ggaatttaag agcacaattg aagtcgcacc 60

aagttaggca acacaatagc cataacgttg aggagttcag atg gca cac agc tac 115
Met Ala His Ser Tyr
1 5

gca gaa caa tta att gac act ttg gaa gct caa ggt gtg aag cga att 163
Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile
10 15 20

tat ggt ttg gtg ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc 211
Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg
25 30 35

caa tca gat att gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg 259
Gln Ser Asp Ile Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala
40 45 50

ttt gca gcc ggt gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt 307
Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys
55 60 65

gct gct tct tgt ggt cct gga aac aca cac ctg att cag ggt ctt tat 355
Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr
70 75 80 85

gat tcg cat cga aat ggt gcg aag gtg ttg gcc atc gct agc cat att 403
Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile
90 95 100

ccg agt gcc cag att ggt tcg acg ttc ttc cag gaa acg cat ccg gag 451
Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu
105 110 115

att ttg ttt aag gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt 499
Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly
120 125 130

gag cag ggt gaa cgc att ttg cat cac gcg att cag tcc acc atg gcg 547
Glu Gln Gly Glu Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala
135 140 145

ggt aaa ggt gtg tcg gtg gta gtg att cct ggt gat atc gct aag gaa 595
Gly Lys Gly Val Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu
150 155 160 165

gac gca ggt gac ggt act tat tcc aat tcc act att tct tct ggc act 643
Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr
170 175 180

cct gtg gtg ttc ccg gat cct act gag gct gca gcg ctg gtg gag gcg 691
Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala
185 190 195

att aac aac gct aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag 739
Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys
200 205 210

```
aat gct cgc gcg cag gtg ttg gag ttg gcg gag aag att aaa tca ccg   787
Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro
    215                 220                 225

atc ggg cat gcg ctg ggt ggt aag cag tac atc cag cat gag aat ccg   835
Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro
230                 235                 240                 245

ttt gag gtc ggc atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat   883
Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp
                250                 255                 260

gcg tcc aat gag gcg gat ctg ctg att cta ttg ggt acg gat ttc cct   931
Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro
            265                 270                 275

tat tct gat ttc ctt cct aaa gac aac gtt gcc cag gtg gat atc aac   979
Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn
        280                 285                 290

ggt gcg cac att ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt  1027
Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly
    295                 300                 305

gat gtt gct gca aca atc gaa aat att ttg cct cat gtg aag gaa aaa  1075
Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys
310                 315                 320                 325

aca gat cgt tcc ttc ctt gat cgg atg ctc aag gca cac gag cgt aag  1123
Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys
                330                 335                 340

ttg agc tcg gtg gta gag acg tac aca cat aac gtc gag aag cat gtg  1171
Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val
            345                 350                 355

cct att cac cct gaa tac gtt gcc tct att ttg aac gag ctg gcg gat  1219
Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp
        360                 365                 370

aag gat gcg gtg ttt act gtg gat acc ggc atg tgc aat gtg tgg cat  1267
Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His
    375                 380                 385

gcg agg tac atc gag aat ccg gag gga acg cgc gac ttt gtg ggt tca  1315
Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser
390                 395                 400                 405

ttc cgc cac ggc acg atg gct aat gcg ttg cct cat gcg att ggt gcg  1363
Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala
                410                 415                 420

caa agt gtt gat cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt  1411
Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly
            425                 430                 435

ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa  1459
Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln
        440                 445                 450
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ctt ccg ctg aag gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg   1507
Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val
    455                 460                 465

aag ttg gag atg ctc gtg gag gga cag cca gaa ttt ggt act gac cat   1555
Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His
470                 475                 480                 485

gag gaa gtg aat ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg   1603
Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser
                490                 495                 500

gta cgc atc acc gat ccg aag aaa gtt cgc gag cag cta gct gag gca   1651
Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala
            505                 510                 515

ttg gca tat cct gga cct gta ctg atc gat atc gtc acg gat cct aat   1699
Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn
        520                 525                 530

gcg ctg tcg atc cca cca acc atc acg tgg gaa cag gtc atg gga ttc   1747
Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe
    535                 540                 545

agc aag gcg gcc acc cga acc gtc ttt ggt gga gga gta gga gcg atg   1795
Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met
550                 555                 560                 565

atc gat ctg gcc cgt tcg aac ata agg aat att cct act cca           1837
Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro
                570                 575

tgatgattga tacacctgct gtt                                        1860
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<210> 86
<211> 579
<212> PRT
<213> Corynebacterium glutamicum

<400> 86

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Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
  1               5                  10                  15

Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
             20                  25                  30

Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
         35                  40                  45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
     50                  55                  60

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
 65                  70                  75                  80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
                 85                  90                  95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
            100                 105                 110
```

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
115 120 125

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
130 135 140

Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
145 150 155 160

Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
165 170 175

Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
180 185 190

Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
195 200 205

Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
210 215 220

Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
225 230 235 240

Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
245 250 255

Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
260 265 270

Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
275 280 285

Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
290 295 300

Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
305 310 315 320

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
325 330 335

Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
340 345 350

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
355 360 365

Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
370 375 380

Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
385 390 395 400

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
405 410 415

His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
420 425 430

Sequence Listing

```
Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
        435                 440                 445

Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
    450                 455                 460

Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
465                 470                 475                 480

Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
                485                 490                 495

Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
            500                 505                 510

Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
        515                 520                 525

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
    530                 535                 540

Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
545                 550                 555                 560

Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
                565                 570                 575

Pro Thr Pro
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US-09-895-150-87

<210> 87
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (88)..(552)
<223> FRXA02807

<400> 87
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caatagccat aacgttgagg agttcagatg gca cac agc tac gca gaa caa tta 114
                               Met Ala His Ser Tyr Ala Glu Gln Leu
                                 1   5

att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 162
Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
 10   15   20   25

ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 210
Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
                 30   35   40

gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt 258
Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly
             45   50   55

gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt 306
```
```

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Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys
          60                  65                  70

ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga   354
Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg
     75                  80                  85

aat ggt gcg aag gtg ttg gcc atc gct agc cat att ccg agt gcc cag   402
Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln
 90                  95                 100                 105

att ggt tcg acg ttc ttc cag gaa acg cat ccg gag att ttg ttt aag   450
Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys
                110                 115                 120

gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt gag cag ggt gaa   498
Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu
            125                 130                 135

cgc att ttg cat cac gcg att cag tcc acc atg gcg ggt aaa ggt gtg   546
Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val
        140                 145                 150

tcg gtg                                                          552
Ser Val
    155
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09/25/2003 15:50:50

<210> 88
<211> 155
<212> PRT
<213> Corynebacterium glutamicum

<400> 88

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Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
  1               5                  10                  15

Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
            20                  25                  30

Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
        35                  40                  45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
    50                  55                  60

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
65                  70                  75                  80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
                85                  90                  95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
            100                 105                 110

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
        115                 120                 125

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
    130                 135                 140
```

```
Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val
145                 150                 155


<210> 89
<211> 944
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(921)
<223> FRXA00635

<400> 89
ggt acg gat ttc cct tat tct gat ttc ctt cct aaa gac aac gtt gcc   48
Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
  1               5                  10                  15

cag gtg gat atc aac ggt gcg cac att ggt cga cgt acc acg gtg aag   96
Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
             20                  25                  30

tat ccg gtg acc ggt gat gtt gct gca aca atc gaa aat att ttg cct   144
Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
         35                  40                  45

cat gtg aag gaa aaa aca gat cgt tcc ttc ctt gat cgg atg ctc aag   192
His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
     50                  55                  60

gca cac gag cgt aag ttg agc tcg gtg gta gag acg tac aca cat aac   240
Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 65                  70                  75                  80

gtc gag aag cat gtg cct att cac cct gaa tac gtt gcc tct att ttg   288
Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
                 85                  90                  95

aac gag ctg gcg gat aag gat gcg gtg ttt act gtg gat acc ggc atg   336
Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
            100                 105                 110

tgc aat gtg tgg cat gcg agg tac atc gag aat ccg gag gga acg cgc   384
Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
        115                 120                 125

gac ttt gtg ggt tca ttc cgc cac ggc acg atg gct aat gcg ttg cct   432
Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
    130                 135                 140

cat gcg att ggt gcg caa agt gtt gat cga aac cgc cag gtg atc gcg   480
His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
145                 150                 155                 160

atg tgt ggc gat ggt ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc   528
Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
                165                 170                 175

gtt aag ctg cac caa ctt ccg ctg aag gct gtg gtg ttt aac aac agt   576
Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
```

```
            180                 185                 190

tct ttg ggc atg gtg aag ttg gag atg ctc gtg gag gga cag cca gaa   624
Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
        195                 200                 205

ttt ggt act gac cat gag gaa gtg aat ttc gca gag att gcg gcg gct   672
Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
    210                 215                 220

gcg ggt atc aaa tcg gta cgc atc acc gat ccg aag aaa gtt cgc gag   720
Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
225                 230                 235                 240

cag cta gct gag gca ttg gca tat cct gga cct gta ctg atc gat atc   768
Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
                245                 250                 255

gtc acg gat cct aat gcg ctg tcg atc cca cca acc atc acg tgg gaa   816
Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
            260                 265                 270

cag gtc atg gga ttc agc aag gcg gcc acc cga acc gtc ttt ggt gga   864
Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
        275                 280                 285

gga gta gga gcg atg atc gat ctg gcc cgt tcg aac ata agg aat att   912
Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
    290                 295                 300

cct act cca tgatgattga tacacctgct gtt                            944
Pro Thr Pro
305


<210> 90
<211> 307
<212> PRT
<213> Corynebacterium glutamicum

<400> 90
Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
  1               5                  10                  15

Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
             20                  25                  30

Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
         35                  40                  45

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
     50                  55                  60

Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 65                  70                  75                  80

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
                 85                  90                  95

Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
            100                 105                 110
```

```
Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
        115                 120                 125

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
    130                 135                 140

His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
145                 150                 155                 160

Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
                165                 170                 175

Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
            180                 185                 190

Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
        195                 200                 205

Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
    210                 215                 220

Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
225                 230                 235                 240

Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
                245                 250                 255

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
            260                 265                 270

Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
        275                 280                 285

Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
    290                 295                 300

Pro Thr Pro
305
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Sequence Listing

<210> 91
<211> 954
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(931)
<223> RXN03044

<400> 91
tacgccaccc acggcaaggc catgattccg ctgtacatct tctactcgat gttcgggatt 60

ccagcgcacc ggtgactcca tctgggcagc agccgatcag atg gca cgt ggc ttc 115
                                                Met Ala Arg Gly Phe
                                                  1   5

ctc ttg ggc gct acc gca ggt cgc acc acc ctg acc ggt gaa ggc ctc 163
Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu
                 10   15   20

```
cag cac atg gat gga cac tcc cct gtc ttg gct tcc acc aac gag ggt   211
Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly
             25                  30                  35

gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt   259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val
         40                  45                  50

cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt   307
His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val
     55                  60                  65

atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag   355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu
 70                  75                  80                  85

cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac   403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr
                 90                  95                 100

tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt   451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly
            105                 110                 115

gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac   499
Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp
        120                 125                 130

tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg   547
Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu
    135                 140                 145

gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt   595
Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly
150                 155                 160                 165

gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc   643
Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser
                170                 175                 180

ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag   691
Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln
            185                 190                 195

atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc   739
Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly
        200                 205                 210

ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc   787
Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile
    215                 220                 225

gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa   835
Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu
230                 235                 240                 245

ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag   883
Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys
                250                 255                 260
```

```
ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa   931
Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
            265                 270                 275

taaatcacct caagggacag ata                                       954
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<210> 92
<211> 277
<212> PRT
<213> Corynebacterium glutamicum

<400> 92

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Met Ala Arg Gly Phe Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu
  1               5                  10                  15

Thr Gly Glu Gly Leu Gln His Met Asp Gly His Ser Pro Val Leu Ala
             20                  25                  30

Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu
         35                  40                  45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
     50                  55                  60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65                  70                  75                  80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
                 85                  90                  95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
            100                 105                 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
        115                 120                 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
    130                 135                 140

Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
145                 150                 155                 160

Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
                165                 170                 175

Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
            180                 185                 190

Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
        195                 200                 205

Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
    210                 215                 220

Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
225                 230                 235                 240

Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
                245                 250                 255
```

```
Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
            260                 265                 270

Asn Ala Pro Glu Glu
        275
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<210> 93
<211> 302
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(279)
<223> FRXA02852

<400> 93

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gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag atc cgt gaa   48
Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
  1               5                  10                  15

tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc   96
Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
             20                  25                  30

tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag   144
Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
         35                  40                  45

tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc   192
Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
     50                  55                  60

gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat   240
Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65                  70                  75                  80

cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct   289
Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
                 85                  90

caagggacag ata                                                  302
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<210> 94
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 94

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Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
  1               5                  10                  15

Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
             20                  25                  30

Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
         35                  40                  45

Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
```

```
     50                  55                  60

Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65                  70                  75                  80

Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
                 85                  90


<210> 95
<211> 954
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(931)
<223> FRXA00268

<400> 95
tacgccaccc acggcaaggc catgattccg ctgtacatct tctactcgat gttcgggatt 60

ccagcgcacc ggtgactcca tttgggcagc agccgatcag atg gca cgt ggc ttc   115
                                            Met Ala Arg Gly Phe
                                              1               5

ttt ttg ggc gct acc gca ggt cgc acc acc ttg acc ggt gaa ggc ctc   163
Phe Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu
                 10                  15                  20

cag cac atg gat gga cac tcc cct gtt ttg gct tcc acc aac gag ggt   211
Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly
             25                  30                  35

gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt   259
Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val
         40                  45                  50

cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt   307
His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val
     55                  60                  65

atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag   355
Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu
 70                  75                  80                  85

cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac   403
Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr
                 90                  95                 100

tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt   451
Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly
            105                 110                 115

gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac   499
Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp
        120                 125                 130

tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg   547
Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu
    135                 140                 145
```

```
gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt   595
Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly
150                 155                 160                 165

gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc   643
Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser
                170                 175                 180

ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag   691
Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln
            185                 190                 195

atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc   739
Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly
        200                 205                 210

ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc   787
Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile
    215                 220                 225

gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa   835
Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu
230                 235                 240                 245

ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag   883
Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys
                250                 255                 260

ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa   931
Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
            265                 270                 275

taaatcacct caagggacag ata                                        954
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<210> 96
<211> 277
<212> PRT
<213> Corynebacterium glutamicum

<400> 96

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Met Ala Arg Gly Phe Phe Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu
  1               5                  10                  15

Thr Gly Glu Gly Leu Gln His Met Asp Gly His Ser Pro Val Leu Ala
             20                  25                  30

Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu
         35                  40                  45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
     50                  55                  60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65                  70                  75                  80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
                 85                  90                  95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
```

```
          100                 105                 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
        115                 120                 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
    130                 135                 140

Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
145                 150                 155                 160

Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
                165                 170                 175

Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
            180                 185                 190

Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
        195                 200                 205

Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
    210                 215                 220

Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
225                 230                 235                 240

Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
                245                 250                 255

Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
            260                 265                 270

Asn Ala Pro Glu Glu
        275


<210> 97
<211> 508
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXN03086

<400> 97
ttcgtgcact tcggcgtgtc acaattaggt acgaccaaga atgggaccgg gaaaccggga 60

cgtataaacg aaataaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca   115
                                        Met Ala Asp Gln Ala
                                          1               5

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc   163
Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
                  10                  15                  20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac   211
Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
              25                  30                  35
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gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa   259
Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
         40                  45                  50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag   307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
     55                  60                  65

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att   355
Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
 70                  75                  80                  85

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag   403
Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
                 90                  95                 100

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc   451
Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
            105                 110                 115

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca   499
Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala
        120                 125                 130

ggc gca gcc                                                       508
Gly Ala Ala
    135
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DO NOT ENTER

<210> 98
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 98

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Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
  1               5                  10                  15

Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
             20                  25                  30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
         35                  40                  45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
     50                  55                  60

Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65                  70                  75                  80

Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
                 85                  90                  95

Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
            100                 105                 110

Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
        115                 120                 125

Ile Ser Thr Tyr Ala Gly Ala Ala
    130                 135
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<210> 99
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(508)
<223> FRXA02887

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cgtataaacg aaataaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca 115
Met Ala Asp Gln Ala
1 5

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
10 15 20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
25 30 35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
40 45 50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
55 60 65

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
70 75 80 85

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
90 95 100

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451
Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
105 110 115

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala
120 125 130

ggc gca gcc 508
Gly Ala Ala
135

<210> 100
<211> 136
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<213> Corynebacterium glutamicum

<400> 100
Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
1 5 10 15

Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
20 25 30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
35 40 45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
50 55 60

Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
65 70 75 80

Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
85 90 95

Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
100 105 110

Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
115 120 125

Ile Ser Thr Tyr Ala Gly Ala Ala
130 135

<210> 101
<211> 1385
<212> DNA
<213> Corynebacterium glutamicum

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<223> RXN03043

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1 5 10 15

ccg tcc tac cct cac cca cac ggt atg aag gac ttc tgg gag ttc cca 96
Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
20 25 30

act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt 144
Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
35 40 45

ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
50 55 60

cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240
His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
65 70 75 80

cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288

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Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
                 85                  90                  95

ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt   336
Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
            100                 105                 110

aac acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggc gca ggc   384
Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
        115                 120                 125

tgg tct gtg atc aag gtt gtt tgg ggt cgc gag tgg gat gaa ctt ctg   432
Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
    130                 135                 140

gag aag gac cag gat ggt gca ctt gtt gag atc atg aac aac acc tcc   480
Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
145                 150                 155                 160

gat ggt gac tac cag acc ttc aag gct aac gac ggc gca tat gtt cgt   528
Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
                165                 170                 175

gag cac ttc ttc gga cgt gac cca cgc acc gca aag ctc gtt gag aac   576
Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
            180                 185                 190

atg acc gac gaa gaa atc tgg aag ctt cca cgt ggc ggc cac gat tac   624
Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
        195                 200                 205

cgc aag gtt tac gca gcc tac aag cga gct ctt gag acc aag gat cgc   672
Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
    210                 215                 220

cca acc gtc atc ctt gct cac acc att aag ggc tac gga ctc ggc cac   720
Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
225                 230                 235                 240

aac ttc gaa ggc cgt aac gca acc cac cag atg aag aag ctg acg ctt   768
Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
                245                 250                 255

gat gat ctg aag ttg ttc cgc gac aag cag ggc atc cca atc acc gat   816
Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
            260                 265                 270

gag cag ctg gag aag gat cct tac ctt cct cct tac tac cac cca ggt   864
Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
        275                 280                 285

gaa gac gct cct gaa atc aag tac atg aag gaa cgt cgc gca gcg ctc   912
Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
    290                 295                 300

ggt ggc tac ctg cca gag cgt cgt gag aac tac gat cca att cag gtt   960
Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
305                 310                 315                 320

cca cca ctg gat aag ctt cgc tct gtc cgt aag ggc tcc ggc aag cag  1008
Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
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                325                 330                 335

cag atc gct acc acc atg gcg act gtt cgt acc ttc aag gaa ctg atg   1056
Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
            340                 345                 350

cgc gat aag ggc ttg gct gat cgc ctt gtc cca atc att cct gat gag   1104
Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
        355                 360                 365

gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac   1152
Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
    370                 375                 380

aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc   1200
Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
385                 390                 395                 400

tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac   1248
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
                405                 410                 415

gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc tcc tac gcc   1296
Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala
            420                 425                 430

acc cac ggc aag gcc atg att ccg ctg tac atc ttc tac tcg atg ttc   1344
Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe
        435                 440                 445

ggg att cca gcg cac cgg tgactccatc tgggcagcag ccg                 1385
Gly Ile Pro Ala His Arg
    450
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09509160.030502



Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
115 120 125

Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
130 135 140

Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
145 150 155 160

Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
165 170 175

Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
180 185 190

Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
195 200 205

Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
210 215 220

Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
225 230 235 240

Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
245 250 255

Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
260 265 270

Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
275 280 285

Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
290 295 300

Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
305 310 315 320

Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
325 330 335

Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
340 345 350

Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
355 360 365

Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
370 375 380

Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
385 390 395 400

Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
405 410 415

Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala
420 425 430

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Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe
        435                 440                 445

Gly Ile Pro Ala His Arg
    450


<210> 103
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<223> FRXA02897

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Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg Glu Gln Gly Gly Ile
  1               5                  10                  15

ccg tcc tac cct cac cca cac ggt atg aag gac ttc tgg gag ttc cca   96
Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
             20                  25                  30

act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt   144
Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
         35                  40                  45

ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag   192
Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
     50                  55                  60

cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca   240
His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65                  70                  75                  80

cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc   288
Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
                 85                  90                  95

ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt   336
Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
            100                 105                 110

aac acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggc gca ggc   384
Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
        115                 120                 125

tgg tct gtg atc aag gtt gtt tgg ggt cgc gag tgg gat gaa ctt ctg   432
Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
    130                 135                 140

gag aag gac cag gat ggt gca ctt gtt gag atc atg aac aac acc tcc   480
Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
145                 150                 155                 160

gat ggt gac tac cag acc ttc aag gct aac gac ggc gca tat gtt cgt   528
Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
                165                 170                 175
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gag cac ttc ttc gga cgt gac cca cgc acc gca aag ctc gtt gag aac   576
Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
            180                 185                 190

atg acc gac gaa gaa atc tgg aag ctt cca cgt ggc ggc cac gat tac   624
Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
        195                 200                 205

cgc aag gtt tac gca gcc tac aag cga gct ctt gag acc aag gat cgc   672
Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
    210                 215                 220

cca acc gtc atc ctt gct cac acc att aag ggc tac gga ctc ggc cac   720
Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
225                 230                 235                 240

aac ttc gaa ggc cgt aac gca acc cac cag atg aag aag ctg acg ctt   768
Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
                245                 250                 255

gat gat ctg aag ttg ttc cgc gac aag cag ggc atc cca atc acc gat   816
Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
            260                 265                 270

gag cag ctg gag aag gat cct tac ctt cct cct tac tac cac cca ggt   864
Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
        275                 280                 285

gaa gac gct cct gaa atc aag tac atg aag gaa cgt cgc gca gcg ctc   912
Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
    290                 295                 300

ggt ggc tac ctg cca gag cgt cgt gag aac tac gat cca att cag gtt   960
Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
305                 310                 315                 320

cca cca ctg gat aag ctt cgc tct gtc cgt aag ggc tcc ggc aag cag  1008
Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
                325                 330                 335

cag atc gct acc acc atg gcg act gtt cgt acc ttc aag gaa ctg atg  1056
Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
            340                 345                 350

cgc gat aag ggc ttg gct gat cgc ctt gtc cca atc att cct gat gag  1104
Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
        355                 360                 365

gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac  1152
Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
    370                 375                 380

aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc  1200
Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
385                 390                 395                 400

tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac  1248
Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
                405                 410                 415
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gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc                1287
Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr
            420                 425


<210> 104
<211> 429
<212> PRT
<213> Corynebacterium glutamicum

<400> 104
Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg Glu Gln Gly Gly Ile
  1               5                  10                  15

Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
             20                  25                  30

Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
         35                  40                  45

Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
     50                  55                  60

His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65                  70                  75                  80

Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
                 85                  90                  95

Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
            100                 105                 110

Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
        115                 120                 125

Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
    130                 135                 140

Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
145                 150                 155                 160

Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
                165                 170                 175

Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
            180                 185                 190

Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
        195                 200                 205

Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
    210                 215                 220

Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
225                 230                 235                 240

Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
                245                 250                 255

Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
            260                 265                 270
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```
Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
        275                 280                 285

Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
    290                 295                 300

Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
305                 310                 315                 320

Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
                325                 330                 335

Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
            340                 345                 350

Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
        355                 360                 365

Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
    370                 375                 380

Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
385                 390                 395                 400

Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
                405                 410                 415

Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr
            420                 425


<210> 105
<211> 1133
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (88)..(1110)
<223> RXN03083

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ccagctcaca cgtgtggagg tgccttaatg gca aag agg atc gta att atc ggc  114
                               Met Ala Lys Arg Ile Val Ile Ile Gly
                                 1               5

ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt   162
Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
 10                  15                  20                  25

gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc   210
Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
                30                  35                  40

acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc   258
Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
            45                  50                  55
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```
aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt   306
Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
         60                  65                  70

gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac   354
Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp
     75                  80                  85

ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca   402
Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser
 90                  95                 100                 105

gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc   450
Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr
                110                 115                 120

aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa   498
Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu
            125                 130                 135

gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc   546
Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro
        140                 145                 150

cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg   594
Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp
    155                 160                 165

cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt   642
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val
170                 175                 180                 185

ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc   690
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu
                190                 195                 200

ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac   738
Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His
            205                 210                 215

gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc   786
Asp Asp Ala Asp Ala Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg
        220                 225                 230

gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc   834
Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr
    235                 240                 245

gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac   882
Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr
250                 255                 260                 265

ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat   930
Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp
                270                 275                 280

ctt ggc ctg gag aac atc ggt gtt gag ctg gca cca tcc ggc cat atc   978
Leu Gly Leu Glu Asn Ile Gly Val Glu Leu Ala Pro Ser Gly His Ile
            285                 290                 295

aag gtt gac cgg tct ccc gca cca aca tcc ccg gtg tgt acg cag cag   1026
```

```
Lys Val Asp Arg Ser Pro Ala Pro Thr Ser Pro Val Cys Thr Gln Gln
        300                 305                 310

gtg act gta ctg acc tat tcc cac tgg cgt ccg ttg cag cga tgc agg   1074
Val Thr Val Leu Thr Tyr Ser His Trp Arg Pro Leu Gln Arg Cys Arg
    315                 320                 325

gcc gta tcg cca tgt atc acg cac tcg gtg aag gcg tgagccccat        1120
Ala Val Ser Pro Cys Ile Thr His Ser Val Lys Ala
330                 335                 340

ccgtttgaag act                                                   1133


<210> 106
<211> 341
<212> PRT
<213> Corynebacterium glutamicum

<400> 106
Met Ala Lys Arg Ile Val Ile Ile Gly Gly Gly Pro Ala Gly Tyr Glu
  1               5                  10                  15

Ala Ala Leu Ala Gly Ala Lys Tyr Gly Ala Glu Val Thr Val Ile Glu
            20                  25                  30

Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
        35                  40                  45

Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
    50                  55                  60

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
65                  70                  75                  80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
                85                  90                  95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly
            100                 105                 110

Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile
        115                 120                 125

Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu
    130                 135                 140

Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu
145                 150                 155                 160

Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu
                165                 170                 175

Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala
            180                 185                 190

Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val
        195                 200                 205

Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp
    210                 215                 220
```

```
Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His
225                 230                 235                 240

Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val
                245                 250                 255

Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr
            260                 265                 270

Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly
        275                 280                 285

Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Ser Pro Ala
    290                 295                 300

Pro Thr Ser Pro Val Cys Thr Gln Gln Val Thr Val Leu Thr Tyr Ser
305                 310                 315                 320

His Trp Arg Pro Leu Gln Arg Cys Arg Ala Val Ser Pro Cys Ile Thr
                325                 330                 335

His Ser Val Lys Ala
            340
```

EP 1 505 148 A2

<210> 107
<211> 1518
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (89)..(1495)
<223> FRXA02853

<400> 107

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aattcagcag taatcattta gacttggaac cgcttaccag tggtttcaac aatgcattca 60

cccagctcac acgtgtggag gtgccttaatg gca aag agg atc gta att atc ggc 115
                               Met Ala Lys Arg Ile Val Ile Ile Gly
                                 1               5

ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt   163
Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
 10                  15                  20                  25

gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc   211
Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
                30                  35                  40

acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc   259
Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
            45                  50                  55

aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt   307
Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
        60                  65                  70

gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac   355
Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp
```

```
     75                  80                  85

ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca   403
Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser
 90                  95                 100                 105

gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc   451
Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr
                110                 115                 120

aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa   499
Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu
            125                 130                 135

gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc   547
Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro
        140                 145                 150

cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg   595
Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp
    155                 160                 165

cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt   643
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val
170                 175                 180                 185

ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc   691
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu
                190                 195                 200

ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac   739
Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His
            205                 210                 215

gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc   787
Asp Asp Ala Asp Ala Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg
        220                 225                 230

gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc   835
Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr
    235                 240                 245

gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac   883
Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr
250                 255                 260                 265

ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat   931
Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp
                270                 275                 280

ctt ggc ctg gag aac atc ggt gtt gag ctg gca cca tcc ggc cat atc   979
Leu Gly Leu Glu Asn Ile Gly Val Glu Leu Ala Pro Ser Gly His Ile
            285                 290                 295

aag gtt gac cgn gtc tcc cgc acc aac atc ccc ggt gtg tac gca gca   1027
Lys Val Asp Arg Val Ser Arg Thr Asn Ile Pro Gly Val Tyr Ala Ala
        300                 305                 310

ggt gac tgt act gac cta ttc cca ctg gcg tcc gtt gca gcg atg cag   1075
Gly Asp Cys Thr Asp Leu Phe Pro Leu Ala Ser Val Ala Ala Met Gln
    315                 320                 325
```

```
ggc cgt atc gcc atg tat cac gca ctc ggt gaa ggc gtg agc ccc atc   1123
Gly Arg Ile Ala Met Tyr His Ala Leu Gly Glu Gly Val Ser Pro Ile
330                 335                 340                 345

cgt ttg aag act gtt gcc acc gca gtg ttt acc cgc cca gag atc gca   1171
Arg Leu Lys Thr Val Ala Thr Ala Val Phe Thr Arg Pro Glu Ile Ala
                350                 355                 360

gca gta ggt atc acc cat gca caa gtt gat tcc ggc gaa gtg tct gct   1219
Ala Val Gly Ile Thr His Ala Gln Val Asp Ser Gly Glu Val Ser Ala
            365                 370                 375

cgc gtg att gtg ctt cct ttg gct act aac cca cgc gcc aag atg cgt   1267
Arg Val Ile Val Leu Pro Leu Ala Thr Asn Pro Arg Ala Lys Met Arg
        380                 385                 390

tcc ctg cgc cac ggt ttt gtg aag ctg ttc tgc cgc cgt aac tct ggc   1315
Ser Leu Arg His Gly Phe Val Lys Leu Phe Cys Arg Arg Asn Ser Gly
    395                 400                 405

ctg atc atc ggt ggt gtc gtg gtg gca ccg acc gcg tct gag ctg atc   1363
Leu Ile Ile Gly Gly Val Val Val Ala Pro Thr Ala Ser Glu Leu Ile
410                 415                 420                 425

cta ccg atc gct gtg gca gtg acc aac cgt ctg aca gtt gct gat ctg   1411
Leu Pro Ile Ala Val Ala Val Thr Asn Arg Leu Thr Val Ala Asp Leu
                430                 435                 440

gct gat acc ttc gcg gtg tac cca tca ttg tca ggt tcg att act gaa   1459
Ala Asp Thr Phe Ala Val Tyr Pro Ser Leu Ser Gly Ser Ile Thr Glu
            445                 450                 455

gca gca cgt cag ctg gtt caa cat gat gat cta ggc taatttttct        1505
Ala Ala Arg Gln Leu Val Gln His Asp Asp Leu Gly
        460                 465

gagtcttaga ttt                                                   1518
```

<210> 108
<211> 469
<212> PRT
<213> Corynebacterium glutamicum

<400> 108

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Met Ala Lys Arg Ile Val Ile Ile Gly Gly Gly Pro Ala Gly Tyr Glu
  1               5                  10                  15

Ala Ala Leu Ala Gly Ala Lys Tyr Gly Ala Glu Val Thr Val Ile Glu
             20                  25                  30

Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
         35                  40                  45

Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
     50                  55                  60

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65                  70                  75                  80
```

```
Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
                  85                  90                  95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly
            100                 105                 110

Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile
        115                 120                 125

Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu
    130                 135                 140

Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu
145                 150                 155                 160

Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu
                165                 170                 175

Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala
            180                 185                 190

Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val
        195                 200                 205

Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp
    210                 215                 220

Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His
225                 230                 235                 240

Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val
                245                 250                 255

Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr
            260                 265                 270

Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly
        275                 280                 285

Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Val Ser Arg
    290                 295                 300

Thr Asn Ile Pro Gly Val Tyr Ala Ala Gly Asp Cys Thr Asp Leu Phe
305                 310                 315                 320

Pro Leu Ala Ser Val Ala Ala Met Gln Gly Arg Ile Ala Met Tyr His
                325                 330                 335

Ala Leu Gly Glu Gly Val Ser Pro Ile Arg Leu Lys Thr Val Ala Thr
            340                 345                 350

Ala Val Phe Thr Arg Pro Glu Ile Ala Ala Val Gly Ile Thr His Ala
        355                 360                 365

Gln Val Asp Ser Gly Glu Val Ser Ala Arg Val Ile Val Leu Pro Leu
    370                 375                 380

Ala Thr Asn Pro Arg Ala Lys Met Arg Ser Leu Arg His Gly Phe Val
385                 390                 395                 400

Lys Leu Phe Cys Arg Arg Asn Ser Gly Leu Ile Ile Gly Gly Val Val
```

```
                405                 410                 415

Val Ala Pro Thr Ala Ser Glu Leu Ile Leu Pro Ile Ala Val Ala Val
            420                 425                 430

Thr Asn Arg Leu Thr Val Ala Asp Leu Ala Asp Thr Phe Ala Val Tyr
        435                 440                 445

Pro Ser Leu Ser Gly Ser Ile Thr Glu Ala Ala Arg Gln Leu Val Gln
    450                 455                 460

His Asp Asp Leu Gly
465
```

<210> 109
<211> 2895
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2872)
<223> RXA02259

<400> 109

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atgagcccat gaaagccatc gaaatcaatc gcccagctaa acacctgttt tgctgggtga 60

ttttttatct catgcacgcc aacaccctca atgtgaaaga gtg ttt aaa gta gtt   115
                                            Val Phe Lys Val Val
                                              1               5

atg act gat ttt tta cgc gat gac atc agg ttc ctc ggt caa atc ctc   163
Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe Leu Gly Gln Ile Leu
                10                  15                  20

ggt gag gta att gcg gaa caa gaa ggc cag gag gtt tat gaa ctg gtc   211
Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu Val Tyr Glu Leu Val
            25                  30                  35

gaa caa gcg cgc ctg act tct ttt gat atc gcc aag ggc aac gcc gaa   259
Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala Lys Gly Asn Ala Glu
        40                  45                  50

atg gat agc ctg gtt cag gtt ttc gac ggc att act cca gcc aag gca   307
Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile Thr Pro Ala Lys Ala
    55                  60                  65

aca ccg att gct cgc gca ttt tcc cac ttc gct ctg ctg gct aac ctg   355
Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala Leu Leu Ala Asn Leu
70                  75                  80                  85

gcg gaa gac ctc tac gat gaa gag ctt cgt gaa cag gct ctc gat gca   403
Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu Gln Ala Leu Asp Ala
                90                  95                  100

ggc gac acc cct ccg gac agc act ctt gat gcc acc tgg ctg aaa ctc   451
Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala Thr Trp Leu Lys Leu
            105                 110                 115

aat gag ggc aat gtt ggc gca gaa gct gtg gcc gat gtg ctg cgc aat   499
```

```
Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala Asp Val Leu Arg Asn
        120                 125                 130

gct gag gtg gcg ccg gtt ctg act gcg cac cca act gag act cgc cgc   547
Ala Glu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg
    135                 140                 145

cgc act gtt ttt gat gcg caa aag tgg atc acc acc cac atg cgt gaa   595
Arg Thr Val Phe Asp Ala Gln Lys Trp Ile Thr Thr His Met Arg Glu
150                 155                 160                 165

cgc cac gct ttg cag tct gcg gag cct acc gct cgt acg caa agc aag   643
Arg His Ala Leu Gln Ser Ala Glu Pro Thr Ala Arg Thr Gln Ser Lys
                170                 175                 180

ttg gat gag atc gag aag aac atc cgc cgt cgc atc acc att ttg tgg   691
Leu Asp Glu Ile Glu Lys Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp
            185                 190                 195

cag acc gcg ttg att cgt gtg gcc cgc cca cgt atc gag gac gag atc   739
Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Ile
        200                 205                 210

gaa gta ggg ctg cgc tac tac aag ctg agc ctt ttg gaa gag att cca   787
Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Glu Glu Ile Pro
    215                 220                 225

cgt atc aac cgt gat gtg gct gtt gag ctt cgt gag cgt ttc ggc gag   835
Arg Ile Asn Arg Asp Val Ala Val Glu Leu Arg Glu Arg Phe Gly Glu
230                 235                 240                 245

ggt gtt cct ttg aag ccc gtg gtc aag cca ggt tcc tgg att ggt gga   883
Gly Val Pro Leu Lys Pro Val Val Lys Pro Gly Ser Trp Ile Gly Gly
                250                 255                 260

gac cac gac ggt aac cct tat gtc acc gcg gaa aca gtt gag tat tcc   931
Asp His Asp Gly Asn Pro Tyr Val Thr Ala Glu Thr Val Glu Tyr Ser
            265                 270                 275

act cac cgc gct gcg gaa acc gtg ctc aag tac tat gca cgc cag ctg   979
Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Ala Arg Gln Leu
        280                 285                 290

cat tcc ctc gag cat gag ctc agc ctg tcg gac cgc atg aat aag gtc   1027
His Ser Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Lys Val
    295                 300                 305

acc ccg cag ctg ctt gcg ctg gca gat gca ggg cac aac gac gtg cca   1075
Thr Pro Gln Leu Leu Ala Leu Ala Asp Ala Gly His Asn Asp Val Pro
310                 315                 320                 325

agc cgc gtg gat gag cct tat cga cgc gcc gtc cat ggc gtt cgc gga   1123
Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val His Gly Val Arg Gly
                330                 335                 340

cgt atc ctc gcg acg acg gcc gag ctg atc ggc gag gac gcc gtt gag   1171
Arg Ile Leu Ala Thr Thr Ala Glu Leu Ile Gly Glu Asp Ala Val Glu
            345                 350                 355

ggc gtg tgg ttc aag gtc ttt act cca tac gca tct ccg gaa gaa ttc   1219
Gly Val Trp Phe Lys Val Phe Thr Pro Tyr Ala Ser Pro Glu Glu Phe
```

```
        360                 365                 370

tta aac gat gcg ttg acc att gat cat tct ctg cgt gaa tcc aag gac   1267
Leu Asn Asp Ala Leu Thr Ile Asp His Ser Leu Arg Glu Ser Lys Asp
    375                 380                 385

gtt ctc att gcc gat gat cgt ttg tct gtg ctg att tct gcc atc gag   1315
Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu Ile Ser Ala Ile Glu
390                 395                 400                 405

agc ttt gga ttc aac ctt tac gca ctg gat ctg cgc caa aac tcc gaa   1363
Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu Arg Gln Asn Ser Glu
                410                 415                 420

agc tac gag gac gtc ctc acc gag ctt ttc gaa cgc gcc caa gtc acc   1411
Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu Arg Ala Gln Val Thr
            425                 430                 435

gca aac tac cgc gag ctg tct gaa gca gag aag ctt gag gtg ctg ctg   1459
Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys Leu Glu Val Leu Leu
        440                 445                 450

aag gaa ctg cgc agc cct cgt ccg ctg atc ccg cac ggt tca gat gaa   1507
Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro His Gly Ser Asp Glu
    455                 460                 465

tac agc gag gtc acc gac cgc gag ctc ggc atc ttc cgc acc gcg tcg   1555
Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile Phe Arg Thr Ala Ser
470                 475                 480                 485

gag gct gtt aag aaa ttc ggg cca cgg atg gtg cct cac tgc atc atc   1603
Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val Pro His Cys Ile Ile
                490                 495                 500

tcc atg gca tca tcg gtc acc gat gtg ctc gag ccg atg gtg ttg ctc   1651
Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu Pro Met Val Leu Leu
            505                 510                 515

aag gaa ttc gga ctc atc gca gcc aac ggc gac aac cca cgc ggc acc   1699
Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp Asn Pro Arg Gly Thr
        520                 525                 530

gtc gat gtc atc cca ctg ttc gaa acc atc gaa gat ctc cag gcc ggc   1747
Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu Asp Leu Gln Ala Gly
    535                 540                 545

gcc gga atc ctc gac gaa ctg tgg aaa att gat ctc tac cgc aac tac   1795
Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp Leu Tyr Arg Asn Tyr
550                 555                 560                 565

ctc ctg cag cgc gac aac gtc cag gaa gtc atg ctc ggt tac tcc gat   1843
Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp
                570                 575                 580

tcc aac aag gat ggc gga tat ttc tcc gca aac tgg gcg ctt tac gac   1891
Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn Trp Ala Leu Tyr Asp
            585                 590                 595

gcg gaa ctg cag ctc gtc gaa cta tgc cga tca gcc ggg gtc aag ctt   1939
Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser Ala Gly Val Lys Leu
        600                 605                 610
```

```
cgc ctg ttc cac ggc cgt ggt ggc acc gtc ggc cgc ggt ggc gga cct   1987
Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro
    615                 620                 625

tcc tac gac gcg att ctt gcc cag ccc agg ggg gct gtc caa ggt tcc   2035
Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly Ala Val Gln Gly Ser
630                 635                 640                 645

gtg cgc atc acc gag cag ggc gag atc atc tcc gct aag tac ggc aac   2083
Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn
                650                 655                 660

ccc gaa acc gcg cgc cga aac ctc gaa gcc ctg gtc tca gcc acg ctt   2131
Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu
            665                 670                 675

gag gca tcg ctt ctc gac gtc tcc gaa ctc acc gat cac caa cgc gcg   2179
Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr Asp His Gln Arg Ala
        680                 685                 690

tac gac atc atg agt gag atc tct gag ctc agc ttg aag aag tac gcc   2227
Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser Leu Lys Lys Tyr Ala
    695                 700                 705

tcc ttg gtg cac gag gat caa ggc ttc atc gat tac ttc acc cag tcc   2275
Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp Tyr Phe Thr Gln Ser
710                 715                 720                 725

acg ccg ctg cag gag att gga tcc ctc aac atc gga tcc agg cct tcc   2323
Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser
                730                 735                 740

tca cgc aag cag acc tcc tcg gtg gaa gat ttg cga gcc atc cca tgg   2371
Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu Arg Ala Ile Pro Trp
            745                 750                 755

gtg ctc agc tgg tca cag tct cgt gtc atg ctg cca ggc tgg ttt ggt   2419
Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly
        760                 765                 770

gtc gga acc gca tta gag cag tgg att ggc gaa ggg gag cag gcc acc   2467
Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu Gly Glu Gln Ala Thr
    775                 780                 785

caa cgc att gcc gag ctg caa aca ctc aat gag tcc tgg cca ttt ttc   2515
Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu Ser Trp Pro Phe Phe
790                 795                 800                 805

acc tca gtg ttg gat aac atg gct cag gtg atg tcc aag gca gag ctg   2563
Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu
                810                 815                 820

cgt ttg gca aag ctc tac gca gac ctg atc cca gat acg gaa gta gcc   2611
Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro Asp Thr Glu Val Ala
            825                 830                 835

gag cga gtc tat tcc gtc atc cgc gag gag tac ttc ctg acc aag aag   2659
Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr Phe Leu Thr Lys Lys
        840                 845                 850
```

```
atg ttc tgc gta atc acc ggc tct gat gat ctg ctt gat gac aac cca   2707
Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu Leu Asp Asp Asn Pro
    855                 860                 865

ctt ctc gca cgc tct gtc cag cgc cga tac ccc tac ctg ctt cca ctc   2755
Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro Tyr Leu Leu Pro Leu
870                 875                 880                 885

aac gtg atc cag gta gag atg atg cga cgc tac cga aaa ggc gac caa   2803
Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Lys Gly Asp Gln
                890                 895                 900

agc gag caa gtg tcc cgc aac att cag ctg acc atg aac ggt ctt tcc   2851
Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr Met Asn Gly Leu Ser
            905                 910                 915

act gcg ctg cgc aac tcc ggc tagtccagcc ggctgggtag tac            2895
Thr Ala Leu Arg Asn Ser Gly
        920
```

US20040265956A1

<210> 110
<211> 924
<212> PRT
<213> Corynebacterium glutamicum

<400> 110

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Val Phe Lys Val Val Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe
  1               5                  10                  15

Leu Gly Gln Ile Leu Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu
            20                  25                  30

Val Tyr Glu Leu Val Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala
        35                  40                  45

Lys Gly Asn Ala Glu Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile
    50                  55                  60

Thr Pro Ala Lys Ala Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala
65                  70                  75                  80

Leu Leu Ala Asn Leu Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu
                85                  90                  95

Gln Ala Leu Asp Ala Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala
            100                 105                 110

Thr Trp Leu Lys Leu Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala
        115                 120                 125

Asp Val Leu Arg Asn Ala Glu Val Ala Pro Val Leu Thr Ala His Pro
    130                 135                 140

Thr Glu Thr Arg Arg Arg Thr Val Phe Asp Ala Gln Lys Trp Ile Thr
145                 150                 155                 160

Thr His Met Arg Glu Arg His Ala Leu Gln Ser Ala Glu Pro Thr Ala
                165                 170                 175

Arg Thr Gln Ser Lys Leu Asp Glu Ile Glu Lys Asn Ile Arg Arg Arg
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            180                 185                 190

Ile Thr Ile Leu Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg
        195                 200                 205

Ile Glu Asp Glu Ile Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu
    210                 215                 220

Leu Glu Glu Ile Pro Arg Ile Asn Arg Asp Val Ala Val Glu Leu Arg
225                 230                 235                 240

Glu Arg Phe Gly Glu Gly Val Pro Leu Lys Pro Val Val Lys Pro Gly
                245                 250                 255

Ser Trp Ile Gly Gly Asp His Asp Gly Asn Pro Tyr Val Thr Ala Glu
            260                 265                 270

Thr Val Glu Tyr Ser Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr
        275                 280                 285

Tyr Ala Arg Gln Leu His Ser Leu Glu His Glu Leu Ser Leu Ser Asp
    290                 295                 300

Arg Met Asn Lys Val Thr Pro Gln Leu Leu Ala Leu Ala Asp Ala Gly
305                 310                 315                 320

His Asn Asp Val Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val
                325                 330                 335

His Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Glu Leu Ile Gly
            340                 345                 350

Glu Asp Ala Val Glu Gly Val Trp Phe Lys Val Phe Thr Pro Tyr Ala
        355                 360                 365

Ser Pro Glu Glu Phe Leu Asn Asp Ala Leu Thr Ile Asp His Ser Leu
    370                 375                 380

Arg Glu Ser Lys Asp Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu
385                 390                 395                 400

Ile Ser Ala Ile Glu Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu
                405                 410                 415

Arg Gln Asn Ser Glu Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu
            420                 425                 430

Arg Ala Gln Val Thr Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys
        435                 440                 445

Leu Glu Val Leu Leu Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro
    450                 455                 460

His Gly Ser Asp Glu Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile
465                 470                 475                 480

Phe Arg Thr Ala Ser Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val
                485                 490                 495

Pro His Cys Ile Ile Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu
            500                 505                 510
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Ala Val Gln Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser
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Val Ser Ala Thr Leu Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr
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Asp His Gln Arg Ala Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser
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Leu Lys Lys Tyr Ala Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp
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Tyr Phe Thr Gln Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile
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Gly Ser Arg Pro Ser Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu
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Arg Ala Ile Pro Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu
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Pro Gly Trp Phe Gly Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu
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Gly Glu Gln Ala Thr Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu
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Ser Trp Pro Phe Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met
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Tyr Leu Leu Pro Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr
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Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu
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Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu
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Ser Val Asp Gly Lys Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys
                250                 255                 260

gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
            265                 270

ccc                                                               939


<210> 112
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 112
Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
  1               5                  10                  15

Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
             20                  25                  30

Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
         35                  40                  45
```

```
Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
     50                  55                  60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
 65                  70                  75                  80

Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
                 85                  90                  95

Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
            100                 105                 110

Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
        115                 120                 125

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
    130                 135                 140

Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
145                 150                 155                 160

Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
                165                 170                 175

Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
            180                 185                 190

Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
        195                 200                 205

Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
    210                 215                 220

Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
225                 230                 235                 240

Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
                245                 250                 255

Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
            260                 265                 270
```

<210> 113
<211> 939
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(916)
<223> FRXA02326

<400> 113
ccaggcggac agttgtccaa cctgcgtgca caggccaccg cactgggcct tgcggatcgt 60

ttcgaactca tcgaagacaa ctacgcaagc cgttaatgag atg ctg gga cgc cca 115
Met Leu Gly Arg Pro

```
                                                    1               5

acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac   163
Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His
                10                  15                  20

ctc gtt ggt gcg ggt gtg gat cca gca gac ttt gct gcc gat cca caa   211
Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln
            25                  30                  35

aag tac gac atc cca gac tct gtc atc gcg ttc ctg cgc ggc gag ctt   259
Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu
        40                  45                  50

ggt aac cct cca ggt ggc tgg cca gag cca ctg cgc acc cgc gca ctg   307
Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu
    55                  60                  65

gaa ggc cgc tcc gaa ggc aag gca cct ctg acg gaa gtt cct gag gaa   355
Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr Glu Val Pro Glu Glu
70                  75                  80                  85

gag cag gcg cac ctc gac gct gat gat tcc aag gaa cgt cgc aat agc   403
Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser
                90                  95                  100

ctc aac cgc ctg ctg ttc ccg aag cca acc gaa gag ttc ctc gag cac   451
Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His
            105                 110                 115

cgt cgc cgc ttc ggc aac acc tct gcg ctg gat gat cgt gaa ttc ttc   499
Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe
        120                 125                 130

tac ggc ctg gtc gaa ggc cgc gag act ttg atc cgc ctg cca gat gtg   547
Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val
    135                 140                 145

cgc acc cca ctg ctt gtt cgc ctg gat gcg atc tct gag cca gac gat   595
Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp
150                 155                 160                 165

aag ggt atg cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca   643
Lys Gly Met Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro
                170                 175                 180

atg cgt gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa   691
Met Arg Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu
            185                 190                 195

aag gca gat tcc tcc aac aag ggc cat gtt gct gca cca ttc gct ggt   739
Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly
        200                 205                 210

gtt gtc acc gtg act gtt gct gaa ggt gat gag gtc aag gct gga gat   787
Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly Asp
    215                 220                 225

gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc act gct   835
Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala
230                 235                 240                 245
```

```
tct gtt gac ggc aaa atc gat cgc gtt gtg gtt cct gct gca acg aag   883
Ser Val Asp Gly Lys Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys
                250                 255                 260

gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
            265                 270

ccc                                                               939
```

<210> 114
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 114

```
Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
  1               5                  10                  15

Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
            20                  25                  30

Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
        35                  40                  45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
    50                  55                  60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
65                  70                  75                  80

Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
                85                  90                  95

Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
            100                 105                 110

Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
        115                 120                 125

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
    130                 135                 140

Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
145                 150                 155                 160

Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
                165                 170                 175

Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
            180                 185                 190

Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
        195                 200                 205

Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
    210                 215                 220

Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
```

```
225                 230                 235                 240

Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
                245                 250                 255

Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
            260                 265                 270
```

<210> 115
<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> RXN02327

<400> 115

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accgctgaag cagcttggcc cagccgcgtt tgctcgtgat ctccgtgagc aggacgcact 60

ggcagttact gataccacct tccgcgatgc acaccagtct ttg ctt gcg acc cga   115
                                              Leu Leu Ala Thr Arg
                                                1               5

gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg   163
Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
                10                  15                  20

act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat   211
Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
            25                  30                  35

gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag   259
Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
        40                  45                  50

ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc   307
Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
    55                  60                  65

cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg   355
Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
70                  75                  80                  85

ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc   403
Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
                90                  95                  100

gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc   451
Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
            105                 110                 115

ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt   499
Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
        120                 125                 130
```

```
gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta   547
Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
    135                 140                 145

aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att   595
Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
150                 155                 160                 165

aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc   643
Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
                170                 175                 180

acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac   691
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
            185                 190                 195

gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct   739
Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala
        200                 205                 210

ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac   787
Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His
    215                 220                 225

ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc   835
Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
230                 235                 240                 245

cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg   883
Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
                250                 255                 260

tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc   931
Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
            265                 270                 275

cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag   979
Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
        280                 285                 290

ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt   1027
Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg
    295                 300                 305

ttc gaa ctc atc gaa gac aac tac gca agc cgt taatgagatg ctgggacgcc 1080
Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
310                 315                 320

caa                                                               1083
```

<210> 116
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 116

```
Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu
  1               5                  10                  15

Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly
```

```
            20                  25                  30

Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp
         35                  40                  45

Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
     50                  55                  60

Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
 65                  70                  75                  80

Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
                 85                  90                  95

Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
            100                 105                 110

Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
        115                 120                 125

Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
    130                 135                 140

Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
145                 150                 155                 160

His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
                165                 170                 175

Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
            180                 185                 190

His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
        195                 200                 205

Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
    210                 215                 220

Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
225                 230                 235                 240

Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
                245                 250                 255

Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
            260                 265                 270

Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
        275                 280                 285

Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu
    290                 295                 300

Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
305                 310                 315                 320
```

<210> 117

<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> FRXA02327

<400> 117
accgctgaag cagcttggcc cagccgcgtt tgctcgtgat ctccgtgagc aggacgcact 60

```
ggcagttact gataccacct tccgcgatgc acaccagtct ttg ctt gcg acc cga   115
                                              Leu Leu Ala Thr Arg
                                                1               5

gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg   163
Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
                 10                  15                  20

act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat   211
Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
             25                  30                  35

gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag   259
Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
         40                  45                  50

ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc   307
Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
     55                  60                  65

cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg   355
Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
 70                  75                  80                  85

ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc   403
Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
                 90                  95                 100

gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc   451
Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
            105                 110                 115

ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt   499
Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
        120                 125                 130

gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta   547
Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
    135                 140                 145

aag atg gca gag gag atc gtc aag tct ggc gct cac atc ttg gcc att   595
Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
150                 155                 160                 165

aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc   643
Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
                170                 175                 180

acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac   691
```

```
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His
            185                 190                 195

gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct   739
Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala
        200                 205                 210

ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac   787
Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His
    215                 220                 225

ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc   835
Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr
230                 235                 240                 245

cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg   883
Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro
                250                 255                 260

tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc   931
Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr
            265                 270                 275

cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag   979
Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
        280                 285                 290

ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt   1027
Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg
    295                 300                 305

ttc gaa ctc atc gaa gac aac tac gca agc cgt taatgagatg ctgggacgcc 1080
Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
310                 315                 320

caa                                                               1083
```

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<210> 118
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 118

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Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu
  1               5                  10                  15

Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly
            20                  25                  30

Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp
        35                  40                  45

Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
    50                  55                  60

Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
65                  70                  75                  80

Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
                85                  90                  95
```

Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
100 105 110

Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
115 120 125

Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
130 135 140

Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
145 150 155 160

His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
165 170 175

Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
180 185 190

His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
195 200 205

Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr
210 215 220

Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
225 230 235 240

Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
245 250 255

Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
260 265 270

Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
275 280 285

Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu
290 295 300

Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg
305 310 315 320

<210> 119
<211> 1719
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1696)
<223> RXN02328

<400> 119
gaagtcgtgc aggtcagggg agtgttgccc gaaaacattg agaggaaaac aaaaaccgat 60

gtttgattgg gggaatcggg ggttacgata ctaggacgca gtg act gct atc acc 115

```
                                                  Val Thr Ala Ile Thr
                                                    1               5

ctt ggc ggt ctc ttg ttg aaa gga ata att act cta gtg tcg act cac   163
Leu Gly Gly Leu Leu Leu Lys Gly Ile Ile Thr Leu Val Ser Thr His
                  10                  15                  20

aca tct tca acg ctt cca gca ttc aaa aag atc ttg gta gca aac cgc   211
Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu Val Ala Asn Arg
              25                  30                  35

ggc gaa atc gcg gtc cgt gct ttc cgt gca gca ctc gaa acc ggt gca   259
Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu Glu Thr Gly Ala
          40                  45                  50

gcc acg gta gct att tac ccc cgt gaa gat cgg gga tca ttc cac cgc   307
Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly Ser Phe His Arg
      55                  60                  65

tct ttt gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc   355
Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val
  70                  75                  80                  85

aag gcg tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt   403
Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val
                  90                  95                 100

aaa gca gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc   451
Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala
              105                 110                 115

cag ctt gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca   499
Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro
          120                 125                 130

acc cca gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc   547
Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr
      135                 140                 145

gcc gcg aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc   595
Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser
  150                 155                 160                 165

aaa aac atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc   643
Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro
                  170                 175                 180

atc ttt gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt   691
Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe
              185                 190                 195

gtt gct tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt   739
Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg
          200                 205                 210

gaa gct gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct   787
Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala
      215                 220                 225

gtg att aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act   835
Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr
```

```
230                 235                 240                 245

gga gaa gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt   883
Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg
                250                 255                 260

cac caa aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa   931
His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu
            265                 270                 275

ctg cgt gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att   979
Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile
        280                 285                 290

ggt tac cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc   1027
Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly
    295                 300                 305

aac cac gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc   1075
Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr
310                 315                 320                 325

gtg act gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc   1123
Val Thr Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg
                330                 335                 340

ttg gct gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag   1171
Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys
            345                 350                 355

atc aag acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat   1219
Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp
        360                 365                 370

cca aac aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc   1267
Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg
    375                 380                 385

tca cca ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt   1315
Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly
390                 395                 400                 405

ggc gaa atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc   1363
Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys
                410                 415                 420

cgt ggt tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg   1411
Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu
            425                 430                 435

gct gag ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt   1459
Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg
        440                 445                 450

gcg ttg ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga   1507
Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly
    455                 460                 465

ttc att gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat   1555
Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp
470                 475                 480                 485
```

```
gag cag gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag   1603
Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys
                490                 495                 500

cct cat ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg   1651
Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu
            505                 510                 515

cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc       1696
Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
        520                 525                 530

tgaagcagct tggcccagcc gcg                                        1719
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<210> 120
<211> 532
<212> PRT
<213> Corynebacterium glutamicum

<400> 120

```
Val Thr Ala Ile Thr Leu Gly Gly Leu Leu Leu Lys Gly Ile Ile Thr
  1               5                  10                  15

Leu Val Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile
            20                  25                  30

Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala
        35                  40                  45

Leu Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg
    50                  55                  60

Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr
65                  70                  75                  80

Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly
                85                  90                  95

Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe
            100                 105                 110

Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile
        115                 120                 125

Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys
    130                 135                 140

Ser Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala
145                 150                 155                 160

Glu Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu
                165                 170                 175

Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly
            180                 185                 190

Arg Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala
        195                 200                 205
```

EP 1 505 148 A2

Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val
210 215 220

Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile
225 230 235 240

Leu Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys
245 250 255

Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln
260 265 270

His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys
275 280 285

Phe Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu
290 295 300

Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile
305 310 315 320

Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val
325 330 335

Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly
340 345 350

Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg
355 360 365

Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr
370 375 380

Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly
385 390 395 400

Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu
405 410 415

Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg
420 425 430

Ala Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn
435 440 445

Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys
450 455 460

Arg Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala
465 470 475 480

Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp
485 490 495

Val Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala
500 505 510

Pro Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly
515 520 525

Ser Arg Asp Arg

09529200.1-1605

530

<210> 121
<211> 1406
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1383)
<223> FRXA02328

<400> 121

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gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc aag gcg   48
Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala
  1               5                  10                  15

tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt aaa gca   96
Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala
            20                  25                  30

gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc cag ctt  144
Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
        35                  40                  45

gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca acc cca  192
Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro
    50                  55                  60

gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc gcc gcg  240
Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala
65                  70                  75                  80

aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc aaa aac  288
Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn
                85                  90                  95

atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc atc ttt  336
Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe
            100                 105                 110

gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt gtt gct  384
Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala
        115                 120                 125

tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt gaa gct  432
Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala
    130                 135                 140

gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct gtg att  480
Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile
145                 150                 155                 160

aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act gga gaa  528
Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu
                165                 170                 175

gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt cac caa  576
Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln
            180                 185                 190
```

```
aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa ctg cgt   624
Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg
        195                 200                 205

gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att ggt tac   672
Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr
    210                 215                 220

cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc aac cac   720
Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His
225                 230                 235                 240

gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc gtg act   768
Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr
                245                 250                 255

gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc ttg gct   816
Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala
            260                 265                 270

gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag atc aag   864
Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys
        275                 280                 285

acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat cca aac   912
Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn
    290                 295                 300

aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc tca cca   960
Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro
305                 310                 315                 320

ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt ggc gaa  1008
Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu
                325                 330                 335

atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc cgt ggt  1056
Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly
            340                 345                 350

tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg gct gag  1104
Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu
        355                 360                 365

ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt gcg ttg  1152
Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu
    370                 375                 380

ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga ttc att  1200
Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile
385                 390                 395                 400

gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat gag cag  1248
Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln
                405                 410                 415

gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag cct cat  1296
Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His
            420                 425                 430
```

```
ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg cct aac   1344
Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn
        435                 440                 445

atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc tgaagcagct   1393
Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
    450                 455                 460

tggcccagcc gcg                                                  1406
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<210> 122
<211> 461
<212> PRT
<213> Corynebacterium glutamicum

<400> 122

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Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala
  1               5                  10                  15

Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala
            20                  25                  30

Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
        35                  40                  45

Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro
    50                  55                  60

Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala
65                  70                  75                  80

Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn
                85                  90                  95

Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe
            100                 105                 110

Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala
        115                 120                 125

Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala
    130                 135                 140

Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile
145                 150                 155                 160

Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu
                165                 170                 175

Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln
            180                 185                 190

Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg
        195                 200                 205

Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr
    210                 215                 220

Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His
225                 230                 235                 240
```

```
Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr
                245                 250                 255

Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala
            260                 265                 270

Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys
        275                 280                 285

Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn
    290                 295                 300

Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro
305                 310                 315                 320

Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu
                325                 330                 335

Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly
            340                 345                 350

Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu
        355                 360                 365

Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu
    370                 375                 380

Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile
385                 390                 395                 400

Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln
                405                 410                 415

Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His
            420                 425                 430

Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn
        435                 440                 445

Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
    450                 455                 460
```

<210> 123
<211> 1347
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1324)
<223> RXN01048

<400> 123
agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
                                              Met Thr Ile Asp Leu
                                                1   5

```
cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac   163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
                10                  15                  20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg   211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
            25                  30                  35

cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa   259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
        40                  45                  50

gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga   307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly
    55                  60                  65

aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc   355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly
70                  75                  80                  85

gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag   403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln
                90                  95                  100

ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac   451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp
            105                 110                 115

gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct   499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro
        120                 125                 130

tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc   547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
    135                 140                 145

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac   595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
150                 155                 160                 165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac   643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
                170                 175                 180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att   691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
            185                 190                 195

tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac   739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
        200                 205                 210

gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac   787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
    215                 220                 225

gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag   835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
230                 235                 240                 245

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc   883
```

```
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
                250                 255                 260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct   931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
            265                 270                 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca   979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
        280                 285                 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc   1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
    295                 300                 305

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg   1075
Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala
310                 315                 320                 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc   1123
Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile
                330                 335                 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag   1171
Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln
            345                 350                 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc   1219
Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro
        360                 365                 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc   1267
Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
    375                 380                 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg   1315
Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
390                 395                 400                 405

cca ata ttt taagagcaaa cttgaggccc aca                            1347
Pro Ile Phe
```

<210> 124
<211> 408
<212> PRT
<213> Corynebacterium glutamicum

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<400> 124
Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
  1               5                  10                  15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
             20                  25                  30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
         35                  40                  45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
     50                  55                  60
```

```
His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65                  70                  75                  80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
                85                  90                  95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
            100                 105                 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
        115                 120                 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
    130                 135                 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
145                 150                 155                 160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
                165                 170                 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
            180                 185                 190

Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
        195                 200                 205

Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
    210                 215                 220

Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
225                 230                 235                 240

Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
                245                 250                 255

Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
            260                 265                 270

Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
        275                 280                 285

Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
    290                 295                 300

Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile
305                 310                 315                 320

Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala
                325                 330                 335

Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln
            340                 345                 350

Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu
        355                 360                 365

Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg
    370                 375                 380
```

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```
Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser
385                 390                 395                 400

Leu Pro Val Glu Ala Pro Ile Phe
                405
```

<210> 125
<211> 311
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(288)
<223> FRXA01048

<400> 125

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cgc tct gac ttg cct aac cag atc aac aac gtg ctg gcg ttc cca gga   48
Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
  1               5                  10                  15

att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag   96
Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
             20                  25                  30

atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc   144
Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
         35                  40                  45

tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc   192
Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
     50                  55                  60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt   240
Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65                  70                  75                  80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt   288
Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
                 85                  90                  95

taagagcaaa cttgaggccc aca                                        311
```

<210> 126
<211> 96
<212> PRT
<213> Corynebacterium glutamicum

<400> 126

```
Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
  1               5                  10                  15

Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
             20                  25                  30

Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
         35                  40                  45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
```

```
     50                  55                  60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65                  70                  75                  80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
                 85                  90                  95
```

<210> 127
<211> 1063
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1063)
<223> FRXA00290

<400> 127

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agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg   115
                                            Met Thr Ile Asp Leu
                                              1               5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac   163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
                 10                  15                  20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg   211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
             25                  30                  35

cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa   259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
         40                  45                  50

gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga   307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly
     55                  60                  65

aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc   355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly
 70                  75                  80                  85

gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag   403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln
                 90                  95                 100

ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac   451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp
            105                 110                 115

gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct   499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro
        120                 125                 130
```

```
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc   547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
    135                 140                 145

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac   595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
150                 155                 160                 165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac   643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
                170                 175                 180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att   691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
            185                 190                 195

tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac   739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
        200                 205                 210

gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac   787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
    215                 220                 225

gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag   835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
230                 235                 240                 245

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc   883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
                250                 255                 260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct   931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
            265                 270                 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca   979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
        280                 285                 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc   1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
    295                 300                 305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca                   1063
Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
310                 315                 320
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<210> 128
<211> 321
<212> PRT
<213> Corynebacterium glutamicum

<400> 128

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Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
  1               5                  10                  15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
             20                  25                  30
```

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
130 135 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
145 150 155 160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
165 170 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
180 185 190

Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
195 200 205

Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
210 215 220

Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
225 230 235 240

Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
245 250 255

Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
260 265 270

Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
275 280 285

Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
290 295 300

Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg
305 310 315 320

Ser

<210> 129
<211> 1065
<212> DNA

09520470.050502

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1042)
<223> RXA02694

<400> 129
attaaaggtg taacaaagga atccgggcac aagctcttgc tgattttctg agctgctttg 60

tgggttgtcc ggttagggaa atcaggaagt gggatcgaaa atg aaa gaa acc gtc 115
Met Lys Glu Thr Val
1 5

ggt aac aag att gtc ctc att ggc gca gga gat gtt gga gtt gca tac 163
Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp Val Gly Val Ala Tyr
10 15 20

gca tac gca ctg atc aac cag ggc atg gca gat cac ctt gcg atc atc 211
Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp His Leu Ala Ile Ile
25 30 35

gac atc gat gaa aag aaa ctc gaa ggc aac gtc atg gac tta aac cat 259
Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val Met Asp Leu Asn His
40 45 50

ggt gtt gtg tgg gcc gat tcc cgc acc cgc gtc acc aag ggc acc tac 307
Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val Thr Lys Gly Thr Tyr
55 60 65

gct gac tgc gaa gac gca gcc atg gtt gtc att tgt gcc ggc gca gcc 355
Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile Cys Ala Gly Ala Ala
70 75 80 85

caa aag cca ggc gag acc cgc ctc cag ctg gtg gac aaa aac gtc aag 403
Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val Asp Lys Asn Val Lys
90 95 100

att atg aaa tcc atc gtc ggc gat gtc atg gac agc gga ttc gac ggc 451
Ile Met Lys Ser Ile Val Gly Asp Val Met Asp Ser Gly Phe Asp Gly
105 110 115

atc ttc ctc gtg gcg tcc aac cca gtg gat atc ctg acc tac gca gtg 499
Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile Leu Thr Tyr Ala Val
120 125 130

tgg aaa ttc tcc ggc ttg gaa tgg aac cgc gtg atc ggc tcc gga act 547
Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val Ile Gly Ser Gly Thr
135 140 145

gtc ctg gac tcc gct cga ttc cgc tac atg ctg ggc gaa ctc tac gaa 595
Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu Gly Glu Leu Tyr Glu
150 155 160 165

gtg gca cca agc tcc gtc cac gcc tac atc atc ggc gaa cac ggc gac 643
Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile Gly Glu His Gly Asp
170 175 180

act gaa ctt cca gtc ctg tcc tcc gcg acc atc gca ggc gta tcg ctt 691
Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile Ala Gly Val Ser Leu
185 190 195

```
agc cga atg ctg gac aaa gac cca gag ctt gag ggc cgt cta gag aaa   739
Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu Gly Arg Leu Glu Lys
        200                 205                 210

att ttc gaa gac acc cgc gac gct gcc tat cac att atc gac gcc aag   787
Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His Ile Ile Asp Ala Lys
    215                 220                 225

ggc tcc act tcc tac ggc atc ggc atg ggt ctt gct cgc atc acc cgc   835
Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu Ala Arg Ile Thr Arg
230                 235                 240                 245

gca atc cta cag aac caa gac gtt gca gtc cca gtc tct gca ctg ctc   883
Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro Val Ser Ala Leu Leu
                250                 255                 260

cac ggt gaa tac ggt gag gaa gac atc tac atc ggc acc cca gct gtg   931
His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile Gly Thr Pro Ala Val
            265                 270                 275

gtg aac cgc cga ggc atc cgc cgc gtt gtc gaa cta gaa atc acc gac   979
Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu Leu Glu Ile Thr Asp
        280                 285                 290

cac gag atg gaa cgc ttc aag cat tcc gca aat acc ctg cgc gaa att  1027
His Glu Met Glu Arg Phe Lys His Ser Ala Asn Thr Leu Arg Glu Ile
    295                 300                 305

cag aag cag ttc ttc taaatctttg gcgcctagtt ggc                   1065
Gln Lys Gln Phe Phe
310
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<210> 130
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 130

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Met Lys Glu Thr Val Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp
  1               5                  10                  15

Val Gly Val Ala Tyr Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp
            20                  25                  30

His Leu Ala Ile Ile Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val
        35                  40                  45

Met Asp Leu Asn His Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val
    50                  55                  60

Thr Lys Gly Thr Tyr Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile
65                  70                  75                  80

Cys Ala Gly Ala Ala Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val
                85                  90                  95

Asp Lys Asn Val Lys Ile Met Lys Ser Ile Val Gly Asp Val Met Asp
            100                 105                 110
```

Ser Gly Phe Asp Gly Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile
115 120 125

Leu Thr Tyr Ala Val Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val
130 135 140

Ile Gly Ser Gly Thr Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu
145 150 155 160

Gly Glu Leu Tyr Glu Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile
165 170 175

Gly Glu His Gly Asp Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile
180 185 190

Ala Gly Val Ser Leu Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu
195 200 205

Gly Arg Leu Glu Lys Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His
210 215 220

Ile Ile Asp Ala Lys Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu
225 230 235 240

Ala Arg Ile Thr Arg Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro
245 250 255

Val Ser Ala Leu Leu His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile
260 265 270

Gly Thr Pro Ala Val Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu
275 280 285

Leu Glu Ile Thr Asp His Glu Met Glu Arg Phe Lys His Ser Ala Asn
290 295 300

Thr Leu Arg Glu Ile Gln Lys Gln Phe Phe
305 310

<210> 131
<211> 2967
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2944)
<223> RXN00296

<400> 131
tttttgttgg catgtctgac attatcgcac aattcaccac agtaaccggt aacatgttac 60

tcaaagcccg cttggatcga atttcacaaa aggacccacc atg act cac acc atc 115
Met Thr His Thr Ile
1 5

aaa ttc aac aga ctc gac cca gaa gta ttt agc cag cat tct cgc gcg 163
Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser Arg Ala
10 15 20

```
aag ctg cgc acg gat atg aca acc cgt gca gca tat tct tct gat gca   211
Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser Asp Ala
            25                  30                  35

gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa aat gtg   259
Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu Asn Val
        40                  45                  50

gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg tgg tct   307
Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly Trp Ser
    55                  60                  65

gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg atc ggt   355
Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala Ile Gly
70                  75                  80                  85

gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att tta gat   403
Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile Leu Asp
                90                  95                  100

att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg gtg tgt   451
Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val Val Cys
            105                 110                 115

gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac ggc ccg   499
Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr Gly Pro
        120                 125                 130

gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt gcc aac   547
Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val Ala Asn
    135                 140                 145

aat gcg tgt ggt tca cac tcg gtt gca ttc ggt aca gct gcg gaa aat   595
Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala Glu Asn
150                 155                 160                 165

ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc act gtg   643
Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val Thr Val
                170                 175                 180

aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc acc gac   691
Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu Thr Asp
            185                 190                 195

tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt cgt ttc   739
Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly Arg Phe
        200                 205                 210

cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac gac atg   787
Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His Asp Met
    215                 220                 225

gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att act cgg   835
Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile Thr Arg
230                 235                 240                 245

ttg acg gtg aag ttg gtt cca aca ccc aaa gtg aaa gcg ctt gct gtc   883
Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu Ala Val
                250                 255                 260

ctg gct ttc gac acg gtt ttt gac gcc gcc cga gca gcc gcc aaa ttg   931
```

```
Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala Lys Leu
            265                 270                 275

cga ctg cct ggg gta gca acc att gaa ggc atg ggc gga gat ctc ctc   979
Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp Leu Leu
        280                 285                 290

gct gcg ctg cgc agt aaa cag gga caa tca gaa gct ggg cag aat ctt   1027
Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln Asn Leu
    295                 300                 305

cca gga aac cgc atc ggc att gaa gcc ggc gga tgg ttg tac tgc gag   1075
Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr Cys Glu
310                 315                 320                 325

aca gga agt gac acc ctg cag gcc gcg gta caa gcc gcc gag gaa gtc   1123
Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu Glu Val
                330                 335                 340

gca acc gcc gtt gac acc att gat tac gtg gtc gtg tct gag cct tct   1171
Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu Pro Ser
            345                 350                 355

gaa atg cgg gaa ttg tgg cgc atc cgt gaa tcc tcg gcg ggc att gtc   1219
Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly Ile Val
        360                 365                 370

acg cgc tta gct gat ggt ggg gaa gcg tgg ccg aat tgg gaa gac tcg   1267
Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu Asp Ser
    375                 380                 385

gcg gtg cct cca gag aat tta gct gat tat ctc cgc gat ctt tat gcg   1315
Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu Tyr Ala
390                 395                 400                 405

ctg atg gat aag ttc gat tac cag ggt att cca ttt gga cac ttt gga   1363
Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His Phe Gly
                410                 415                 420

gaa ggc tgc gtc cac gtt cgc atc agt ttt gat ttc tct acc aag gaa   1411
Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr Lys Glu
            425                 430                 435

ggc ctg aag aaa ttc gag gcg ttc atg aat gaa gcc tcc acc ttg gtg   1459
Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr Leu Val
        440                 445                 450

gcg tct tat ggt ggc agc ctc tcg ggc gag cat gga gac ggt cgc gcc   1507
Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly Arg Ala
    455                 460                 465

cgc tca tcc ttc ctt gac cgc atg tat tca gca gaa atg cgt gca ctc   1555
Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg Ala Leu
470                 475                 480                 485

ttc gaa gaa ttc aag ctg att ttc gat ccc cag cgc atc ttc aat ccg   1603
Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe Asn Pro
                490                 495                 500

gga gtg ttg gtc tgg gca gat cct gtc atg caa gga ctt cgc atg gac   1651
Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg Met Asp
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                505                 510                 515

ccg ggc cag cgc gcc ctc gac atc acg ccc gta cac aaa ttc tct aaa   1699
Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe Ser Lys
        520                 525                 530

gac aaa ggt tcc atg atc aac gcg gtg aat cgc tgc gtg ggt gta tcc   1747
Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly Val Ser
    535                 540                 545

gca tgc cgc tca gaa tcc gac gcg atg tgc ccg tcc ttc caa atc acc   1795
Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln Ile Thr
550                 555                 560                 565

ggc gac gaa gta cat tcc acc aga ggc cgc gcc cgc ttg ctc tct gag   1843
Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu Ser Glu
                570                 575                 580

atg ttc cgc ggt gaa tcc atc gcc gac ggc tac cgc agc gaa gaa gtc   1891
Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu Glu Val
            585                 590                 595

aat gaa gcc ctt gac ctg tgc ctt tcc tgc aaa gca tgc gca tcg gaa   1939
Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala Ser Glu
        600                 605                 610

tgt cca gtc aac gtc gac atg tcc acc tac aaa gcc gaa ttc ctg gac   1987
Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe Leu Asp
    615                 620                 625

aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc atg ggc   2035
Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val Met Gly
630                 635                 640                 645

tgg ctg ccg ctt ctg gga cac gtt gcc cat aaa ata ccg ctt ctt cct   2083
Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu Leu Pro
                650                 655                 660

acg ctt atc gac gcc acc atg cag tca gca ctc acc gcc cca gtg gtg   2131
Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro Val Val
            665                 670                 675

cgc aag gtc ggc ggg ctc gct gat cgc ccg ttg att tcc ttc gcc cac   2179
Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe Ala His
        680                 685                 690

cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa acg gtg   2227
Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu Thr Val
    695                 700                 705

gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga cca gct   2275
Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly Pro Ala
710                 715                 720                 725

cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg gtc atc   2323
His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val Val Ile
                730                 735                 740

cca gat ggc ttc gtc tgc tgt gga ctc acc tgg cat tcc acc ggc caa   2371
Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr Gly Gln
            745                 750                 755
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CN 1950509 A 20070418

```
ttg agc atg aca aag aaa gtc cta gaa caa acg gcg aaa gtg atg aaa   2419
Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val Met Lys
        760                 765                 770

ccc tac ctg gac caa ggt cta aca gtc gtt ggt ttg gaa cct tcg tgc   2467
Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro Ser Cys
    775                 780                 785

acc gtc atg ctt caa gat gag gca aca gaa ctc tcc gat aac cct gat   2515
Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn Pro Asp
790                 795                 800                 805

ctg gca cgc ctt gca gca ctg acc aaa cca ttc gct gag gtc atc gca   2563
Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val Ile Ala
                810                 815                 820

cca aag atc acc gag cta gtc gag tct gga agc ctc cag cta aca gaa   2611
Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu Thr Glu
            825                 830                 835

tca act gcg ctt acc cag gtg cac tgc cac gag cgt tcg cta ggc gac   2659
Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu Gly Asp
        840                 845                 850

cca caa caa tcg gca ctc gtt ctt gaa gct ttg ggt gta aaa gat gaa   2707
Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys Asp Glu
    855                 860                 865

caa att gcc act ggt tgt tgc ggg ctt gcc gga aac tgg ggc ttt gaa   2755
Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly Phe Glu
870                 875                 880                 885

aaa gac cac gct gaa atg tcc ttc gca ctt ggt gaa cga gag ctg ttc   2803
Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu Leu Phe
                890                 895                 900

ccc aag gtc aga aaa gca gaa gga cat gtg att gct gac ggt ttc tcc   2851
Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly Phe Ser
            905                 910                 915

tgc cgc acc cag atc gaa caa ggc acc gga aaa caa gca acg cac ctt   2899
Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr His Leu
        920                 925                 930

gca gag gtg gtc tta agc atc ttg gag caa aac aac atg gca caa       2944
Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala Gln
    935                 940                 945

taacgatcat gcaacaggtg ctc                                       2967
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<210> 132
<211> 948
<212> PRT
<213> Corynebacterium glutamicum

<400> 132

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Met Thr His Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser
  1               5                  10                  15
```

```
Gln His Ser Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala
            20                  25                  30

Tyr Ser Ser Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala
        35                  40                  45

Glu Pro Glu Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val
    50                  55                  60

Ala Arg Gly Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala
65                  70                  75                  80

Gly Asn Ala Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe
                85                  90                  95

Asn Arg Ile Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu
            100                 105                 110

Pro Gly Val Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly
        115                 120                 125

Leu Thr Tyr Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly
    130                 135                 140

Gly Met Val Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly
145                 150                 155                 160

Thr Ala Ala Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly
                165                 170                 175

Arg Glu Val Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn
            180                 185                 190

Gln Lys Leu Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys
        195                 200                 205

Glu Leu Gly Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr
    210                 215                 220

Leu Ala His Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile
225                 230                 235                 240

Gly Ile Ile Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val
                245                 250                 255

Lys Ala Leu Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg
            260                 265                 270

Ala Ala Ala Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met
        275                 280                 285

Gly Gly Asp Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu
    290                 295                 300

Ala Gly Gln Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly
305                 310                 315                 320

Trp Leu Tyr Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln
                325                 330                 335

Ala Ala Glu Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val
```

09529120.050202

```
            340                 345                 350

Val Ser Glu Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser
        355                 360                 365

Ser Ala Gly Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro
    370                 375                 380

Asn Trp Glu Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu
385                 390                 395                 400

Arg Asp Leu Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro
                405                 410                 415

Phe Gly His Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp
            420                 425                 430

Phe Ser Thr Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu
        435                 440                 445

Ala Ser Thr Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His
    450                 455                 460

Gly Asp Gly Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala
465                 470                 475                 480

Glu Met Arg Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln
                485                 490                 495

Arg Ile Phe Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln
            500                 505                 510

Gly Leu Arg Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val
        515                 520                 525

His Lys Phe Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg
    530                 535                 540

Cys Val Gly Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro
545                 550                 555                 560

Ser Phe Gln Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala
                565                 570                 575

Arg Leu Leu Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr
            580                 585                 590

Arg Ser Glu Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys
        595                 600                 605

Ala Cys Ala Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys
    610                 615                 620

Ala Glu Phe Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala
625                 630                 635                 640

His Tyr Val Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys
                645                 650                 655

Ile Pro Leu Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu
            660                 665                 670
```

Sequence Listing

```
Thr Ala Pro Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu
        675                 680                 685

Ile Ser Phe Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn
    690                 695                 700

Ser Gly Glu Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu
705                 710                 715                 720

Asp Thr Gly Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly
                725                 730                 735

Tyr Asn Val Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp
            740                 745                 750

His Ser Thr Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr
        755                 760                 765

Ala Lys Val Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly
    770                 775                 780

Leu Glu Pro Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu
785                 790                 795                 800

Ser Asp Asn Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe
                805                 810                 815

Ala Glu Val Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser
            820                 825                 830

Leu Gln Leu Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu
        835                 840                 845

Arg Ser Leu Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu
    850                 855                 860

Gly Val Lys Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly
865                 870                 875                 880

Asn Trp Gly Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly
                885                 890                 895

Glu Arg Glu Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile
            900                 905                 910

Ala Asp Gly Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys
        915                 920                 925

Gln Ala Thr His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn
    930                 935                 940

Asn Met Ala Gln
945
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<210> 133
<211> 2858
<212> DNA
<213> Corynebacterium glutamicum

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<222> (1)..(2835)
<223> FRXA00296

<400> 133

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acc atc aaa ttc aac aga ctc gac cca gaa gta ttt agc cag cat tct   48
Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser
  1               5                  10                  15

cgc gcg aag ctg cgc acg gat atg aca acc cgt gca gca tat tct tct   96
Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser
            20                  25                  30

gat gca gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa   144
Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu
        35                  40                  45

aat gtg gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg   192
Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly
    50                  55                  60

tgg tct gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg   240
Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala
65                  70                  75                  80

atc ggt gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att   288
Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile
                85                  90                  95

tta gat att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg   336
Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val
            100                 105                 110

gtg tgt gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac   384
Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr
        115                 120                 125

ggc ccg gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt   432
Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val
    130                 135                 140

gcc aac aat gcg tgt ggt tca cac tcg gtt gca ttc ggt aca gct gcg   480
Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala
145                 150                 155                 160

gaa aat ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc   528
Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val
                165                 170                 175

act gtg aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc   576
Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu
            180                 185                 190

acc gac tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt   624
Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly
        195                 200                 205

cgt ttc cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac   672
Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His
    210                 215                 220
```

09529140.030502

```
gac atg gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att   720
Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile
225                 230                 235                 240

act cgg ttg acg gtg aag ttg gtt cca aca ccc aaa gtg aaa gcg ctt   768
Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu
                245                 250                 255

gct gtc ctg gct ttc gac acg gtt ttt gac gcc gcc cga gca gcc gcc   816
Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala
            260                 265                 270

aaa ttg cga ctg cct ggg gta gca acc att gaa ggc atg ggc gga gat   864
Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp
        275                 280                 285

ctc ctc gct gcg ctg cgc agt aaa cag gga caa tca gaa gct ggg cag   912
Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln
    290                 295                 300

aat ctt cca gga aac cgc atc ggc att gaa gcc ggc gga tgg ttg tac   960
Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr
305                 310                 315                 320

tgc gag aca gga agt gac acc ctg cag gcc gcg gta caa gcc gcc gag   1008
Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu
                325                 330                 335

gaa gtc gca acc gcc gtt gac acc att gat tac gtg gtc gtg tct gag   1056
Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu
            340                 345                 350

cct tct gaa atg cgg gaa ttg tgg cgc atc cgt gaa tcc tcg gcg ggc   1104
Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly
        355                 360                 365

att gtc acg cgc tta gct gat ggt ggg gaa gcg tgg ccg aat tgg gaa   1152
Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu
    370                 375                 380

gac tcg gcg gtg cct cca gag aat tta gct gat tat ctc cgc gat ctt   1200
Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu
385                 390                 395                 400

tat gcg ctg atg gat aag ttc gat tac cag ggt att cca ttt gga cac   1248
Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His
                405                 410                 415

ttt gga gaa ggc tgc gtc cac gtt cgc atc agt ttt gat ttc tct acc   1296
Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr
            420                 425                 430

aag gaa ggc ctg aag aaa ttc gag gcg ttc atg aat gaa gcc tcc acc   1344
Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr
        435                 440                 445

ttg gtg gcg tct tat ggt ggc agc ctc tcg ggc gag cat gga gac ggt   1392
Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly
    450                 455                 460
```

```
cgc gcc cgc tca tcc ttc ctt gac cgc atg tat tca gca gaa atg cgt   1440
Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg
465                 470                 475                 480

gca ctc ttc gaa gaa ttc aag ctg att ttc gat ccc cag cgc atc ttc   1488
Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe
                485                 490                 495

aat ccg gga gtg ttg gtc tgg gca gat cct gtc atg caa gga ctt cgc   1536
Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg
            500                 505                 510

atg gac ccg ggc cag cgc gcc ctc gac atc acg ccc gta cac aaa ttc   1584
Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe
        515                 520                 525

tct aaa gac aaa ggt tcc atg atc aac gcg gtg aat cgc tgc gtg ggt   1632
Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly
    530                 535                 540

gta tcc gca tgc cgc tca gaa tcc gac gcg atg tgc ccg tcc ttc caa   1680
Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln
545                 550                 555                 560

atc acc ggc gac gaa gta cat tcc acc aga ggc cgc gcc cgc ttg ctc   1728
Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu
                565                 570                 575

tct gag atg ttc cgc ggt gaa tcc atc gcc gac ggc tac cgc agc gaa   1776
Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu
            580                 585                 590

gaa gtc aat gaa gcc ctt gac ctg tgc ctt tcc tgc aaa gca tgc gca   1824
Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala
        595                 600                 605

tcg gaa tgt cca gtc aac gtc gac atg tcc acc tac aaa gcc gaa ttc   1872
Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe
    610                 615                 620

ctg gac aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc   1920
Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val
625                 630                 635                 640

atg ggc tgg ctg ccg ctt ctg gga cac gtt gcc cat aaa ata ccg ctt   1968
Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu
                645                 650                 655

ctt cct acg ctt atc gac gcc acc atg cag tca gca ctc acc gcc cca   2016
Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro
            660                 665                 670

gtg gtg cgc aag gtc ggc ggg ctc gct gat cgc ccg ttg att tcc ttc   2064
Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe
        675                 680                 685

gcc cac cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa   2112
Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu
    690                 695                 700

acg gtg gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga   2160
```

```
Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly
705                 710                 715                 720

cca gct cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg   2208
Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val
                725                 730                 735

gtc atc cca gat ggc ttc gtc tgc tgt gga ctc acc tgg cat tcc acc   2256
Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr
            740                 745                 750

ggc caa ttg agc atg aca aag aaa gtc cta gaa caa acg gcg aaa gtg   2304
Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val
        755                 760                 765

atg aaa ccc tac ctg gac caa ggt cta aca gtc gtt ggt ttg gaa cct   2352
Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro
    770                 775                 780

tcg tgc acc gtc atg ctt caa gat gag gca aca gaa ctc tcc gat aac   2400
Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn
785                 790                 795                 800

cct gat ctg gca cgc ctt gca gca ctg acc aaa cca ttc gct gag gtc   2448
Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val
                805                 810                 815

atc gca cca aag atc acc gag cta gtc gag tct gga agc ctc cag cta   2496
Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu
            820                 825                 830

aca gaa tca act gcg ctt acc cag gtg cac tgc cac gag cgt tcg cta   2544
Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu
        835                 840                 845

ggc gac cca caa caa tcg gca ctc gtt ctt gaa gct ttg ggt gta aaa   2592
Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys
    850                 855                 860

gat gaa caa att gcc act ggt tgt tgc ggg ctt gcc gga aac tgg ggc   2640
Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly
865                 870                 875                 880

ttt gaa aaa gac cac gct gaa atg tcc ttc gca ctt ggt gaa cga gag   2688
Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu
                885                 890                 895

ctg ttc ccc aag gtc aga aaa gca gaa gga cat gtg att gct gac ggt   2736
Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly
            900                 905                 910

ttc tcc tgc cgc acc cag atc gaa caa ggc acc gga aaa caa gca acg   2784
Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr
        915                 920                 925

cac ctt gca gag gtg gtc tta agc atc ttg gag caa aac aac atg gca   2832
His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala
    930                 935                 940

caa taacgatcat gcaacaggtg ctc                                    2858
Gln
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09252006 - 09:25:56 - 09252006

945

<210> 134
<211> 945
<212> PRT
<213> Corynebacterium glutamicum

<400> 134

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Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser
  1               5                  10                  15

Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser
            20                  25                  30

Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu
        35                  40                  45

Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly
    50                  55                  60

Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala
65                  70                  75                  80

Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile
                85                  90                  95

Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val
            100                 105                 110

Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr
        115                 120                 125

Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val
    130                 135                 140

Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala
145                 150                 155                 160

Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val
                165                 170                 175

Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu
            180                 185                 190

Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly
        195                 200                 205

Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His
    210                 215                 220

Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile
225                 230                 235                 240

Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu
                245                 250                 255

Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala
            260                 265                 270

Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp
```

```
        275                 280                 285

Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln
    290                 295                 300

Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr
305                 310                 315                 320

Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu
                325                 330                 335

Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu
            340                 345                 350

Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly
        355                 360                 365

Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu
    370                 375                 380

Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu
385                 390                 395                 400

Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His
                405                 410                 415

Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr
            420                 425                 430

Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr
        435                 440                 445

Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly
    450                 455                 460

Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg
465                 470                 475                 480

Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe
                485                 490                 495

Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg
            500                 505                 510

Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe
        515                 520                 525

Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly
    530                 535                 540

Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln
545                 550                 555                 560

Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu
                565                 570                 575

Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu
            580                 585                 590

Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala
        595                 600                 605
```

Substitute Sheet (Rule 26)

```
Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe
    610                 615                 620

Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val
625                 630                 635                 640

Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu
                645                 650                 655

Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro
            660                 665                 670

Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe
        675                 680                 685

Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu
    690                 695                 700

Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly
705                 710                 715                 720

Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val
                725                 730                 735

Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr
            740                 745                 750

Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val
        755                 760                 765

Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro
    770                 775                 780

Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn
785                 790                 795                 800

Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val
                805                 810                 815

Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu
            820                 825                 830

Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu
        835                 840                 845

Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys
    850                 855                 860

Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly
865                 870                 875                 880

Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu
                885                 890                 895

Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly
            900                 905                 910

Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr
        915                 920                 925
```

Doc. No. 1-0000-0000-0000

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His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala
    930                 935                 940

Gln
945
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<210> 135
<211> 1383
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1360)
<223> RXA01901

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aactaaaatc taagtaaaac ccctccgaaa ggaaccaccc atg gtg aaa cgt caa   115
                                              Met Val Lys Arg Gln
                                                1               5

ctg ccc aac ccc gca gaa cta ctc gaa ctc atg aag ttc aaa aag cca   163
Leu Pro Asn Pro Ala Glu Leu Leu Glu Leu Met Lys Phe Lys Lys Pro
                10                  15                  20

gag ctc aac ggc aag aaa cga cgc cta gac tcc gcg ctc acc atc tac   211
Glu Leu Asn Gly Lys Lys Arg Arg Leu Asp Ser Ala Leu Thr Ile Tyr
            25                  30                  35

gac ctg cgt aaa att gct aaa cga cgc acc cca gct gcc gcg ttc gac   259
Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro Ala Ala Ala Phe Asp
        40                  45                  50

tac acc gac ggc gca gcc gag gcc gaa ctc tca atc aca cgc gca cgt   307
Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser Ile Thr Arg Ala Arg
    55                  60                  65

gaa gca ttc gaa aac atc gaa ttc cac cca gac atc ctc aag cct gca   355
Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp Ile Leu Lys Pro Ala
70                  75                  80                  85

gaa cac gta gac acc acc acc caa atc ctg ggc gga acc tcc tcc atg   403
Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly Gly Thr Ser Ser Met
                90                  95                  100

cca ttc ggc atc gca cca acc ggc ttc acc cgc ctc atg cag acc gaa   451
Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg Leu Met Gln Thr Glu
            105                 110                 115

ggt gaa atc gca ggt gcc gga gct gca ggc gct gca gga att cct ttc   499
Gly Glu Ile Ala Gly Ala Gly Ala Ala Gly Ala Ala Gly Ile Pro Phe
        120                 125                 130

acc ctg tcc acc ctg ggc act acc tcc atc gaa gac gtc aag gcc acc   547
Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu Asp Val Lys Ala Thr
    135                 140                 145

aac ccc aac ggc cga aac tgg ttc cag ctc tac gtc atg cgc gac cgc   595
```

```
Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr Val Met Arg Asp Arg
150                 155                 160                 165

gaa atc tcc tac ggc ctc gtc gaa cgc gca gcc aaa gca gga ttc gac   643
Glu Ile Ser Tyr Gly Leu Val Glu Arg Ala Ala Lys Ala Gly Phe Asp
                170                 175                 180

acc ctg atg ttc acc gtg gat acc ccc atc gcc ggc tac cgc atc cgc   691
Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala Gly Tyr Arg Ile Arg
            185                 190                 195

gat tcc cgc aac gga ttc tcc atc ccg cca cag ctg acc cca tcc acc   739
Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln Leu Thr Pro Ser Thr
        200                 205                 210

gtg ctc aat gca atc cca cgc cca tgg tgg tgg atc gac ttc ctg acc   787
Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp Ile Asp Phe Leu Thr
    215                 220                 225

acc cca acc ctt gag ttc gca tcc ctt tcc tcg acc ggc gga acc gtg   835
Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Ser Thr Gly Gly Thr Val
230                 235                 240                 245

ggc gac ctc ctc aac tcc gcg atg gat ccc acc att tct tac gaa gac   883
Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr Ile Ser Tyr Glu Asp
                250                 255                 260

ctc aag gtc atc cgt gaa atg tgg cca ggc aag ctc gta gtc aag ggt   931
Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys Leu Val Val Lys Gly
            265                 270                 275

gtc cag aac gtt gaa gac tcc gtc aaa ctc ctc gac caa ggc gtc gac   979
Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu Asp Gln Gly Val Asp
        280                 285                 290

ggc ctc atc ctc tcc aac cac ggt ggc cgt caa ctc gac cgc gca cca  1027
Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln Leu Asp Arg Ala Pro
    295                 300                 305

gtc cca ttc cac ctc ctg cca cag gta cgc aag gaa gtc gga tct gaa  1075
Val Pro Phe His Leu Leu Pro Gln Val Arg Lys Glu Val Gly Ser Glu
310                 315                 320                 325

cca acc atc atg atc gac acc ggc atc atg aac ggc gcc gac atc gtc  1123
Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn Gly Ala Asp Ile Val
                330                 335                 340

gca gcc gta gcc atg ggc gct gac ttc acc ctc atc ggt cgt gcc tac  1171
Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu Ile Gly Arg Ala Tyr
            345                 350                 355

ctc tac gga ctc atg gcc gga ggc cgc gaa ggc gtc gac cgc acc atc  1219
Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly Val Asp Arg Thr Ile
        360                 365                 370

gcc att ctc cgc agc gag atc acc cgc acc atg gct ctc ctc ggt gtt  1267
Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met Ala Leu Leu Gly Val
    375                 380                 385

tcc tcc ctc gaa gaa ctc gag cca cgc cac gtc acc cag ctg gcc aag  1315
Ser Ser Leu Glu Glu Leu Glu Pro Arg His Val Thr Gln Leu Ala Lys
```

390 395 400 405

atg gtt cca gtt tct gac gca act cgt tct gca gcg gcg gag att 1360
Met Val Pro Val Ser Asp Ala Thr Arg Ser Ala Ala Ala Glu Ile
410 415 420

taaaagtttc tctccttagc tat 1383

<210> 136
<211> 420
<212> PRT
<213> Corynebacterium glutamicum

<400> 136
Met Val Lys Arg Gln Leu Pro Asn Pro Ala Glu Leu Leu Glu Leu Met
1 5 10 15

Lys Phe Lys Lys Pro Glu Leu Asn Gly Lys Lys Arg Arg Leu Asp Ser
20 25 30

Ala Leu Thr Ile Tyr Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro
35 40 45

Ala Ala Ala Phe Asp Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser
50 55 60

Ile Thr Arg Ala Arg Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp
65 70 75 80

Ile Leu Lys Pro Ala Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly
85 90 95

Gly Thr Ser Ser Met Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg
100 105 110

Leu Met Gln Thr Glu Gly Glu Ile Ala Gly Ala Gly Ala Ala Gly Ala
115 120 125

Ala Gly Ile Pro Phe Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu
130 135 140

Asp Val Lys Ala Thr Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr
145 150 155 160

Val Met Arg Asp Arg Glu Ile Ser Tyr Gly Leu Val Glu Arg Ala Ala
165 170 175

Lys Ala Gly Phe Asp Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala
180 185 190

Gly Tyr Arg Ile Arg Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln
195 200 205

Leu Thr Pro Ser Thr Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp
210 215 220

Ile Asp Phe Leu Thr Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Ser
225 230 235 240

Thr Gly Gly Thr Val Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr

```
                245                 250                 255

Ile Ser Tyr Glu Asp Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys
            260                 265                 270

Leu Val Val Lys Gly Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu
        275                 280                 285

Asp Gln Gly Val Asp Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln
    290                 295                 300

Leu Asp Arg Ala Pro Val Pro Phe His Leu Leu Pro Gln Val Arg Lys
305                 310                 315                 320

Glu Val Gly Ser Glu Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn
                325                 330                 335

Gly Ala Asp Ile Val Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu
            340                 345                 350

Ile Gly Arg Ala Tyr Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly
        355                 360                 365

Val Asp Arg Thr Ile Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met
    370                 375                 380

Ala Leu Leu Gly Val Ser Ser Leu Glu Glu Leu Glu Pro Arg His Val
385                 390                 395                 400

Thr Gln Leu Ala Lys Met Val Pro Val Ser Asp Ala Thr Arg Ser Ala
                405                 410                 415

Ala Ala Glu Ile
            420
```

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<210> 137
<211> 1836
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1813)
<223> RXN01952

<400> 137
ccatcaaaaa atgaacgacc gcggactagc tcggatcaag gcgacatccc ctcagcatca 60

tgacgcgctt gtgatgcaac tgaatatagg aagcttagag atg acg caa cca gga 115
                                                Met Thr Gln Pro Gly
                                                  1   5

cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163
Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
                  10   15   20

gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211
Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe
              25   30   35
```
```

```
agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc   259
Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg
         40                  45                  50

ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac   307
Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp
     55                  60                  65

aac aac ctc atc gtc atc ccg cag gca tcg aac acg ggc ctg act ggt   355
Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly
 70                  75                  80                  85

gga tcc ggc ccc ggc ttc caa gac tac gat cgc ccc att gtg atc atc   403
Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile
                 90                  95                 100

tcg act cac cgc atc gat gag gtg cac ctc atc aac gac gcg cgc gag   451
Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu
            105                 110                 115

gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc   499
Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu
        120                 125                 130

gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc   547
Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile
    135                 140                 145

ggc gcc tcg gtc atc ggc ggc atc gcg aac aac tcg ggc ggc agc cag   595
Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln
150                 155                 160                 165

att cgc aag ggt ccg gca ttc acg cgc gaa gcg atc ttc gcc cgc gtc   643
Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val
                170                 175                 180

aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc   691
Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu
            185                 190                 195

gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg   739
Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp
        200                 205                 210

tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag   787
Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu
    215                 220                 225

tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat   835
Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn
230                 235                 240                 245

gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg   883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu
                250                 255                 260

atg gtg ttc gcg gtg cgc acc cgc acc ttc cct cgc gaa gtg cac ccg   931
Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro
            265                 270                 275

acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc   979
```

```
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile
        280                 285                 290

cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag   1027
Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu Pro Ile Ser Gly Glu
    295                 300                 305

tac atg ggc cgc agt gcc ttc gac ttg gcc gag aag tac ggc aaa gac   1075
Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu Lys Tyr Gly Lys Asp
310                 315                 320                 325

acc ttc gtc ttc ctg aag ttc atg agt cca gcg ctg cag acg cgc atg   1123
Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala Leu Gln Thr Arg Met
                330                 335                 340

ttc tcg ttc aag acg tgg gcc aac ggc ttg ttc tcg aag att ccc ggc   1171
Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe Ser Lys Ile Pro Gly
            345                 350                 355

att ggt ccg acc ttc gcc gac acg gta tcg caa gcc atg ttc agc gtg   1219
Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln Ala Met Phe Ser Val
        360                 365                 370

ctg ccc aac cag ctg ccc aag cgc atg atg gag tac cgc aac cgt ttc   1267
Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu Tyr Arg Asn Arg Phe
    375                 380                 385

gag cat cac ctg ctg ctc acc gtc agc gag tcg cag aag gcc gcg agc   1315
Glu His His Leu Leu Leu Thr Val Ser Glu Ser Gln Lys Ala Ala Ser
390                 395                 400                 405

gag aag atg ctc aag gag ttc ttc gca gag ccc gag cac act ggt gag   1363
Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro Glu His Thr Gly Glu
                410                 415                 420

ttc ttc atc tgc acg tct gat gaa gaa aag agc gcg tcg ctc aac cgg   1411
Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser Ala Ser Leu Asn Arg
            425                 430                 435

ttc ggc gcg gcc agt gcc gcc act cgc tac gcc gcg ttg aag cgc cgg   1459
Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala Ala Leu Lys Arg Arg
        440                 445                 450

cac atc gca ggg ctc atc ccc atc gat gtg gcc ctg cgt cgc gac gat   1507
His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala Leu Arg Arg Asp Asp
    455                 460                 465

tgg aac tgg ctc gag gtg ctg ccg gag gag atc gac gac cag ctt gag   1555
Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile Asp Asp Gln Leu Glu
470                 475                 480                 485

gtc aag gcg tat tac ggg cac ttc ttc tgc cat gtg atg cac cag gac   1603
Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His Val Met His Gln Asp
                490                 495                 500

tat gtc gcc aag cag ggc gtg gat ctc gag gcg ctg cac gac cgc atc   1651
Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala Leu His Asp Arg Ile
            505                 510                 515

cag cac ctg ctg gag gag cgc ggc gcg aag ctg ccc gcc gag cac aac   1699
Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu Pro Ala Glu His Asn
```

```
        520                 525                 530

tac ggt cgc atg tac aag ctg ccg gag tcc atg gaa gag cac ttc aag   1747
Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His Phe Lys
    535                 540                 545

gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc acg tcg   1795
Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly Thr Ser
550                 555                 560                 565

ccg cac aag gac tgg gcc taagtcccca aggtagcgcg acg                 1836
Pro His Lys Asp Trp Ala
               570
```

<210> 138
<211> 571
<212> PRT
<213> Corynebacterium glutamicum

<400> 138

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Met Thr Gln Pro Gly Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp
  1               5                  10                  15

Ala Phe Lys Arg Ile Val Gly Asp Glu His Val Leu Thr Ser Glu Arg
             20                  25                  30

Ala Thr Met Pro Phe Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val
         35                  40                  45

Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu
     50                  55                  60

Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn
 65                  70                  75                  80

Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg
                 85                  90                  95

Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile
            100                 105                 110

Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His
        115                 120                 125

Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile
    130                 135                 140

Gly Ser Thr Ser Ile Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn
145                 150                 155                 160

Ser Gly Gly Ser Gln Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala
                165                 170                 175

Ile Phe Ala Arg Val Asn Asp Asp Gly Lys Val Glu Leu Val Asn His
            180                 185                 190

Leu Gly Ile Ser Leu Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu
        195                 200                 205

Gln Arg Gly Glu Trp Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp
```

```
    210                 215                 220

Ser Asn Glu Thr Glu Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser
225                 230                 235                 240

Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly
                245                 250                 255

Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro
            260                 265                 270

Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His
        275                 280                 285

Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu
    290                 295                 300

Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu
305                 310                 315                 320

Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala
                325                 330                 335

Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe
            340                 345                 350

Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln
        355                 360                 365

Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
    370                 375                 380

Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
385                 390                 395                 400

Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
                405                 410                 415

Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
            420                 425                 430

Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
        435                 440                 445

Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
    450                 455                 460

Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile
465                 470                 475                 480

Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His
                485                 490                 495

Val Met His Gln Asp Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala
            500                 505                 510

Leu His Asp Arg Ile Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu
        515                 520                 525

Pro Ala Glu His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met
    530                 535                 540
```

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```
Glu Glu His Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly
545                 550                 555                 560

Ile Gly Gly Thr Ser Pro His Lys Asp Trp Ala
                565                 570
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<210> 139
<211> 239
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(216)
<223> FRXA01952

<400> 139

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cca gga cta tgt cgc caa gca ggg cgt gga tct caa ggc gct gac gac   48
Pro Gly Leu Cys Arg Gln Ala Gly Arg Gly Ser Gln Gly Ala Asp Asp
  1               5                  10                  15

cgc atc cag cac ttg ctg gag gag cac ggc aag aag ctg ccc gcc gag   96
Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu
             20                  25                  30

cac aac tac ggt cgc atg tac aag ctg ccg gag tcc atg gaa gag cac   144
His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His
         35                  40                  45

ttc aag gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc   192
Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
     50                  55                  60

acg tcg ccg cac aag gac tgg gcc taagtcccca aggtagcgcg acg         239
Thr Ser Pro His Lys Asp Trp Ala
 65                  70
```

<210> 140
<211> 72
<212> PRT
<213> Corynebacterium glutamicum

<400> 140

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Pro Gly Leu Cys Arg Gln Ala Gly Arg Gly Ser Gln Gly Ala Asp Asp
  1               5                  10                  15

Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu
             20                  25                  30

His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His
         35                  40                  45

Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
     50                  55                  60

Thr Ser Pro His Lys Asp Trp Ala
 65                  70
```

<210> 141
<211> 1699
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1699)
<223> FRXA01955

<400> 141
ccatcaaaaa atgaacgacc gcggactagc tcggatcaag gcgacatccc ctcagcatca 60

tgacgcgctt gtgatgcaac tgaatatagg aagcttagag atg acg caa cca gga 115
Met Thr Gln Pro Gly
1 5

cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163
Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
10 15 20

gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211
Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe
25 30 35

agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259
Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg
40 45 50

ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac 307
Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp
55 60 65

aac aac ctc atc gtc atc ccg cag gca tcg aac acg ggc ctg act ggt 355
Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly
70 75 80 85

gga tcc ggc ccc ggc ttc caa gac tac gat cgc ccc att gtg atc atc 403
Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile
90 95 100

tcg act cac cgc atc gat gag gtg cac ctc atc aac gac gcg cgc gag 451
Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu
105 110 115

gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc 499
Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu
120 125 130

gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc 547
Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile
135 140 145

ggc gcc tcg gtc atc ggc ggc atc gcg aac aac tcg ggc ggc agc cag 595
Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln
150 155 160 165

att cgc aag ggt ccg gca ttc acg cgc gaa gcg atc ttc gcc cgc gtc 643
Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val
170 175 180

```
aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc   691
Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu
            185                 190                 195

gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg   739
Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp
        200                 205                 210

tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag   787
Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu
    215                 220                 225

tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat   835
Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn
230                 235                 240                 245

gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg   883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu
                250                 255                 260

atg gtg ttc gcg gtg cgc acc cgc acc ttc cct cgc gaa gtg cac ccg   931
Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro
            265                 270                 275

acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc   979
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile
        280                 285                 290

cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag   1027
Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu Pro Ile Ser Gly Glu
    295                 300                 305

tac atg ggc cgc agt gcc ttc gac ttg gcc gag aag tac ggc aaa gac   1075
Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu Lys Tyr Gly Lys Asp
310                 315                 320                 325

acc ttc gtc ttc ctg aag ttc atg agt cca gcg ctg cag acg cgc atg   1123
Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala Leu Gln Thr Arg Met
                330                 335                 340

ttc tcg ttc aag acg tgg gcc aac ggc ttg ttc tcg aag att ccc ggc   1171
Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe Ser Lys Ile Pro Gly
            345                 350                 355

att ggt ccg acc ttc gcc gac acg gta tcg caa gcc atg ttc agc gtg   1219
Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln Ala Met Phe Ser Val
        360                 365                 370

ctg ccc aac cag ctg ccc aag cgc atg atg gag tac cgc aac cgt ttc   1267
Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu Tyr Arg Asn Arg Phe
    375                 380                 385

gag cat cac ctg ctg ctc acc gtc agc gag tcg cag aag gcc gcg agc   1315
Glu His His Leu Leu Leu Thr Val Ser Glu Ser Gln Lys Ala Ala Ser
390                 395                 400                 405

gag aag atg ctc aag gag ttc ttc gca gag ccc gag cac act ggt gag   1363
Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro Glu His Thr Gly Glu
                410                 415                 420
```

```
ttc ttc atc tgc acg tct gat gaa gaa aag agc gcg tcg ctc aac cgg   1411
Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser Ala Ser Leu Asn Arg
            425                 430                 435

ttc ggc gcg gcc agt gcc gcc act cgc tac gcc gcg ttg aag cgc cgg   1459
Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala Ala Leu Lys Arg Arg
        440                 445                 450

cac atc gca ggg ctc atc ccc atc gat gtg gcc ctg cgt cgc gac gat   1507
His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala Leu Arg Arg Asp Asp
    455                 460                 465

tgg aac tgg ctc gag gtg ctg ccg gag gag atc gac gac cag ctt gag   1555
Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile Asp Asp Gln Leu Glu
470                 475                 480                 485

gtc aag gcg tat tac ggg cac ttc ttc tgc cat gtg atg cac cag gac   1603
Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His Val Met His Gln Asp
                490                 495                 500

tat gtc gcc aag cag ggc gtg gat ctc gag gcg ctg cac gac cgc atc   1651
Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala Leu His Asp Arg Ile
            505                 510                 515

cag cac ctg ctg gag gag cgc ggc gcg aag ctg ccc gcc gag cac aac   1699
Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu Pro Ala Glu His Asn
        520                 525                 530
```

<210> 142
<211> 533
<212> PRT
<213> Corynebacterium glutamicum

<400> 142

```
Met Thr Gln Pro Gly Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp
  1               5                  10                  15

Ala Phe Lys Arg Ile Val Gly Asp Glu His Val Leu Thr Ser Glu Arg
            20                  25                  30

Ala Thr Met Pro Phe Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val
        35                  40                  45

Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu
    50                  55                  60

Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn
65                  70                  75                  80

Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg
                85                  90                  95

Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile
            100                 105                 110

Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His
        115                 120                 125

Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile
    130                 135                 140
```

```
Gly Ser Thr Ser Ile Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn
145                 150                 155                 160

Ser Gly Gly Ser Gln Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala
                165                 170                 175

Ile Phe Ala Arg Val Asn Asp Asp Gly Lys Val Glu Leu Val Asn His
            180                 185                 190

Leu Gly Ile Ser Leu Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu
        195                 200                 205

Gln Arg Gly Glu Trp Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp
    210                 215                 220

Ser Asn Glu Thr Glu Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser
225                 230                 235                 240

Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly
                245                 250                 255

Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro
            260                 265                 270

Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His
        275                 280                 285

Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu
    290                 295                 300

Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu
305                 310                 315                 320

Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala
                325                 330                 335

Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe
            340                 345                 350

Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln
        355                 360                 365

Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
    370                 375                 380

Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
385                 390                 395                 400

Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
                405                 410                 415

Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
            420                 425                 430

Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
        435                 440                 445

Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
    450                 455                 460
```

```
Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile
465                 470                 475                 480

Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His
                485                 490                 495

Val Met His Gln Asp Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala
            500                 505                 510

Leu His Asp Arg Ile Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu
        515                 520                 525

Pro Ala Glu His Asn
    530
```

<210> 143
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXA00293

<400> 143

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agagattgtt gattcggcac caactttacc cacgagggta gaaatgaagc attcaggatg 60

acaaaaccca acctcacacc aacaacctat cctggagccc atg aaa atc ttt gtt   115
                                            Met Lys Ile Phe Val
                                              1               5

ggt ttt ggc gat tat cca ctc acc acc aag gcc ctt aag gag gca ggc   163
Gly Phe Gly Asp Tyr Pro Leu Thr Thr Lys Ala Leu Lys Glu Ala Gly
                  10                  15                  20

gca gaa ata gtg gac tcc ctc gaa aaa gcc gag ggg ttt gtc ttc act   211
Ala Glu Ile Val Asp Ser Leu Glu Lys Ala Glu Gly Phe Val Phe Thr
              25                  30                  35

caa aca cca ggc aca gaa ttt ccc cta ctt ccc gac gga gtg agg tgg   259
Gln Thr Pro Gly Thr Glu Phe Pro Leu Leu Pro Asp Gly Val Arg Trp
          40                  45                  50

gtg caa ttt ccc aat gcg ggg ctc aac gca tat ttc aca gct ggg cag   307
Val Gln Phe Pro Asn Ala Gly Leu Asn Ala Tyr Phe Thr Ala Gly Gln
      55                  60                  65

att gat gac aaa cgc cgg tgg tca aat gca tca ggg gtg tat ggc caa   355
Ile Asp Asp Lys Arg Arg Trp Ser Asn Ala Ser Gly Val Tyr Gly Gln
  70                  75                  80                  85

cag gta gcc gaa gca gca atg gct ctt ttg ctg gga ctg att cat atg   403
Gln Val Ala Glu Ala Ala Met Ala Leu Leu Leu Gly Leu Ile His Met
                  90                  95                 100

cac ccc acc atg gtg cgt gcc gat agt tgg gca cca agc act caa ata   451
His Pro Thr Met Val Arg Ala Asp Ser Trp Ala Pro Ser Thr Gln Ile
              105                 110                 115
```

```
gat cag cag acc aga tgg ctt gat ggt gca aca gtt gcc att gtg gga   499
Asp Gln Gln Thr Arg Trp Leu Asp Gly Ala Thr Val Ala Ile Val Gly
        120                 125                 130

gct ggt gga atc ggt aaa cat ctg gca gcc atg ttg aaa cct ttt ggc   547
Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met Leu Lys Pro Phe Gly
    135                 140                 145

gca aag tct tta gca gta agc agg acc ggt aca ccc acc caa gat ttt   595
Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr Pro Thr Gln Asp Phe
150                 155                 160                 165

gat gca acg gaa cct ata tcc aac ctg cac caa gta ctt gcc gac gcc   643
Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln Val Leu Ala Asp Ala
                170                 175                 180

gac cat gtg gtg ttg tgc gta ccg ctt acc gca gac acc tat cat ctg   691
Asp His Val Val Leu Cys Val Pro Leu Thr Ala Asp Thr Tyr His Leu
            185                 190                 195

atc gga aaa gca gag ctt aaa gca atg cag tcc act gca att ttg atc   739
Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser Thr Ala Ile Leu Ile
        200                 205                 210

aac gtg gct cgc gga gaa gta gta gat aca gaa gca tta gtt gac gcc   787
Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu Ala Leu Val Asp Ala
    215                 220                 225

tta gat gcc caa gaa ata tcc ggg gca ggc tta gat gtc acc gat cct   835
Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu Asp Val Thr Asp Pro
230                 235                 240                 245

gaa cca ttg ccg gac gat cat cca ctg tgg ggg cgc agc aat gtg atc   883
Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly Arg Ser Asn Val Ile
                250                 255                 260

att acc ccg cac gta gcc aac acg ttg acc tcg atg gat cgc atg ctt   931
Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser Met Asp Arg Met Leu
            265                 270                 275

gcc cca gtg gtg gca gaa aac tac cga cgg ttt ctc gct gga gaa aag   979
Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe Leu Ala Gly Glu Lys
        280                 285                 290

atg ctg acc gag gtg gac atc cac aaa ggt tac tagagcagtg gctttgaata 1032
Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
    295                 300

tag                                                               1035


<210> 144
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 144
Met Lys Ile Phe Val Gly Phe Gly Asp Tyr Pro Leu Thr Thr Lys Ala
  1               5                  10                  15

Leu Lys Glu Ala Gly Ala Glu Ile Val Asp Ser Leu Glu Lys Ala Glu
```

```
            20                  25                  30

Gly Phe Val Phe Thr Gln Thr Pro Gly Thr Glu Phe Pro Leu Leu Pro
        35                  40                  45

Asp Gly Val Arg Trp Val Gln Phe Pro Asn Ala Gly Leu Asn Ala Tyr
    50                  55                  60

Phe Thr Ala Gly Gln Ile Asp Asp Lys Arg Arg Trp Ser Asn Ala Ser
65                  70                  75                  80

Gly Val Tyr Gly Gln Gln Val Ala Glu Ala Ala Met Ala Leu Leu Leu
                85                  90                  95

Gly Leu Ile His Met His Pro Thr Met Val Arg Ala Asp Ser Trp Ala
            100                 105                 110

Pro Ser Thr Gln Ile Asp Gln Gln Thr Arg Trp Leu Asp Gly Ala Thr
        115                 120                 125

Val Ala Ile Val Gly Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met
    130                 135                 140

Leu Lys Pro Phe Gly Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr
145                 150                 155                 160

Pro Thr Gln Asp Phe Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln
                165                 170                 175

Val Leu Ala Asp Ala Asp His Val Val Leu Cys Val Pro Leu Thr Ala
            180                 185                 190

Asp Thr Tyr His Leu Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser
        195                 200                 205

Thr Ala Ile Leu Ile Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu
    210                 215                 220

Ala Leu Val Asp Ala Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu
225                 230                 235                 240

Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly
                245                 250                 255

Arg Ser Asn Val Ile Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser
            260                 265                 270

Met Asp Arg Met Leu Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe
        275                 280                 285

Leu Ala Gly Glu Lys Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
    290                 295                 300
```

<210> 145
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (62)..(664)
<223> RXN01130

<400> 145
agttcgtggc ggatgctgtg aacgtttccg gtggtcgcgt gggcgaagag gttctgtgtg 60

gatg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109
Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
1 5 10 15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
20 25 30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
35 40 45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
50 55 60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
65 70 75 80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
85 90 95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
100 105 110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
115 120 125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
130 135 140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
145 150 155 160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
165 170 175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
180 185 190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct 684
Ala Thr Ser Phe Gln Val Asp Leu Asp
195 200

tga 687

<210> 146
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 146
Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
1 5 10 15

Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
20 25 30

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
35 40 45

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
50 55 60

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
65 70 75 80

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
85 90 95

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
100 105 110

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
115 120 125

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
130 135 140

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
145 150 155 160

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
165 170 175

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
180 185 190

Ala Thr Ser Phe Gln Val Asp Leu Asp
195 200

<210> 147
<211> 326
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(303)
<223> FRXA01130

<400> 147
gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag atc acc cgc atc 48

```
Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile
  1               5                  10                  15

aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg aac ctc ttc ctg   96
Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu
             20                  25                  30

cag tac act gac gct cct ggt gca ctg ggt acc gtt ggt acc aag ctg   144
Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
         35                  40                  45

ggt gct gct ggc atc aac atc gag gct gct gcg ttg act cag gct gag   192
Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
     50                  55                  60

aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag tcc gct gtc tct   240
Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
 65                  70                  75                  80

gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt gct act tcc ttc   288
Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
                 85                  90                  95

cag gtt gat ctt gac taattagaga tccatttgct tga                    326
Gln Val Asp Leu Asp
            100
```

Doc#: 1-1-1-

<220>
<221> CDS
<222> (101)..(604)
<223> RXN03112

<400> 149
gtgagcacgc aatttctttg ctgctgtcta ctgctcgcca gatcctgctg ctgatgcgac 60

gctgcgtgag ggcgagtgga agcggtcttc tttcaacggt gtg gaa att ttc gga 115
Val Glu Ile Phe Gly
1 5

aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163
Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
10 15 20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211
Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
25 30 35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
40 45 50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
55 60 65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser
70 75 80 85

aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat 403
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
90 95 100

gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct 451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
105 110 115

ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc 499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
120 125 130

aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa 547
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
135 140 145

gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag 595
Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys
150 155 160 165

gcg ctg gct 604
Ala Leu Ala

<210> 150
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 150
Val Glu Ile Phe Gly Lys Thr Val Gly Ile Val Gly Phe Gly His Ile
1 5 10 15

Gly Gln Leu Phe Ala Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val
20 25 30

Ala Tyr Asp Pro Tyr Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val
35 40 45

Glu Leu Val Glu Leu Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr
50 55 60

Ile His Leu Pro Lys Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His
65 70 75 80

Leu Leu Ala Lys Ser Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg
85 90 95

Gly Gly Leu Val Asp Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly
100 105 110

His Ile Arg Gly Ala Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr
115 120 125

Asp Ser Pro Leu Phe Lys Leu Pro Gln Val Val Val Thr Pro His Leu
130 135 140

Gly Ala Ser Thr Glu Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala
145 150 155 160

Asp Ser Val Leu Lys Ala Leu Ala
165

<210> 151
<211> 649
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> FRXA01133

<400> 151
tgtttctagt cgcacgccaa aacccggcgt ggacacgtct gcagccgacg cggtcgtgcc 60

tgttgtagac ggacattcct agtttttcca ggagtaactt gtg agc cag aat ggc 115
Val Ser Gln Asn Gly
1 5

cgt ccg gta gtc ctc atc gcc gat aag ctt gcg cag tcc act gtt gac 163
Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala Gln Ser Thr Val Asp
10 15 20

gcg ctt gga gat gca gta gaa gtc cgt tgg gtt gac gga cct aac cgc 211
Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp Gly Pro Asn Arg
25 30 35

```
cca gaa ctg ctt gat gca gtt aag gaa gcg gac gca ctg ctc gtg cgt   259
Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp Ala Leu Leu Val Arg
         40                  45                  50

tct gct acc act gtc gat gct gaa gtc atc gcc gct gcc cct aac ttg   307
Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala Ala Ala Pro Asn Leu
     55                  60                  65

aag atc gtc ggt cgt gcc ggc gtg ggc ttg gac aac gtt gac atc cct   355
Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp Ile Pro
 70                  75                  80                  85

gct gcc act gaa gct ggc gtc atg gtt gct aac gca ccg acc tct aat   403
Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn Ala Pro Thr Ser Asn
                 90                  95                 100

att cac tcc gct tgt gag cac gca att tct ttg ctg ctg tct act gct   451
Ile His Ser Ala Cys Glu His Ala Ile Ser Leu Leu Leu Ser Thr Ala
            105                 110                 115

cgc cag atc ctg ctg ctg atg cga cgc tgc gtg agg gcg agt gga agc   499
Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val Arg Ala Ser Gly Ser
        120                 125                 130

ggt ctt ctt tca acg gtg tgg aaa ttt tcg gaa aaa ctg tcg gta tcg   547
Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu Lys Leu Ser Val Ser
    135                 140                 145

tcg gtt ttg gcc aca ttg gtc agt tgt ttg ctc agc gtc ttg ctg cgt   595
Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu Ser Val Leu Leu Arg
150                 155                 160                 165

ttg aga cca cca ttg ttg ctt acg atc ctt acg cta acc ctg ctt cgt   643
Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr Leu Thr Leu Leu Arg
                170                 175                 180

gcg ggt                                                          649
Ala Gly
```

<210> 152
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 152

```
Val Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
  1               5                  10                  15

Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val
             20                  25                  30

Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
         35                  40                  45

Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
     50                  55                  60

Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
 65                  70                  75                  80
```

```
Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
                 85                  90                  95

Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
            100                 105                 110

Leu Leu Ser Thr Ala Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val
        115                 120                 125

Arg Ala Ser Gly Ser Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu
    130                 135                 140

Lys Leu Ser Val Ser Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu
145                 150                 155                 160

Ser Val Leu Leu Arg Leu Arg Pro Pro Leu Leu Leu Thr Ile Leu Thr
                165                 170                 175

Leu Thr Leu Leu Arg Ala Gly
            180
```

<210> 153
<211> 1011
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(988)
<223> RXN00871

<400> 153

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gggaaaaggc gatcaccagc cgttggctcg acccagcaac ccacggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat   115
                                              Met Arg Trp Phe His
                                                1               5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc   163
Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
                10                  15                  20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc   211
Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
            25                  30                  35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc   259
Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
        40                  45                  50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc   307
Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
    55                  60                  65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc   355
His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
70                  75                  80                  85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc   403
```

```
Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
                 90                  95                 100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc   451
Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
            105                 110                 115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc   499
Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
        120                 125                 130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga   547
Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
    135                 140                 145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac   595
Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
150                 155                 160                 165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg   643
Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
                170                 175                 180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg   691
Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg
            185                 190                 195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca   739
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser
        200                 205                 210

cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc   787
Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile
    215                 220                 225

gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc   835
Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly
230                 235                 240                 245

tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga   883
Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg
                250                 255                 260

atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca   931
Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr
            265                 270                 275

tgg acc ggg caa gca ttt gat gat cgc ttg cca tat gag aac gca aac   979
Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro Tyr Glu Asn Ala Asn
        280                 285                 290

aag gag gga taaaatttca tggctgaaac gaa                            1011
Lys Glu Gly
    295
```

<210> 154
<211> 296
<212> PRT
<213> Corynebacterium glutamicum

<400> 154
Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln
1 5 10 15

Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg
20 25 30

Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly
35 40 45

Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His
50 55 60

His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly
65 70 75 80

Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser
85 90 95

Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys
100 105 110

Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly
115 120 125

Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala
130 135 140

Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu
145 150 155 160

Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly
165 170 175

His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
180 185 190

Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
195 200 205

Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
210 215 220

Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
225 230 235 240

Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
245 250 255

Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
260 265 270

Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
275 280 285

Tyr Glu Asn Ala Asn Lys Glu Gly
290 295

<210> 155
<211> 964

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(964)
<223> FRXA00871

<400> 155
gggaaaaggc gatcaccagc cgttggctcg acccagcaac ccacggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
Met Arg Trp Phe His
1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
55 60 65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
70 75 80 85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
90 95 100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451
Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
105 110 115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499
Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
120 125 130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547
Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
135 140 145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595
Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
150 155 160 165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643
Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
170 175 180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691
Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg

```
            185                 190                 195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca   739
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser
        200                 205                 210

cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc   787
Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile
    215                 220                 225

gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc   835
Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly
230                 235                 240                 245

tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga   883
Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg
                250                 255                 260

atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca   931
Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr
            265                 270                 275

tgg acc ggg caa gca ttt gat gat cgc ttg cca                       964
Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
        280                 285


<210> 156
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 156
Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln
  1               5                  10                  15

Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg
             20                  25                  30

Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly
         35                  40                  45

Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His
     50                  55                  60

His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly
 65                  70                  75                  80

Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser
                 85                  90                  95

Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys
            100                 105                 110

Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly
        115                 120                 125

Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala
    130                 135                 140

Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu
```

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```
145                 150                 155                 160

Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly
                165                 170                 175

His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
            180                 185                 190

Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
        195                 200                 205

Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
    210                 215                 220

Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
225                 230                 235                 240

Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
                245                 250                 255

Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
            260                 265                 270

Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
        275                 280                 285
```

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<210> 157
<211> 373
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(373)
<223> RXN02829

<400> 157
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tttttcgttt aatctcatat ttaaacacgt tccttttaat tggttttata aattgataaa 60

ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att   115
                                            Met Gln Lys Asn Ile
                                              1               5

cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt   163
Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
                  10                  15                  20

tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att   211
Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
              25                  30                  35

gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga   259
Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
          40                  45                  50

gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt   307
Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
```

```
     55                  60                  65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat   355
Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp
 70                  75                  80                  85

gga cat atg acg tgg gat                                           373
Gly His Met Thr Trp Asp
                90
```

<210> 158
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

<400> 158

```
Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
  1               5                  10                  15

Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
             20                  25                  30

Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
         35                  40                  45

Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
     50                  55                  60

Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn
 65                  70                  75                  80

Arg Leu Thr Asp Asp Gly His Met Thr Trp Asp
                85                  90
```

<210> 159
<211> 376
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(376)
<223> FRXA02829

<400> 159

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tttttcgttt aatctcatat ttaaacacgt tccttttaat tggttttata aattgataaa 60

ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att   115
                                            Met Gln Lys Asn Ile
                                              1               5

cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt   163
Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
                10                  15                  20

tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att   211
Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
            25                  30                  35
```

```
gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga   259
Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
         40                  45                  50

gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt   307
Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
     55                  60                  65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat   355
Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp
 70                  75                  80                  85

gga cat atg acg tgg gga tcc                                      376
Gly His Met Thr Trp Gly Ser
                 90
```

<210> 160
<211> 92
<212> PRT
<213> Corynebacterium glutamicum

<400> 160

```
Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
  1               5                  10                  15

Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
            20                  25                  30

Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
         35                  40                  45

Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
     50                  55                  60

Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn
 65                  70                  75                  80

Arg Leu Thr Asp Asp Gly His Met Thr Trp Gly Ser
                 85                  90
```

<210> 161
<211> 948
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(925)
<223> RXN01468

<400> 161

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tgccaaggat ttgaccaccg tgcaggattt gattgacttt attaacacca ataaggctga 60

ttagcgggaa aatttcgccc aaaacaggga caatggtgtt atg aca gtg aac att   115
                                              Met Thr Val Asn Ile
                                                1               5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata   163
Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
```

```
                  10                  15                  20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg   211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val
            25                  30                  35

gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt   259
Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu
        40                  45                  50

tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att   307
Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile
    55                  60                  65

tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag   355
Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys
70                  75                  80                  85

gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg   403
Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu
                90                  95                 100

cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc   451
His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val
            105                 110                 115

ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata   499
Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile
        120                 125                 130

aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc   547
Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val
    135                 140                 145

act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc   595
Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala
150                 155                 160                 165

gca ctt att acc gca gct act ggc gct gag cct tat tac atc ggc aag   643
Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys
                170                 175                 180

cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat   691
Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His
            185                 190                 195

tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa   739
Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys
        200                 205                 210

tct ggt ttg gaa gcc ggc ctg agc acc gtg ctg gtt cga agc gga att   787
Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile
    215                 220                 225

tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg   835
Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val
230                 235                 240                 245

atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt   883
Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly
                250                 255                 260
```

```
gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac          925
Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp
            265                 270                 275

tagtattctg taggtcatgg cat                                       948
```

<210> 162
<211> 275
<212> PRT
<213> Corynebacterium glutamicum

<400> 162

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Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
  1               5                  10                  15

Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
            20                  25                  30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
        35                  40                  45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
    50                  55                  60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
65                  70                  75                  80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
                85                  90                  95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
            100                 105                 110

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
        115                 120                 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
    130                 135                 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
145                 150                 155                 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
                165                 170                 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
            180                 185                 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
        195                 200                 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
    210                 215                 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
225                 230                 235                 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
                245                 250                 255
```

```
Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
            260                 265                 270

Phe Thr Asp
        275


<210> 163
<211> 948
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(925)
<223> FRXA01468

<400> 163
tgccaaggat ttgaccaccg tgcaggattt gattgacttt attaacacca ataaggctga 60

ttagcgggaa aatttcgccc aaaacaggga caatggtgtt atg aca gtg aac att   115
                                              Met Thr Val Asn Ile
                                                1               5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata   163
Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
                10                  15                  20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg   211
Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val
            25                  30                  35

gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt   259
Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu
        40                  45                  50

tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att   307
Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile
    55                  60                  65

tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag   355
Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys
70                  75                  80                  85

gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg   403
Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu
                90                  95                  100

cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc   451
His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val
            105                 110                 115

ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata   499
Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile
        120                 125                 130

aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc   547
Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val
    135                 140                 145
```

```
act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc   595
Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala
150                 155                 160                 165

gca ctt att acc gca gct act ggc gct gag cct tat tac atc ggc aag   643
Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys
                170                 175                 180

cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat   691
Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His
            185                 190                 195

tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa   739
Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys
        200                 205                 210

tct ggt ttg gaa gcc ggc ctg agc acc gtg ctg gtt cga agc gga att   787
Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile
    215                 220                 225

tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg   835
Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val
230                 235                 240                 245

atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt   883
Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly
                250                 255                 260

gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac           925
Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp
            265                 270                 275

tagtattctg taggtcatgg cat                                        948
```

<210> 164
<211> 275
<212> PRT
<213> Corynebacterium glutamicum

<400> 164

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Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
  1               5                  10                  15

Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
             20                  25                  30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
         35                  40                  45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
     50                  55                  60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
 65                  70                  75                  80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
                 85                  90                  95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
            100                 105                 110
```

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
260 265 270

Phe Thr Asp
275

<210> 165
<211> 1128
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1105)
<223> RXA00794

<400> 165
gcgggttgat acagcccaag cgccgataca tttataatgc gcctagatac gtgcaaccca 60

cgtaaccagg tcagatcaag tgccccagga ggcccttcag atg aac cta aag aac 115
Met Asn Leu Lys Asn
1 5

ccc gaa acg cca gac cgt aac ctt gct atg gag ctg gtg cga gtt acg 163
Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu Leu Val Arg Val Thr
10 15 20

gaa gca gct gca ctg gct tct gga cgt tgg gtt gga cgt ggc atg aag 211
Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val Gly Arg Gly Met Lys
25 30 35

aat gaa ggc gac ggt gcc gct gtt gac gcc atg cgc cag ctc atc aac 259

```
Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met Arg Gln Leu Ile Asn
         40                  45                  50

tca gtg acc atg aag ggc gtc gtt gtt atc ggc gag ggc gaa aaa gac   307
Ser Val Thr Met Lys Gly Val Val Val Ile Gly Glu Gly Glu Lys Asp
     55                  60                  65

gaa gct cca atg ctg tac aac ggc gaa gag gtc gga acc ggc ttt gga   355
Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val Gly Thr Gly Phe Gly
 70                  75                  80                  85

cct gag gtt gat atc gca gtt gac cca gtt gac ggc acc acc ctg atg   403
Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp Gly Thr Thr Leu Met
                 90                  95                 100

gct gag ggt cgc ccc aac gca att tcc att ctc gca gct gca gag cgt   451
Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu Ala Ala Ala Glu Arg
            105                 110                 115

ggc acc atg tac gat cca tcc tcc gtc ttc tac atg aag aag atc gcc   499
Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr Met Lys Lys Ile Ala
        120                 125                 130

gtg gga cct gag gcc gca ggc aag atc gac atc gaa gct cca gtt gcc   547
Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile Glu Ala Pro Val Ala
    135                 140                 145

cac aac atc aac gcg gtg gca aag tcc aag gga atc aac cct tcc gac   595
His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly Ile Asn Pro Ser Asp
150                 155                 160                 165

gtc acc gtt gtc gtg ctt gac cgt cct cgc cac atc gaa ctg atc gca   643
Val Thr Val Val Val Leu Asp Arg Pro Arg His Ile Glu Leu Ile Ala
                170                 175                 180

gac att cgt cgt gca ggc gca aag gtt cgt ctc atc tcc gac ggc gac   691
Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu Ile Ser Asp Gly Asp
            185                 190                 195

gtt gca ggt gca gtt gca gca gct cag gat tcc aac tcc gtg gac atc   739
Val Ala Gly Ala Val Ala Ala Ala Gln Asp Ser Asn Ser Val Asp Ile
        200                 205                 210

atg atg ggc acc ggc gga acc cca gaa ggc atc atc act gcg tgc gcc   787
Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile Ile Thr Ala Cys Ala
    215                 220                 225

atg aag tgc atg ggt ggc gaa atc cag ggc atc ctg gcc cca atg aac   835
Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile Leu Ala Pro Met Asn
230                 235                 240                 245

gat ttc gag cgc cag aag gca cac gac gct ggt ctg gtt ctt gat cag   883
Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly Leu Val Leu Asp Gln
                250                 255                 260

gtt ctg cac acc aac gat ctg gtg agc tcc gac aac tgc tac ttc gtg   931
Val Leu His Thr Asn Asp Leu Val Ser Ser Asp Asn Cys Tyr Phe Val
            265                 270                 275

gca acc ggt gtg acc aac ggt gac atg ctc cgt ggc gtt tcc tac cgc   979
Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg Gly Val Ser Tyr Arg
```

```
        280                 285                 290

gca aac ggc gca acc acc cgt tcc ctg gtt atg cgc gca aag tca ggc   1027
Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met Arg Ala Lys Ser Gly
    295                 300                 305

acc atc cgc cac atc gag tct gtc cac cag ctg tcc aag ctg cag gaa   1075
Thr Ile Arg His Ile Glu Ser Val His Gln Leu Ser Lys Leu Gln Glu
310                 315                 320                 325

tac tcc gtg gtt gac tac acc acc gcg acc taagagctct tagttcgaaa     1125
Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
                330                 335

aac                                                               1128
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<210> 166
<211> 335
<212> PRT
<213> Corynebacterium glutamicum

<400> 166

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Met Asn Leu Lys Asn Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu
  1               5                  10                  15

Leu Val Arg Val Thr Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val
            20                  25                  30

Gly Arg Gly Met Lys Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met
        35                  40                  45

Arg Gln Leu Ile Asn Ser Val Thr Met Lys Gly Val Val Val Ile Gly
    50                  55                  60

Glu Gly Glu Lys Asp Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val
65                  70                  75                  80

Gly Thr Gly Phe Gly Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp
                85                  90                  95

Gly Thr Thr Leu Met Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu
            100                 105                 110

Ala Ala Ala Glu Arg Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr
        115                 120                 125

Met Lys Lys Ile Ala Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile
    130                 135                 140

Glu Ala Pro Val Ala His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly
145                 150                 155                 160

Ile Asn Pro Ser Asp Val Thr Val Val Val Leu Asp Arg Pro Arg His
                165                 170                 175

Ile Glu Leu Ile Ala Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu
            180                 185                 190

Ile Ser Asp Gly Asp Val Ala Gly Ala Val Ala Ala Ala Gln Asp Ser
        195                 200                 205
```

```
Asn Ser Val Asp Ile Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile
    210                 215                 220

Ile Thr Ala Cys Ala Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile
225                 230                 235                 240

Leu Ala Pro Met Asn Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly
                245                 250                 255

Leu Val Leu Asp Gln Val Leu His Thr Asn Asp Leu Val Ser Ser Asp
            260                 265                 270

Asn Cys Tyr Phe Val Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg
        275                 280                 285

Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met
    290                 295                 300

Arg Ala Lys Ser Gly Thr Ile Arg His Ile Glu Ser Val His Gln Leu
305                 310                 315                 320

Ser Lys Leu Gln Glu Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
                325                 330                 335
```

09892460.090306

<210> 167
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXN02920

<400> 167

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tgcatgcaga ttatctgtcc aactacgcca gccgcgcgta aagcgcgggc ctgctggtgg 60

cgggtggcgt cgaaaagcat ttttaaagga gtttaagacg atg aag ttt gtt atg   115
                                            Met Lys Phe Val Met
                                              1               5

tat ccg cat ttg tgg gag tcc acg acc gct gtc att gag ggt ggc gga   163
Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val Ile Glu Gly Gly Gly
                 10                  15                  20

cat gag cgg gtt gag gat att aaa gat gca gac ttc att ttc ttt aat   211
His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp Phe Ile Phe Phe Asn
             25                  30                  35

ggt tca gcg ccg gag ttc ccg gat ttg ccg gag aac atc aag ttc gtg   259
Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu Asn Ile Lys Phe Val
         40                  45                  50

cag gcc tcc atg gcg ggt att gat gcg ctg gtc aag cgt ggt gtc gtc   307
Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val Lys Arg Gly Val Val
     55                  60                  65

aat gag aag gca cgt tgg gca aac gcg gct ggc ctg tac gct gac acc   355
Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
```

```
70                  75                  80                  85

gtt gct gag tcc acc att ggt tta att ctg gcg cag atg cac atg cat   403
Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His
                 90                  95                 100

gcg acg act cgt ttg gct aag tcg tgg agc gtg cgg cct gag gtg gaa   451
Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu
            105                 110                 115

aac aac aag tca tgg ctg cat gac aat aaa act gtc gct att ttg ggc   499
Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly
        120                 125                 130

gcc ggt ggc att ggc gtg cgt ctg ctg gaa atg ctc aag ccg ttc aac   547
Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn
    135                 140                 145

gtg aag acc att gcg gtt aat aac tct ggt cgt ccg gtg gaa ggt gca   595
Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala
150                 155                 160                 165

gat gaa acc ttc gcc atg gat aag gct gag cac gtg tgg gct gag gct   643
Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala
                170                 175                 180

gat gtg ttt gtg ctc atc ctg ccg ctg act gat gcc act tat cag atc   691
Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile
            185                 190                 195

gtc aat gca gaa act ttg ggc aag atg aag cct tct gcc gtg gtg gtc   739
Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val
        200                 205                 210

aat gtg ggg cgt ggc ccg ctg atc aac acc gat gat ctg gtg gat gca   787
Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala
    215                 220                 225

ttg aac aac ggc acc att gcg ggt gct gcg ctg gac gtt acc gat cct   835
Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro
230                 235                 240                 245

gag cca ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt   883
Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val
                250                 255                 260

atc act cct cat act gca aac acg aat gag agg att cgt gct ttg acc   931
Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr
            265                 270                 275

ggc gaa ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag   979
Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln
        280                 285                 290

atg gcc acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat 1032
Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
    295                 300

ccg                                                               1035
```

<210> 168
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 168

```
Met Lys Phe Val Met Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val
  1               5                  10                  15

Ile Glu Gly Gly Gly His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp
             20                  25                  30

Phe Ile Phe Phe Asn Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu
         35                  40                  45

Asn Ile Lys Phe Val Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val
     50                  55                  60

Lys Arg Gly Val Val Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly
 65                  70                  75                  80

Leu Tyr Ala Asp Thr Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala
                 85                  90                  95

Gln Met His Met His Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val
            100                 105                 110

Arg Pro Glu Val Glu Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr
        115                 120                 125

Val Ala Ile Leu Gly Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met
    130                 135                 140

Leu Lys Pro Phe Asn Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg
145                 150                 155                 160

Pro Val Glu Gly Ala Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His
                165                 170                 175

Val Trp Ala Glu Ala Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp
            180                 185                 190

Ala Thr Tyr Gln Ile Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro
        195                 200                 205

Ser Ala Val Val Val Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp
    210                 215                 220

Asp Leu Val Asp Ala Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu
225                 230                 235                 240

Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu
                245                 250                 255

Met Asp Asn Val Val Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg
            260                 265                 270

Ile Arg Ala Leu Thr Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe
        275                 280                 285

Glu Ala Gly Glu Gln Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
```

290 295 300

<210> 169
<211> 779
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (52)..(756)
<223> FRXA02379

<400> 169

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tgcaggcctc catggcgggt attgatgcgc tggtcaagcg tggtgtcgtc aatg aga    57
                                                          Met Arg
                                                            1

aag cac cgt tgg gca aac gcg gct ggc ctg tac gct gac acc gtt gct    105
Lys His Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr Val Ala
          5                  10                  15

gag tcc acc att ggt tta att ctg gcg cag atg cac atg cat gcg acg    153
Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His Ala Thr
     20                  25                  30

act cgt ttg gct aag tcg tgg agc gtg cgg cct gag gtg gaa aac aac    201
Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu Asn Asn
 35                  40                  45                  50

aag tca tgg ctg cat gac aat aaa act gtc gct att ttg ggc gcc ggt    249
Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly Ala Gly
                 55                  60                  65

ggc att ggc gtg cgt ctg ctg gaa atg ctc aag ccg ttc aac gtg aag    297
Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn Val Lys
            70                  75                  80

acc att gcg gtt aat aac tct ggt cgt ccg gtg gaa ggt gca gat gaa    345
Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala Asp Glu
         85                  90                  95

acc ttc gcc atg gat aag gct gag cac gtg tgg gct gag gct gat gtg    393
Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala Asp Val
    100                 105                 110

ttt gtg ctc atc ctg ccg ctg act gat gcc act tat cag atc gtc aat    441
Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile Val Asn
115                 120                 125                 130

gca gaa act ttg ggc aag atg aag cct tct gcc gtg gtg gtc aat gtg    489
Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val Asn Val
                135                 140                 145

ggg cgt ggc ccg ctg atc aac acc gat gat ctg gtg gat gca ttg aac    537
Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala Leu Asn
            150                 155                 160
```

```
aac ggc acc att gcg ggt gct gcg ctg gac gtt acc gat cct gag cca   585
Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro Glu Pro
        165                 170                 175

ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt atc act   633
Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val Ile Thr
    180                 185                 190

cct cat act gca aac acg aat gag agg att cgt gct ttg acc ggc gaa   681
Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr Gly Glu
195                 200                 205                 210

ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag atg gcc   729
Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln Met Ala
                215                 220                 225

acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat         776
Thr Glu Val Asp Val Val Ala Gly Tyr
            230                 235

ccg                                                               779
```

<210> 170
<211> 235
<212> PRT
<213> Corynebacterium glutamicum

<400> 170

```
Met Arg Lys His Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr
  1               5                  10                  15

Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His
             20                  25                  30

Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu
         35                  40                  45

Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly
     50                  55                  60

Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn
 65                  70                  75                  80

Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala
                 85                  90                  95

Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala
            100                 105                 110

Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile
        115                 120                 125

Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val
    130                 135                 140

Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala
145                 150                 155                 160

Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro
                165                 170                 175
```

```
Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val
            180                 185                 190

Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr
        195                 200                 205

Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln
    210                 215                 220

Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
225                 230                 235


<210> 171
<211> 792
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(769)
<223> RXN02688

<400> 171
gtgcggaaga cagcacgccc caaaccgacc aactagctaa gctacacaag gcggacgaat 60

gggttcgcgc agcaagcgaa ggaaggaaac ttaactagcc atg gcc ggc cgg att   115
                                        Met Ala Gly Arg Ile
                                          1               5

att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg   163
Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu
                10                  15                  20

gac acc cgc cca cca gga gct gaa ctc acc gac ctg ggc cgt aaa caa   211
Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln
            25                  30                  35

gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc   259
Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu
        40                  45                  50

gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg   307
Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val
    55                  60                  65

ctt gcc acc tct acc ttt gaa aaa gct cgc gac atg cag tcc ggt gcg   355
Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala
70                  75                  80                  85

att cca ctc gac gtt gtg gaa ggc att cag gaa atc aac gtc ggc gac   403
Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu Ile Asn Val Gly Asp
                90                  95                  100

ttt gaa atg cgc ggc gat gaa gaa gcc cac atg aat tac tcc cgc gca   451
Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala
            105                 110                 115

ctc aac ggc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc ggc ggt   499
Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly
```

```
        120                 125                 130

gag acc tac aaa gac gtg ctg aac cgc tac cag ccg act ctt gat cga   547
Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln Pro Thr Leu Asp Arg
    135                 140                 145

atc atg gac agc cac gac ctt gac gac gac cgc gac gtt gcc gtt gtc   595
Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val
150                 155                 160                 165

agc cac ggc gcc gtc atc cgc atc gtg gca aca cac gca act ggt gtg   643
Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val
                170                 175                 180

gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg   691
Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val
            185                 190                 195

gtg ctg gag cca aac ggt aag aaa ttc agc caa tgg gat gtt gtg cgc   739
Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg
        200                 205                 210

tgg act gac agc cca ctg cca tgg cag gag taattgagac caaaggctcg     789
Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
    215                 220

gat                                                               792


<210> 172
<211> 223
<212> PRT
<213> Corynebacterium glutamicum

<400> 172
Met Ala Gly Arg Ile Ile Leu Leu Arg His Gly Gln Thr His Asn Asn
  1               5                  10                  15

Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp
             20                  25                  30

Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr
         35                  40                  45

Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala
     50                  55                  60

Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp
 65                  70                  75                  80

Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu
                 85                  90                  95

Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met
            100                 105                 110

Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala
        115                 120                 125

Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln
    130                 135                 140
```

```
Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg
145                 150                 155                 160

Asp Val Ala Val Val Ser His Gly Ala Val Ile Arg Ile Val Ala Thr
                165                 170                 175

His Ala Thr Gly Val Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly
            180                 185                 190

Asn Cys Arg Phe Val Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln
        195                 200                 205

Trp Asp Val Val Arg Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
    210                 215                 220
```

<210> 173
<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> RXN03087

<400> 173
gttgccgcca gccgttccag ggcgcttgag ctggtcagcg acatcgcaat gatcaaccag 60

gaatacctgg aaaagagctg atattgatag ggtttaagtc atg aag atc tac gca 115
                                        Met Lys Ile Tyr Ala
                                          1   5

cct ttt gct gga atc gtc cac tat ttt gtc gat gaa ggc gat ccc gtg 163
Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp Glu Gly Asp Pro Val
                10   15   20

gaa acc ggc atg caa ctg gga acg gta gaa acc atc aaa ctc gag gca 211
Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr Ile Lys Leu Glu Ala
            25   30   35

cca atc atg gca ccg gga cct ggc atc gta gct aag gtt tct ttt gat 259
Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala Lys Val Ser Phe Asp
        40   45   50

gat ttc tcc gac gtc acc ggc ggc gat gaa ctc ctc gaa ttg gag gca 307
Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu Leu Glu Leu Glu Ala
    55   60   65

aag aac taatgggtca aacccgcatc att   336
Lys Asn
 70

<210> 174
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 174
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```

```
Met Lys Ile Tyr Ala Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp
 1               5                  10                  15

Glu Gly Asp Pro Val Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr
            20                  25                  30

Ile Lys Leu Glu Ala Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala
        35                  40                  45

Lys Val Ser Phe Asp Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu
    50                  55                  60

Leu Glu Leu Glu Ala Lys Asn
65                  70
```

<210> 175
<211> 310
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(310)
<223> RXN03186

<400> 175
ttcgtgcact tcggcgtgtc acaattaggt acgaccaaga atgggaccgg gaaaccggga 60

cgtataaacg aaataaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca 115
Met Ala Asp Gln Ala
  1   5

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
            10   15   20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
        25   30   35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
    40   45   50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
55   60   65

cgc 310
Arg
 70

<210> 176
<211> 70
<212> PRT
<213> Corynebacterium glutamicum

<400> 176
Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn

```
  1               5                  10                  15

Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
            20                  25                  30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
        35                  40                  45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
    50                  55                  60

Arg Ala Ser Ala Lys Arg
65                  70
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<210> 177
<211> 302
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(279)
<223> RXN03187

<400> 177

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gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag atc cgt gaa   48
Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
  1               5                  10                  15

tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc   96
Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
            20                  25                  30

tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag   144
Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
        35                  40                  45

tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc   192
Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
    50                  55                  60

gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat   240
Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
65                  70                  75                  80

cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct    289
Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
                85                  90

caagggacag ata                                                   302
```

<210> 178
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 178

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Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
  1               5                  10                  15
```

```
Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
            20                  25                  30

Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
        35                  40                  45

Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
    50                  55                  60

Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
65                  70                  75                  80

Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
                85                  90
```

<210> 179
<211> 1953
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1930)
<223> RXN02591

<400> 179

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atgtgtccgt tgtctcacct aaagttttaa ctagttctgt atctgaaagc tacgctaggg 60

ggcgagaact ctgtcgaatg acacaaaatc tggagaagta atg act act gct gca   115
                                            Met Thr Thr Ala Ala
                                              1               5

atc agg ggc ctt cag ggc gag gcg ccg acc aag aat aag gaa ctg ctg   163
Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys Asn Lys Glu Leu Leu
                10                  15                  20

aac tgg atc gca gac gcc gtc gag ctc ttc cag cct gag gct gtt gtg   211
Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln Pro Glu Ala Val Val
            25                  30                  35

ttc gtt gat gga tcc cag gct gag tgg gat cgc atg gcg gag gat ctt   259
Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg Met Ala Glu Asp Leu
        40                  45                  50

gtt gaa gcc ggt acc ctc atc aag ctc aac gag gaa aag cgt ccg aac   307
Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu Glu Lys Arg Pro Asn
    55                  60                  65

agc tac cta gct cgt tcc aac cca tct gac gtt gcg cgc gtt gag tcc   355
Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val Ala Arg Val Glu Ser
70                  75                  80                  85

cgc acc ttc atc tgc tcc gag aag gaa gaa gat gct ggc cca acc aac   403
Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala Gly Pro Thr Asn
                90                  95                  100

aac tgg gct cca cca cag gca atg aag gac gaa atg tcc aag cat tac   451
Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu Met Ser Lys His Tyr
            105                 110                 115
```

```
gct ggt tcc atg aag ggg cgc acc atg tac gtc gtg cct ttc tgc atg   499
Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val Val Pro Phe Cys Met
        120                 125                 130

ggt cca atc agc gat ccg gac cct aag ctt ggt gtg cag ctc act gac   547
Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly Val Gln Leu Thr Asp
    135                 140                 145

tcc gag tac gtt gtc atg tcc atg cgc atc atg acc cgc atg ggt att   595
Ser Glu Tyr Val Val Met Ser Met Arg Ile Met Thr Arg Met Gly Ile
150                 155                 160                 165

gaa gcg ctg gac aag atc ggc gcg aac ggc agc ttc gtc agg tgc ctc   643
Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser Phe Val Arg Cys Leu
                170                 175                 180

cac tcc gtt ggt gct cct ttg gag cca ggc cag gaa gac gtt gca tgg   691
His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln Glu Asp Val Ala Trp
            185                 190                 195

cct tgc aac gac acc aag tac atc acc cag ttc cca gag acc aag gaa   739
Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe Pro Glu Thr Lys Glu
        200                 205                 210

att tgg tcc tac ggt tcc ggc tac ggc gga aac gca atc ctg gca aag   787
Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn Ala Ile Leu Ala Lys
    215                 220                 225

aag tgc tac gca ctg cgt atc gca tct gtc atg gct cgc gaa gaa gga   835
Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met Ala Arg Glu Glu Gly
230                 235                 240                 245

tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc   883
Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly
                250                 255                 260

aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc   931
Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr
            265                 270                 275

aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt   979
Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val
        280                 285                 290

gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac   1027
Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr
    295                 300                 305

gca gtt aac cca gaa aat ggt ttc ttc ggt gtt gct cca ggc acc aac   1075
Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn
310                 315                 320                 325

tac gca tcc aac cca atc gcg atg aag acc atg gaa cca ggc aac acc   1123
Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr
                330                 335                 340

ctg ttc acc aac gtg gca ctc acc gac gac ggc gac atc tgg tgg gaa   1171
Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu
            345                 350                 355
```

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```
ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac   1219
Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn
        360                 365                 370

gac tgg acc cca gag tcc gac gaa aac gct gct cac cct aac tcc cgt   1267
Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg
    375                 380                 385

tac tgc gta gca atc gac cag tcc cca gca gca gca cct gag ttc aac   1315
Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn
390                 395                 400                 405

gac tgg gaa ggc gtc aag atc gac gca atc ctc ttc ggt gga cgt cgc   1363
Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg
                410                 415                 420

gca gac acc gtc cca ctg gtt acc cag acc tac gac tgg gag cac ggc   1411
Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly
            425                 430                 435

acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca   1459
Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala
        440                 445                 450

gaa gca aag gtc ggc aca ctc cgc cac gac cca atg gca atg ctc cca   1507
Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro
    455                 460                 465

ttc att ggc tac aac gct ggt gaa tac ctg cag aac tgg att gac atg   1555
Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met
470                 475                 480                 485

ggt aac aag ggt ggc gac aag atg cca tcc atc ttc ctg gtc aac tgg   1603
Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp
                490                 495                 500

ttc cgc cgt ggc gaa gat gga cgc ttc ctg tgg cct ggc ttc ggc gac   1651
Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp
            505                 510                 515

aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt   1699
Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val
        520                 525                 530

ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc   1747
Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu
    535                 540                 545

gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg   1795
Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu
550                 555                 560                 565

acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag   1843
Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu
                570                 575                 580

tac ctc act ttc ctc gga cca cgt gtt cct gca gag gtt cac agc cag   1891
Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln
            585                 590                 595

ttc gat gct ctg aag gcc cgc att tca gca gct cac gct taaagttcac    1940
```

```
Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala
        600                 605                 610

gcttaagaac tgc                                                    1953


<210> 180
<211> 610
<212> PRT
<213> Corynebacterium glutamicum

<400> 180
Met Thr Thr Ala Ala Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys
  1               5                  10                  15

Asn Lys Glu Leu Leu Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln
             20                  25                  30

Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg
         35                  40                  45

Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu
     50                  55                  60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val
 65                  70                  75                  80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp
                 85                  90                  95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu
            100                 105                 110

Met Ser Lys His Tyr Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val
        115                 120                 125

Val Pro Phe Cys Met Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly
    130                 135                 140

Val Gln Leu Thr Asp Ser Glu Tyr Val Val Met Ser Met Arg Ile Met
145                 150                 155                 160

Thr Arg Met Gly Ile Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser
                165                 170                 175

Phe Val Arg Cys Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln
            180                 185                 190

Glu Asp Val Ala Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe
        195                 200                 205

Pro Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn
    210                 215                 220

Ala Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met
225                 230                 235                 240

Ala Arg Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu
                245                 250                 255

Ile Asn Pro Glu Gly Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser
```

```
            260                 265                 270

Ala Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly
        275                 280                 285

Trp Thr Ala Gln Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg
    290                 295                 300

Glu Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val
305                 310                 315                 320

Ala Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met
                325                 330                 335

Glu Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly
            340                 345                 350

Asp Ile Trp Trp Glu Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile
        355                 360                 365

Asp Trp Met Gly Asn Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala
    370                 375                 380

His Pro Asn Ser Arg Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala
385                 390                 395                 400

Ala Pro Glu Phe Asn Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu
                405                 410                 415

Phe Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr
            420                 425                 430

Asp Trp Glu His Gly Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln
        435                 440                 445

Thr Ala Ala Ser Ala Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro
    450                 455                 460

Met Ala Met Leu Pro Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln
465                 470                 475                 480

Asn Trp Ile Asp Met Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile
                485                 490                 495

Phe Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp
            500                 505                 510

Pro Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg
        515                 520                 525

Ile Glu Gly His Val Gly Ala Asp Glu Thr Val Val Gly His Thr Ala
    530                 535                 540

Lys Ala Glu Asp Leu Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp
545                 550                 555                 560

Val Lys Glu Ala Leu Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val
                565                 570                 575

Glu Asp Asn Ala Glu Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala
            580                 585                 590
```

```
Glu Val His Ser Gln Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala
        595                 600                 605

His Ala
    610


<210> 181
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXS01260

<400> 181
ctaaacgtgg gctgcattcc ttccaaagtc tctgatcaaa aacgctgaag ttgcccatac 60

ctttacccat gagaagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat   115
                                              Val Thr Phe Asn Tyr
                                                1               5

gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga   163
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
                10                  15                  20

ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt   211
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly
            25                  30                  35

ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag   259
Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys
        40                  45                  50

gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt   307
Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
    55                  60                  65

tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg   355
Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val
70                  75                  80                  85

tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc   403
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
                90                  95                  100

att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt   451
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly
            105                 110                 115

aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt   499
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu
        120                 125                 130

cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag   547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
    135                 140                 145
```

```
aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg   595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
150                 155                 160                 165

gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac   643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
                170                 175                 180

aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc   691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe
            185                 190                 195

cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc   739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu
        200                 205                 210

acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc   787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val
    215                 220                 225

gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct   835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
230                 235                 240                 245

cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt   883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly
                250                 255                 260

gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc   931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
            265                 270                 275

ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc   979
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala
        280                 285                 290

aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc   1027
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
    295                 300                 305

tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca   1075
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala
310                 315                 320                 325

aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg   1123
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu
                330                 335                 340

gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag   1171
Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln
            345                 350                 355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac   1219
Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
        360                 365                 370

cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga   1267
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly
    375                 380                 385

cac atg atc aac ttc tagaatccac ctcgttggcc ctg                    1305
```

09529.0052-00000

His Met Ile Asn Phe
390

<210> 182
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 182
Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser
1 5 10 15

Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile
20 25 30

Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu
35 40 45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys
50 55 60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
65 70 75 80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe
115 120 125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile
130 135 140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala
145 150 155 160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
165 170 175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met
180 185 190

Val Ser Val Gly Phe Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn
195 200 205

Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr
210 215 220

Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala
225 230 235 240

Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val Ala Ala
245 250 255

Glu Thr Ile Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met
260 265 270

```
Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr
        275                 280                 285

Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val
    290                 295                 300

Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu
305                 310                 315                 320

Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu
                325                 330                 335

Leu Gly Ala His Leu Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu
            340                 345                 350

Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg
        355                 360                 365

Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala
    370                 375                 380

His Gly Ile Ser Gly His Met Ile Asn Phe
385                 390


<210> 183
<211> 294
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> RXS01261

<400> 183
gtgggtgttt ttcatttttct tccactctaa aattaagtat ggaaaaccaa ccgcacccgg 60

atgcacgaca atgacccact aaacacgtat ccttgaatgc gtg act gaa cat tat   115
                                            Val Thr Glu His Tyr
                                              1               5

gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc   163
Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile
                  10                  15                  20

cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac   211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr
              25                  30                  35

tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct   259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser
          40                  45                  50

gat caa aaa cgc tgaagttgcc catacctta ccc                         294
Asp Gln Lys Arg
     55


<210> 184
<211> 57
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<212> PRT
<213> Corynebacterium glutamicum

<400> 184
Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
1 5 10 15

Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
20 25 30

Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
35 40 45

Pro Ser Lys Val Ser Asp Gln Lys Arg
50 55

<210> 185
<211> 1650
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1627)
<223> RXA02640

<400> 185
accaacgacg acgccggtgt agcagatgta ttggagtggt ggttctaata ggtggtgtta 60

aaacactgct tagtggccca atacgtgcaa aaataaggcc atg aga atc tca aag 115
Met Arg Ile Ser Lys
1 5

gcc aat gcg tat gtt gca gcg att gac caa ggc acc act tcc act cgg 163
Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly Thr Thr Ser Thr Arg
10 15 20

tgc atc ttc att gat gcc caa gga aaa gtg gtg tct tct gct tcc aag 211
Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val Ser Ser Ala Ser Lys
25 30 35

gag cac cgc caa atc ttc cca caa cag ggc tgg gta gag cac gat cct 259
Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp Val Glu His Asp Pro
40 45 50

gaa gaa att tgg gac aac att cga tct gtc gtc agc cag gcg atg gtc 307
Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val Ser Gln Ala Met Val
55 60 65

tcc att gac atc acc cca cac gag gtt gca tcg ctg gga gtc acc aac 355
Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser Leu Gly Val Thr Asn
70 75 80 85

cag cgc gaa acc acc gtg gtg tgg gac aag cac acc ggc gaa cct gtc 403
Gln Arg Glu Thr Thr Val Val Trp Asp Lys His Thr Gly Glu Pro Val
90 95 100

tac aac gca atc gtg tgg caa gac acc cgc acc tct gac att tgc cta 451
Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Ser Asp Ile Cys Leu
105 110 115

```
gag atc gcg ggc gaa gaa ggc cag gaa aag tgg ctt gac cgc acc ggc   499
Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp Leu Asp Arg Thr Gly
        120                 125                 130

ctg ctg atc aac tcc tac cca tcg ggg ccc aaa atc aag tgg att ctc   547
Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys Ile Lys Trp Ile Leu
    135                 140                 145

gac aac gtt gag gga gct cgc gaa cgc gcc gaa aag ggc gac ctt ttg   595
Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu Lys Gly Asp Leu Leu
150                 155                 160                 165

ttt ggc acc atg gat acc tgg gtg ctg tgg aac ctg acc ggc ggt gtc   643
Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Val
                170                 175                 180

cgc ggc gac gac ggt gat gat gcc atc cac gtc acc gat gtc acc aac   691
Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val Thr Asp Val Thr Asn
            185                 190                 195

gca tcc cgc aca cta ttg atg gat ctc cgc acg caa cag tgg gat cca   739
Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr Gln Gln Trp Asp Pro
        200                 205                 210

gaa cta tgc gaa gcc cta gac att ccg atg tcc atg ctc cct gag att   787
Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser Met Leu Pro Glu Ile
    215                 220                 225

cgt ccc tcc gtc gga gaa ttc cgc tcc gtg cgc cac cgc gga acc cta   835
Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg His Arg Gly Thr Leu
230                 235                 240                 245

gcc gac gtc ccg att act ggc gtg ctc ggc gac cag caa gcg gcc ctt   883
Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp Gln Gln Ala Ala Leu
                250                 255                 260

ttt ggt cag ggc gga ttc cac gaa ggt gct gct aaa aat acc tac ggc   931
Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly
            265                 270                 275

acc ggc ctc ttc ctg ctg atg aac acc ggc acc tcg ttg aag att tcc   979
Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser
        280                 285                 290

gag cac ggc ctg ctg tcc acc atc gcc tat caa cgg gaa gga tcc gct  1027
Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala
    295                 300                 305

ccg gtc tac gcg ctg gaa ggt tcc gta tcc atg ggc ggt tcc ttg gtg  1075
Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val
310                 315                 320                 325

cag tgg ctg cgc gac aac cta cag cta atc ccc aac gca cca gcg att  1123
Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile
                330                 335                 340

gaa aac ctc gcc cga gaa gtc gaa gac aac ggt ggc gtt cat gtt gtc  1171
Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly Gly Val His Val Val
            345                 350                 355
```

```
cca gca ttc acc gga ctg ttc gca cca cgt tgg cgc ccc gat gct cgt   1219
Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp Arg Pro Asp Ala Arg
        360                 365                 370

ggc gtc att aca ggc ctc acc cgt ttt gcc aac cgc aaa cac atc gcc   1267
Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn Arg Lys His Ile Ala
    375                 380                 385

cgc gca gtc ctt gaa gcc aac gcc ttc caa acc cgc gaa gtt gtg gac   1315
Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr Arg Glu Val Val Asp
390                 395                 400                 405

gcc atg gcc aaa gac gca ggc aaa gcc ctc gaa tcc ctc cgc gtc gac   1363
Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu Ser Leu Arg Val Asp
                410                 415                 420

ggt gcg atg gtg gaa aat gac ctc ctc atg caa atg caa gcc gac ttc   1411
Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln Met Gln Ala Asp Phe
            425                 430                 435

ctc ggc atc gac gtc caa cgt ctc gag gac gta gaa acc acc gcc gtc   1459
Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val Glu Thr Thr Ala Val
        440                 445                 450

ggc gtc gca ttc gct gca ggt ctc ggc tct gga ttc ttc aaa aca act   1507
Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr
    455                 460                 465

gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac   1555
Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp
470                 475                 480                 485

atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca   1603
Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala
                490                 495                 500

gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta         1650
Val Glu His Ser Tyr Asp Gln Ala
            505
```

D0E3N2V1 = 0E3N2V1

<210> 186
<211> 509
<212> PRT
<213> Corynebacterium glutamicum

<400> 186

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Met Arg Ile Ser Lys Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly
  1               5                  10                  15

Thr Thr Ser Thr Arg Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val
             20                  25                  30

Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp
         35                  40                  45

Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val
     50                  55                  60

Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser
 65                  70                  75                  80
```

Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His
85 90 95

Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr
100 105 110

Ser Asp Ile Cys Leu Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp
115 120 125

Leu Asp Arg Thr Gly Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys
130 135 140

Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu
145 150 155 160

Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn
165 170 175

Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val
180 185 190

Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr
195 200 205

Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser
210 215 220

Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg
225 230 235 240

His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp
245 250 255

Gln Gln Ala Ala Leu Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala
260 265 270

Lys Asn Thr Tyr Gly Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr
275 280 285

Ser Leu Lys Ile Ser Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln
290 295 300

Arg Glu Gly Ser Ala Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met
305 310 315 320

Gly Gly Ser Leu Val Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro
325 330 335

Asn Ala Pro Ala Ile Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly
340 345 350

Gly Val His Val Val Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp
355 360 365

Arg Pro Asp Ala Arg Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn
370 375 380

Arg Lys His Ile Ala Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr
385 390 395 400

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```
Arg Glu Val Val Asp Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu
                405                 410                 415

Ser Leu Arg Val Asp Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln
            420                 425                 430

Met Gln Ala Asp Phe Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val
        435                 440                 445

Glu Thr Thr Ala Val Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly
    450                 455                 460

Phe Phe Lys Thr Thr Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys
465                 470                 475                 480

Val Trp Asn Pro Asp Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala
                485                 490                 495

Glu Trp Asn Arg Ala Val Glu His Ser Tyr Asp Gln Ala
            500                 505
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<210> 187
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXN01025

<400> 187

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gggcagcagc ggcaggtttc caggaggttt ccatgcgggt ggcttgggac atgggctaac 60

ctgagacggt taaatatcgt tttcgaaagg tgggtttcgc gtg gtt tct gta agc   115
                                        Val Val Ser Val Ser
                                          1               5

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct   163
Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
                  10                  15                  20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca   211
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
              25                  30                  35

agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att   259
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
          40                  45                  50

acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta   307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
      55                  60                  65

gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt   355
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
  70                  75                  80                  85

ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg   403
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
```

```
                  90                  95                 100

gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt   451
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser
            105                 110                 115

gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg   499
Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val
        120                 125                 130

ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca   547
Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala
    135                 140                 145

gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag   595
Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln
150                 155                 160                 165

gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg   643
Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val
                170                 175                 180

gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc   691
Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala
            185                 190                 195

tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg   739
Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser
        200                 205                 210

ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg   787
Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu
    215                 220                 225

ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg   835
Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu
230                 235                 240                 245

gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag   883
Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu
                250                 255                 260

cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat   931
Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn
            265                 270                 275

ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt   979
Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu
        280                 285                 290

gcc acc aag ctt ggt gtg gag atg ccg atc acc cag gct gtc tac ggt  1027
Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln Ala Val Tyr Gly
    295                 300                 305

gtg tgc cac cga gat atg aaa gta act gac atg att gtg gct ctc atg  1075
Val Cys His Arg Asp Met Lys Val Thr Asp Met Ile Val Ala Leu Met
310                 315                 320                 325

ggc agg tct aag aag gct gag tagtcttagg ttgtaagctt caa            1119
Gly Arg Ser Lys Lys Ala Glu
                330
```

<210> 188
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 188

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Val Val Ser Val Ser Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu
  1               5                  10                  15

Ala Lys Val Phe Ser Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg
             20                  25                  30

Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
         35                  40                  45

Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
     50                  55                  60

Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
 65                  70                  75                  80

Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro
                 85                  90                  95

Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr
            100                 105                 110

His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro
        115                 120                 125

Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala
    130                 135                 140

Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg
145                 150                 155                 160

Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr
                165                 170                 175

Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn
            180                 185                 190

Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu
        195                 200                 205

Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg
    210                 215                 220

Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala
225                 230                 235                 240

Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn
                245                 250                 255

Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala
            260                 265                 270

Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln
        275                 280                 285
```

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```
Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr
    290                 295                 300

Gln Ala Val Tyr Gly Val Cys His Arg Asp Met Lys Val Thr Asp Met
305                 310                 315                 320

Ile Val Ala Leu Met Gly Arg Ser Lys Lys Ala Glu
                325                 330
```

<210> 189
<211> 1015
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1015)
<223> FRXA01025

<400> 189

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gggcagcagc ggcaggtttc cagraggttt ccatgcgggt ggcttggrac wtgggctaac 60

ctgaracggt taaatatcgt tttcgaaagg tgggtttcgc gtg gtt tct gta agc   115
                                        Val Val Ser Val Ser
                                          1               5

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct   163
Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
                10                  15                  20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca   211
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
            25                  30                  35

agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att   259
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
        40                  45                  50

acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta   307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
    55                  60                  65

gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt   355
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
70                  75                  80                  85

ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg   403
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
                90                  95                  100

gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt   451
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser
            105                 110                 115

gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg   499
Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val
        120                 125                 130

ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca   547
```

```
Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala
    135                 140                 145

gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag   595
Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln
150                 155                 160                 165

gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg   643
Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val
                170                 175                 180

gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc   691
Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala
            185                 190                 195

tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg   739
Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser
        200                 205                 210

ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg   787
Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu
    215                 220                 225

ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg   835
Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu
230                 235                 240                 245

gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag   883
Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu
                250                 255                 260

cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat   931
Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn
            265                 270                 275

ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt   979
Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu
        280                 285                 290

gcc acc aag ctt ggt gtg gag atg ccg atc acc cag                  1015
Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln
    295                 300                 305
```

<210> 190
<211> 305
<212> PRT
<213> Corynebacterium glutamicum

<400> 190

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Val Val Ser Val Ser Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu
  1               5                  10                  15

Ala Lys Val Phe Ser Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg
             20                  25                  30

Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
         35                  40                  45

Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
     50                  55                  60
```

```
Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
 65                  70                  75                  80

Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro
                85                  90                  95

Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr
            100                 105                 110

His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro
        115                 120                 125

Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala
    130                 135                 140

Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg
145                 150                 155                 160

Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr
                165                 170                 175

Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn
            180                 185                 190

Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu
        195                 200                 205

Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg
    210                 215                 220

Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala
225                 230                 235                 240

Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn
                245                 250                 255

Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala
            260                 265                 270

Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln
        275                 280                 285

Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr
    290                 295                 300

Gln
305
```

<210> 191
<211> 1809
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1786)
<223> RXA01851

<400> 191

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ttgtggcctt tttgcagggg aaacttattt aaataattca taagtaaaaa accgtcaatt 60

cacgatgtgg gttggcggtt ttcctattag gctcactttt atg acg agc gca cac   115
                                            Met Thr Ser Ala His
                                              1               5

ttt gaa tcc cgc cgg att ggc cct ccg ctt cgc gat aat tat gac gtc   163
Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg Asp Asn Tyr Asp Val
                 10                  15                  20

att gtg att ggc ggt ggt atc tca ggt gta cag att gcg cga cat gct   211
Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln Ile Ala Arg His Ala
             25                  30                  35

caa ggc cgc ggt tta cgc act gtg atg ttt gag gcc aga gat tat tct   259
Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu Ala Arg Asp Tyr Ser
         40                  45                  50

tct gga aca tca tcg aca acc tcc aag atg att cat ggt ggt ttg cgc   307
Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile His Gly Gly Leu Arg
     55                  60                  65

tat ttg gag cag tac gat ttc ggc gtg gtc cag gaa gcc gtg aag gaa   355
Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln Glu Ala Val Lys Glu
 70                  75                  80                  85

cgc cgg tac cta ggt atc gcc gct ccg cat ttg gtg gct cca cgc agt   403
Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu Val Ala Pro Arg Ser
                 90                  95                 100

ttc atg ctc acg gcg ttt gat tgg tca gag ccg aaa gcc cct atg ttg   451
Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro Lys Ala Pro Met Leu
            105                 110                 115

ggt gct ggt gtg gcg ttg tat gaa acg atg gcg tgg cag cgt aac cag   499
Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala Trp Gln Arg Asn Gln
        120                 125                 130

ggg caa tcg aag gaa aac cac tcg ccg cgt ttc cgg tgg att cct aaa   547
Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe Arg Trp Ile Pro Lys
    135                 140                 145

aat gca ctg ctc aag gaa gtc ccg tgg ctt gac ccg gag ggc ttg aag   595
Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp Pro Glu Gly Leu Lys
150                 155                 160                 165

gga gcg tgg cgc cac gat gat acg ttg aat ctc cat gca gaa cga ctc   643
Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu His Ala Glu Arg Leu
                170                 175                 180

ctc ctc gcg gtg att aaa gct ttt gcg gca gat ggc gga acg gcg atc   691
Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp Gly Gly Thr Ala Ile
            185                 190                 195

aac cac gcc aaa gtc act cgc att ctc cgg aac gtg gaa gaa ggc cgc   739
Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn Val Glu Glu Gly Arg
        200                 205                 210

gtc aag ggt gta gaa gtg act gat cag gtc acc aac acc acg cat gag   787
Val Lys Gly Val Glu Val Thr Asp Gln Val Thr Asn Thr Thr His Glu
    215                 220                 225
```

```
gtg aat gcc cct gtg gtg atc aac gct gcg ggt ccg tgg gtt gcg cag   835
Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly Pro Trp Val Ala Gln
230                 235                 240                 245

gcg ttg ggt gat ttg gcg gag gta acc aag ttg aag gtg cgc caa tcc   883
Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu Lys Val Arg Gln Ser
                250                 255                 260

aag gga gtg cat ttg ctc act ggt gat ttg ggc agc cag agt ggc gtg   931
Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly Ser Gln Ser Gly Val
            265                 270                 275

ttt gtg cgt ggc aaa aac ggc aag cat gtg atc gtg aat ccg tgg atg   979
Phe Val Arg Gly Lys Asn Gly Lys His Val Ile Val Asn Pro Trp Met
        280                 285                 290

ggg cgc acc ctt att ggt cca acc gac acc atg att gac ggt gac gct  1027
Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met Ile Asp Gly Asp Ala
    295                 300                 305

gat gat gcg gct gca gat gaa agc gat atc gat ttg ctg ctt gag acc  1075
Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp Leu Leu Leu Glu Thr
310                 315                 320                 325

atc gat tcg gta cgc gct aca ccg ctt gat cgc aaa gag atc atc tcc  1123
Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg Lys Glu Ile Ile Ser
                330                 335                 340

acg ctg gtg ggt gtg cgc ccg ctt gtt gat gac ggc acc gac acc tac  1171
Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp Gly Thr Asp Thr Tyr
            345                 350                 355

acg tcc tct cgc cgt ttc gat att tcc gat cac gcc aac gtc ggc att  1219
Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His Ala Asn Val Gly Ile
        360                 365                 370

gat ggt ttg gtg tct gtc tct ggc ggc aag tgg acc act tcc cgc gtg  1267
Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp Thr Thr Ser Arg Val
    375                 380                 385

atg ggg tac aag gtg att gag cat gtg gtg gag cac caa gct gcg gtg  1315
Met Gly Tyr Lys Val Ile Glu His Val Val Glu His Gln Ala Ala Val
390                 395                 400                 405

tta cct ccg ctg cgc cac ttt gac tcc agg cag atg ccg ttg agt act  1363
Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln Met Pro Leu Ser Thr
                410                 415                 420

tct ttt ggc gcg tat gag tcc gtg gct gat tcc ttt gag tca gcg ctt  1411
Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser Phe Glu Ser Ala Leu
            425                 430                 435

cgc agc cac ccc gag ctg gat gtg gat gat gaa atc cgc gtg cat ctg  1459
Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu Ile Arg Val His Leu
        440                 445                 450

gcc aga ctg tat gga act gag cat gaa aaa gtg ctg gat ctc gtc gca  1507
Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val Leu Asp Leu Val Ala
    455                 460                 465
```

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aag caa ccc gac ctg ggg cgc cga ctt gac cca gac aac ctt gat atc   1555
Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro Asp Asn Leu Asp Ile
470                 475                 480                 485

gcg gcg cag gcc gtt ttt gct gtc gcc gag gag gcg gcc gtc gac ctg   1603
Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu Ala Ala Val Asp Leu
                490                 495                 500

gcg gac gtg ctg gat cgt cgc atc gtg ctc ggc acg ctg ggt tat gtg   1651
Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly Thr Leu Gly Tyr Val
            505                 510                 515

caa ccg gct gcc gtg cgt gcg acg gcc gaa gca atg gcg cag gtc acc   1699
Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala Met Ala Gln Val Thr
        520                 525                 530

ggg tgg tca gct gag ctt atc gac gcc cag tgc cag tcc tac ctc gcc   1747
Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys Gln Ser Tyr Leu Ala
    535                 540                 545

aag caa gac aaa atc caa gcc gtg tta aag ccg tac cgc taacactccg    1796
Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro Tyr Arg
550                 555                 560

tcatcgacac cgg                                                   1809
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09625136.doc

<210> 192
<211> 562
<212> PRT
<213> Corynebacterium glutamicum

<400> 192

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Met Thr Ser Ala His Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg
  1               5                  10                  15

Asp Asn Tyr Asp Val Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln
             20                  25                  30

Ile Ala Arg His Ala Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu
         35                  40                  45

Ala Arg Asp Tyr Ser Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile
     50                  55                  60

His Gly Gly Leu Arg Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln
 65                  70                  75                  80

Glu Ala Val Lys Glu Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu
                 85                  90                  95

Val Ala Pro Arg Ser Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro
            100                 105                 110

Lys Ala Pro Met Leu Gly Ala Gly Val Ala Leu Tyr Glu Thr Met Ala
        115                 120                 125

Trp Gln Arg Asn Gln Gly Gln Ser Lys Glu Asn His Ser Pro Arg Phe
    130                 135                 140

Arg Trp Ile Pro Lys Asn Ala Leu Leu Lys Glu Val Pro Trp Leu Asp
```

```
145                 150                 155                 160

Pro Glu Gly Leu Lys Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu
                165                 170                 175

His Ala Glu Arg Leu Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp
            180                 185                 190

Gly Gly Thr Ala Ile Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn
        195                 200                 205

Val Glu Glu Gly Arg Val Lys Gly Val Glu Val Thr Asp Gln Val Thr
    210                 215                 220

Asn Thr Thr His Glu Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly
225                 230                 235                 240

Pro Trp Val Ala Gln Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu
                245                 250                 255

Lys Val Arg Gln Ser Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly
            260                 265                 270

Ser Gln Ser Gly Val Phe Val Arg Gly Lys Asn Gly Lys His Val Ile
        275                 280                 285

Val Asn Pro Trp Met Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met
    290                 295                 300

Ile Asp Gly Asp Ala Asp Asp Ala Ala Ala Asp Glu Ser Asp Ile Asp
305                 310                 315                 320

Leu Leu Leu Glu Thr Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg
                325                 330                 335

Lys Glu Ile Ile Ser Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp
            340                 345                 350

Gly Thr Asp Thr Tyr Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His
        355                 360                 365

Ala Asn Val Gly Ile Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp
    370                 375                 380

Thr Thr Ser Arg Val Met Gly Tyr Lys Val Ile Glu His Val Val Glu
385                 390                 395                 400

His Gln Ala Ala Val Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln
                405                 410                 415

Met Pro Leu Ser Thr Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser
            420                 425                 430

Phe Glu Ser Ala Leu Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu
        435                 440                 445

Ile Arg Val His Leu Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val
    450                 455                 460

Leu Asp Leu Val Ala Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro
465                 470                 475                 480
```

09852150 050902

```
Asp Asn Leu Asp Ile Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu
                485                 490                 495

Ala Ala Val Asp Leu Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly
            500                 505                 510

Thr Leu Gly Tyr Val Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala
        515                 520                 525

Met Ala Gln Val Thr Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys
    530                 535                 540

Gln Ser Tyr Leu Ala Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro
545                 550                 555                 560

Tyr Arg
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<210> 193
<211> 900
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(877)
<223> RXA01242

<400> 193

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cgccggcaac caaatgaggc ttttgggcgt tggacagtga gacaatgggt aagaaattcg 60

gacatattta gtaaattggc tttttgcttt aaggagtgac atg tac gca gag gag   115
                                        Met Tyr Ala Glu Glu
                                          1               5

cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat   163
Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn
                  10                  15                  20

gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga   211
Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg
              25                  30                  35

cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac   259
Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His
          40                  45                  50

ggt ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg   307
Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu
      55                  60                  65

gat act cgt ttc agg tct gca tcg tca gca aag tac tcc att gcc aag   355
Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys
  70                  75                  80                  85

gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat   403
Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp
                  90                  95                 100
```

```
gcg gga act act gtt act gct ttg gcc gat ctc att tct gag cat cct   451
Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro
            105                 110                 115

agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt   499
Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu
        120                 125                 130

aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc   547
Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser
    135                 140                 145

gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act   595
Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr
150                 155                 160                 165

ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg   643
Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu
                170                 175                 180

acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg   691
Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met
            185                 190                 195

aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac   739
Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp
        200                 205                 210

tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc   787
Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser
    215                 220                 225

gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt   835
Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val
230                 235                 240                 245

gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa           877
Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu
                250                 255

tgattcttac agtcactgca agt                                        900
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<210> 194
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 194

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Met Tyr Ala Glu Glu Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val
  1               5                  10                  15

Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr
            20                  25                  30

Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
        35                  40                  45

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
    50                  55                  60
```

```
Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
 65                  70                  75                  80

Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly
                 85                  90                  95

Gly Leu Phe Leu Asp Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu
            100                 105                 110

Ile Ser Glu His Pro Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys
        115                 120                 125

Leu Pro Ile Ala Leu Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln
    130                 135                 140

Leu Leu Gly Gly Ser Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp
145                 150                 155                 160

Thr Ala Leu Arg Thr Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile
                165                 170                 175

Gly Thr Asn Ala Leu Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser
            180                 185                 190

Gln Glu Ala Ala Met Lys Ser Ala Met Ile Thr Asn Ala His Lys Val
        195                 200                 205

Val Val Leu Cys Asp Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser
    210                 215                 220

Phe Gly Ala Ile Ser Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala
225                 230                 235                 240

Pro Ala Ser Phe Val Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val
                245                 250                 255

Ile Ala Glu
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US 2005/0196848 A1

<210> 195
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXA02288

<400> 195
aacaacaatc taacgccatc atgttataaa aaagcaagac ctaacataaa aatgttagaa 60

agtgctggat ctaacaacat ttccgtggta acttttttcac atg tcc caa gtg att 115
                                                Met Ser Gln Val Ile
                                                  1   5

ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc 163
Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val
                10   15   20

```
acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag   211
Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu
            25                  30                  35

gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac   259
Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp
        40                  45                  50

aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg   307
Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser
    55                  60                  65

atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt   355
Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val
70                  75                  80                  85

aaa gag gcg ttg tgt act gca gca gca cgg ttg att ccg gag ggc gct   403
Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala
                90                  95                  100

gtg gtg gcg att gat gat tcc acc acg ttg gag tct ttg gtt gag aag   451
Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys
            105                 110                 115

ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca   499
Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr
        120                 125                 130

atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att   547
Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile
    135                 140                 145

gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag   595
Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys
150                 155                 160                 165

gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt   643
Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val
                170                 175                 180

tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat   691
Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His
            185                 190                 195

cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt   739
Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly
        200                 205                 210

agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt   787
Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly
    215                 220                 225

gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat   835
Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp
230                 235                 240                 245

cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg   883
Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala
                250                 255                 260

cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca   931
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Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro
265 270 275

acg gaa gag gat ttt taagatggct ttggttcttg gaa 969
Thr Glu Glu Asp Phe
280

<210> 196
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 196
Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg
1 5 10 15

Ile Val Ser Tyr Val Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu
20 25 30

Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu
35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg
50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His
65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu
85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu
100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr
115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser
130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp
145 150 155 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala
165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val
180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala
195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys
210 215 220

Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp
225 230 235 240

His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu
245 250 255

```
Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu
            260                 265                 270

Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
        275                 280


<210> 197
<211> 887
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(864)
<223> RXN01891

<400> 197
ggt ggc cac tat ggt ttg cct ttc gct cgc tcc act gtc ctc ttc tac   48
Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr
  1               5                  10                  15

tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc cca   96
Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro
            20                  25                  30

gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa gcg   144
Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala
        35                  40                  45

atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac ctt   192
Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu
    50                  55                  60

tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac tct   240
Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser
65                  70                  75                  80

gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca gtt   288
Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val
                85                  90                  95

gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc acc   336
Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr
            100                 105                 110

gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc cag   384
Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln
        115                 120                 125

tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac tgg   432
Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp
    130                 135                 140

ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca acc   480
Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
145                 150                 155                 160

ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt cag   528
Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln
```

```
                165                 170                 175

gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac act   576
Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr
            180                 185                 190

ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat gct   624
Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala
        195                 200                 205

gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca tac   672
Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr
    210                 215                 220

aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac ttc   720
Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe
225                 230                 235                 240

cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg gag   768
Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu
                245                 250                 255

aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag gtt   816
Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val
            260                 265                 270

gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt att   864
Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile
        275                 280                 285

taatccgagc acttcagcta cac                                        887
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20050239.0

<210> 198
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 198

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Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr
  1               5                  10                  15

Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro
             20                  25                  30

Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala
         35                  40                  45

Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu
     50                  55                  60

Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser
 65                  70                  75                  80

Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val
                 85                  90                  95

Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr
            100                 105                 110

Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln
```

```
        115                 120                 125

Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp
    130                 135                 140

Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
145                 150                 155                 160

Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln
                165                 170                 175

Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr
            180                 185                 190

Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala
        195                 200                 205

Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr
    210                 215                 220

Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe
225                 230                 235                 240

Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu
                245                 250                 255

Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val
            260                 265                 270

Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile
        275                 280                 285
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09852-0016

<210> 199
<211> 842
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(819)
<223> FRXA01891

<400> 199

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tac tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc   48
Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly
  1               5                  10                  15

cca gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa   96
Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
             20                  25                  30

gcg atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac  144
Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
         35                  40                  45

ctt tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac  192
Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
```

```
     50                  55                  60

tct gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca   240
Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala
 65                  70                  75                  80

gtt gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc   288
Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser
                85                  90                  95

acc gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc   336
Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile
            100                 105                 110

cag tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac   384
Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp
        115                 120                 125

tgg ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca   432
Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro
    130                 135                 140

acc ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt   480
Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg
145                 150                 155                 160

cag gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac   528
Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn
                165                 170                 175

act ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat   576
Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp
            180                 185                 190

gct gca tct gat cca gat cac gca gca ttc ctc gag gag aac cct gca   624
Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala
        195                 200                 205

tac aac gtt gca gtg gag cag ctt cct gat acc cgt tcc cag gac aac   672
Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn
    210                 215                 220

ttc cgc gtg ctg ctg cca aac ggt gac cgc acc atc ggt gac gca ctg   720
Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu
225                 230                 235                 240

gag aag atc tgc ctg act ggt gca gac atc gat gtc acc ctg gct gag   768
Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu
                245                 250                 255

gtt gag acc aag ctg aac acc atc tac acc cgc gac atc gaa cca ctt   816
Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu
            260                 265                 270

att taatccgagc acttcagcta cac                                    842
Ile
```

20050215-0215200

<210> 200
<211> 273

<212> PRT
<213> Corynebacterium glutamicum

<400> 200
Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly
1 5 10 15

Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
20 25 30

Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
35 40 45

Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
50 55 60

Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala
65 70 75 80

Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser
85 90 95

Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile
100 105 110

Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp
115 120 125

Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro
130 135 140

Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg
145 150 155 160

Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn
165 170 175

Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp
180 185 190

Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala
195 200 205

Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn
210 215 220

Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu
225 230 235 240

Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu
245 250 255

Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu
260 265 270

Ile

<210> 201
<211> 776

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (7)..(753)
<223> RXA02414

<400> 201

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tttaccatg agt tac aac agc ccg tat aac aac acg aat ttc agc acc act 51
      Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr
        1               5                  10                  15

ggc gcg ttc caa cct gct ggt ggg ccg gtg aag ccg tgg aat aag ccc   99
Gly Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro
                20                  25                  30

gat gcc agc ctg aat cag cag ctg aaa aac aaa tcc cgt gtg cgc aca   147
Asp Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr
            35                  40                  45

ggt ctt acc atc gcc atc ggt tat gta gtg gtg att tgg gcg gtg cat   195
Gly Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His
        50                  55                  60

ttg gca tcc atc gtc att gcg ctg ctc act ggc ttc aac ctg acc aac   243
Leu Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn
    65                  70                  75

ttt ggt att cat ccg ctg gat acc agt gca ctg tgg ggt att ttc acc   291
Phe Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr
80                  85                  90                  95

tca ccg ctg ttg cat gga agc ttc agc cac ctc att gga aat acc gtt   339
Ser Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val
                100                 105                 110

cca ggc ttt ata ttc agt ttc ctc atc ggt atg agt ggc aag cgc gtg   387
Pro Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val
            115                 120                 125

ttc tgg gaa gtc acg att atc gca ggt ctc atc ggc ggt ctt ggt aca   435
Phe Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr
        130                 135                 140

tgg att ttc ggt gga atc ggc acc aac cac atc ggt gcg tcc ggc ctg   483
Trp Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu
    145                 150                 155

att tat ggc tgg ctt ggc tac ctg atc gtg cgt gga att ttc aac aag   531
Ile Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys
160                 165                 170                 175

gat att aaa cag ttc ctg ctt ggc ata gtt ttg gcg ttc att tac tcc   579
Asp Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser
                180                 185                 190

ggt ttg ttc tgg ggt ctg cta cct act caa atc ggt gtg tcc tgg cag   627
Gly Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln
            195                 200                 205
```

```
ggc cac ctt ttc ggt gca ctt ggt gga atc ggt gcg ggt gct ttt atc   675
Gly His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile
        210                 215                 220

gcc tcg gat gac ccg gca gcg ttg aaa gcg aag aag caa cag aag aaa   723
Ala Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys
    225                 230                 235

tta gaa aag caa caa cgc caa aga ggc tta tagttttcac ctagcgacta     773
Leu Glu Lys Gln Gln Arg Gln Arg Gly Leu
240                 245

cac                                                               776
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<210> 202
<211> 249
<212> PRT
<213> Corynebacterium glutamicum

<400> 202

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Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr Gly
  1               5                  10                  15

Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro Asp
            20                  25                  30

Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr Gly
        35                  40                  45

Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His Leu
    50                  55                  60

Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn Phe
65                  70                  75                  80

Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr Ser
                85                  90                  95

Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val Pro
            100                 105                 110

Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val Phe
        115                 120                 125

Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr Trp
    130                 135                 140

Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu Ile
145                 150                 155                 160

Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys Asp
                165                 170                 175

Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser Gly
            180                 185                 190

Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln Gly
        195                 200                 205

His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile Ala
```

```
    210                 215                 220

Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys Leu
225                 230                 235                 240

Glu Lys Gln Gln Arg Gln Arg Gly Leu
                245
```

<210> 203
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> RXN01580

<400> 203

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cggtaaacgc ctcattaaag tccaatgcca tgctcataac actaacagtt aaccgtgcgg 60

tcaactttgc tccctatcct taaaaagccc acagaaaagg atg tat aag aat atg   115
                                              Met Tyr Lys Asn Met
                                                1               5

cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctc gaa aac acc   163
His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr
                10                  15                  20

atg acc gct ttc cag gct gcc gcg ccc gct gac gct ttt gag ctg gat   211
Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp
            25                  30                  35

atc cac gcc acc gct gac aat cag gtc gtc gtt atc cac gac cgc acc   259
Ile His Ala Thr Ala Asp Asn Gln Val Val Val Ile His Asp Arg Thr
        40                  45                  50

gca gcg cgt gtt gcc gcg cca gat tcc ctg cac cgc gac acc ccg gtt   307
Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His Arg Asp Thr Pro Val
    55                  60                  65

gcg cgc tta agc gcc gcg caa atc aag gag ata acg ctt atc gac gga   355
Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile Thr Leu Ile Asp Gly
70                  75                  80                  85

tcc ccc gta cca acc ctg gag gaa gtt cta ctc cag acg agc ctg ccg   403
Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu Gln Thr Ser Leu Pro
                90                  95                  100

atc caa gtg gaa atc aaa tct gcc ggt gca gtt cca gca gcc gca gca   451
Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val Pro Ala Ala Ala Ala
            105                 110                 115

tta ttg cag aaa tac cca gag cac ctg gag cgc ctg ctg ttc atc agt   499
Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg Leu Leu Phe Ile Ser
        120                 125                 130

ttc atc gat gca gca ctg gtg gaa atc gtg gat cga ctg cca gaa gct   547
Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp Arg Leu Pro Glu Ala
    135                 140                 145
```

```
cgc gtg gga atc ttg cgc gat gcg tcc atg gat gat ctg cgc att ctt   595
Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp Asp Leu Arg Ile Leu
150                 155                 160                 165

gat tac atc ccg cta aaa aat gtg ggc gcg atc ttg ccc tcg tgg aaa   643
Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile Leu Pro Ser Trp Lys
                170                 175                 180

gca cta aac gtg gcg tca att gct gat cta cat acc aag gga atc aag   691
Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His Thr Lys Gly Ile Lys
            185                 190                 195

gtt ggc tgc tgg aca att cgg gat gaa aat gcg ttt ggg atc gca caa   739
Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala Phe Gly Ile Ala Gln
        200                 205                 210

caa gct ggc gtt gat tac gcc act gtt agc gat ccc tct cgt ttc ctc   787
Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp Pro Ser Arg Phe Leu
    215                 220                 225

gcg ccc tcc cct gct ggg gag ttg cac tgg taaataatct agtgaccaga     837
Ala Pro Ser Pro Ala Gly Glu Leu His Trp
230                 235

ctg                                                               840
```

09629160 - 082502

<210> 204
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 204

```
Met Tyr Lys Asn Met His Ile Val Ala His Arg Gly Ala Glu Asp Leu
  1               5                  10                  15

His Leu Glu Asn Thr Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp
             20                  25                  30

Ala Phe Glu Leu Asp Ile His Ala Thr Ala Asp Asn Gln Val Val Val
         35                  40                  45

Ile His Asp Arg Thr Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His
     50                  55                  60

Arg Asp Thr Pro Val Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile
 65                  70                  75                  80

Thr Leu Ile Asp Gly Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu
                 85                  90                  95

Gln Thr Ser Leu Pro Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val
            100                 105                 110

Pro Ala Ala Ala Ala Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg
        115                 120                 125

Leu Leu Phe Ile Ser Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp
    130                 135                 140
```

```
Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp
145                 150                 155                 160

Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile
                165                 170                 175

Leu Pro Ser Trp Lys Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His
            180                 185                 190

Thr Lys Gly Ile Lys Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala
        195                 200                 205

Phe Gly Ile Ala Gln Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp
    210                 215                 220

Pro Ser Arg Phe Leu Ala Pro Ser Pro Ala Gly Glu Leu His Trp
225                 230                 235


<210> 205
<211> 1314
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1291)
<223> RXA01436

<400> 205
gcctaaacaa accagtcaac gacctttccc gtggcgcaac agtccctgac atcgtcaaca 60

cagtagccat cacagcaatt caggcaggag gacgcagcta atg gca ttg gca ctt   115
                                        Met Ala Leu Ala Leu
                                          1               5

gtt ttg aac tcc ggt tca tct tcc atc aaa ttc cag ctg gtc aac ccc   163
Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe Gln Leu Val Asn Pro
                  10                  15                  20

gaa aac tct gcc atc gac gag cca tat gtt tct ggt ctt gtg gag cag   211
Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser Gly Leu Val Glu Gln
              25                  30                  35

att ggt gag cca aac ggc cgc atc gta ctc aaa ata gag ggt gaa aaa   259
Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys Ile Glu Gly Glu Lys
          40                  45                  50

tat acc cta gag aca ccc atc gca gat cac tcc gaa ggc cta aac ctg   307
Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser Glu Gly Leu Asn Leu
      55                  60                  65

gcg ttc gat ctc atg gac cag cac aac tgt ggt cct tcc caa ctg gaa   355
Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly Pro Ser Gln Leu Glu
  70                  75                  80                  85

atc acc gca gtt gga cac cgc gtg gtc cac ggc gga atc ttg ttc tcc   403
Ile Thr Ala Val Gly His Arg Val Val His Gly Gly Ile Leu Phe Ser
                  90                  95                 100

gca ccg gaa ctt atc act gat gaa atc gtg gaa atg atc cgc gat ctc   451
```

```
Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu Met Ile Arg Asp Leu
            105                 110                 115

att cca ctc gca cca ctg cac aac cct gca aac gtt gac ggc att gat   499
Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn Val Asp Gly Ile Asp
        120                 125                 130

gtt gct cga aaa att ctc ccc gat gtc cca cac gta gct gtc ttt gac   547
Val Ala Arg Lys Ile Leu Pro Asp Val Pro His Val Ala Val Phe Asp
    135                 140                 145

acc ggt ttc ttc cac tca ctt cca cca gca gct gcg ctg tat gcc atc   595
Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala Ala Leu Tyr Ala Ile
150                 155                 160                 165

aac aag gat gtc gca gct gaa cac gga atc agg cgc tat ggt ttc cac   643
Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg Arg Tyr Gly Phe His
                170                 175                 180

ggc acc tcc cat gaa ttt gtg tcc aag cgc gtg gtg gaa att ctg gaa   691
Gly Thr Ser His Glu Phe Val Ser Lys Arg Val Val Glu Ile Leu Glu
            185                 190                 195

aag ccc acc gaa gac atc aac acc atc acc ttc cac ctg ggc aac ggc   739
Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe His Leu Gly Asn Gly
        200                 205                 210

gca tcc atg gct gct gtt caa ggt ggc cgt gcg gta gat act tcc atg   787
Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala Val Asp Thr Ser Met
    215                 220                 225

ggt atg aca cct ctc gcg ggc ctt gtc atg ggt acc cga agc ggt gac   835
Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly Thr Arg Ser Gly Asp
230                 235                 240                 245

att gat cca ggt atc gtc ttc cac ctt tcc cgc acc gct ggc atg agc   883
Ile Asp Pro Gly Ile Val Phe His Leu Ser Arg Thr Ala Gly Met Ser
                250                 255                 260

atc gat gag atc gat aat ctg ctg aac aaa aag tcg ggt gta aag gga   931
Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys Ser Gly Val Lys Gly
            265                 270                 275

ctt tcc ggt gtt aat gat ttc cgt gaa ctg cgg gaa atg atc gac aac   979
Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg Glu Met Ile Asp Asn
        280                 285                 290

aat gat caa gat gcc tgg tcc gcg tac aac att tac ata cac caa ctc   1027
Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile Tyr Ile His Gln Leu
    295                 300                 305

cgc cgc tac ctc ggt tcc tac atg gtg gca ctg gga cgg gta gac acc   1075
Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu Gly Arg Val Asp Thr
310                 315                 320                 325

atc gtg ttc acc gcc ggt gtc ggt gaa aat gcc cag ttt gtc cgt gag   1123
Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala Gln Phe Val Arg Glu
                330                 335                 340

gat gcc ttg gca ggt ttg gaa atg tac gga att gag atc gat cca gag   1171
Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile Glu Ile Asp Pro Glu
```

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```
            345                 350                 355

cgt aac gca ttg cca aac gat ggt cct cga ttg att tcc acc gat gcc   1219
Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu Ile Ser Thr Asp Ala
        360                 365                 370

tcc aag gtg aag gtg ttt gtt att cca act aat gaa gag tta gct atc   1267
Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu Leu Ala Ile
    375                 380                 385

gct agg tac gcg gtg aag ttc gct tagctctcct ggttaggatc cac         1314
Ala Arg Tyr Ala Val Lys Phe Ala
390                 395
```

<210> 206
<211> 397
<212> PRT
<213> Corynebacterium glutamicum

<400> 206

```
Met Ala Leu Ala Leu Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe
  1               5                  10                  15

Gln Leu Val Asn Pro Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser
             20                  25                  30

Gly Leu Val Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys
         35                  40                  45

Ile Glu Gly Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser
     50                  55                  60

Glu Gly Leu Asn Leu Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly
 65                  70                  75                  80

Pro Ser Gln Leu Glu Ile Thr Ala Val Gly His Arg Val Val His Gly
                 85                  90                  95

Gly Ile Leu Phe Ser Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu
            100                 105                 110

Met Ile Arg Asp Leu Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn
        115                 120                 125

Val Asp Gly Ile Asp Val Ala Arg Lys Ile Leu Pro Asp Val Pro His
    130                 135                 140

Val Ala Val Phe Asp Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala
145                 150                 155                 160

Ala Leu Tyr Ala Ile Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg
                165                 170                 175

Arg Tyr Gly Phe His Gly Thr Ser His Glu Phe Val Ser Lys Arg Val
            180                 185                 190

Val Glu Ile Leu Glu Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe
        195                 200                 205

His Leu Gly Asn Gly Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala
```

Doc. No. 1000000000000

```
    210                 215                 220

Val Asp Thr Ser Met Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly
225                 230                 235                 240

Thr Arg Ser Gly Asp Ile Asp Pro Gly Ile Val Phe His Leu Ser Arg
                245                 250                 255

Thr Ala Gly Met Ser Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys
            260                 265                 270

Ser Gly Val Lys Gly Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg
        275                 280                 285

Glu Met Ile Asp Asn Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile
    290                 295                 300

Tyr Ile His Gln Leu Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu
305                 310                 315                 320

Gly Arg Val Asp Thr Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala
                325                 330                 335

Gln Phe Val Arg Glu Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile
            340                 345                 350

Glu Ile Asp Pro Glu Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu
        355                 360                 365

Ile Ser Thr Asp Ala Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn
    370                 375                 380

Glu Glu Leu Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala
385                 390                 395


<210> 207
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXA00686

<400> 207
ataggcttga acaatacgtc gttacactgg ccgatttgat acctttcaaa acttttaccc 60

ttcatcggag tgccagggga acttagagga gcattaaata atg gcg gga gga aat   115
                                        Met Ala Gly Gly Asn
                                          1               5

cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga   163
Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly
                10                  15                  20

gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag   211
Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu
            25                  30                  35
```

```
ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta   259
Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu
         40                  45                  50

acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg   307
Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu
     55                  60                  65

ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc   355
Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg
 70                  75                  80                  85

gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag   403
Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu
                 90                  95                 100

act gcg cag cta gtg gtc cgc gat aaa gat gaa gca ctt ttg att gac   451
Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp
            105                 110                 115

cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt   499
Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly
        120                 125                 130

cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt   547
Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe
    135                 140                 145

gat gag cca tgg gta aaa cag tcc tat ctc aag ctg cca ctc aac gcc   595
Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala
150                 155                 160                 165

tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg   643
Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu
                170                 175                 180

aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga   691
Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg
            185                 190                 195

atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg   739
Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu
        200                 205                 210

gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt   787
Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu
    215                 220                 225

gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa   835
Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys
230                 235                 240                 245

gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat   883
Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn
                250                 255                 260

gca gaa cga aaa ggc gat acc taaacccgcc ctccatctgc ata             927
Ala Glu Arg Lys Gly Asp Thr
            265
```

<210> 208
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 208
Met Ala Gly Gly Asn Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val
1 5 10 15

Ile Ala Val Leu Gly Ala Phe Glu His Thr Met Arg Pro Leu Gly Val
20 25 30

Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg
35 40 45

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp
50 55 60

Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr
65 70 75 80

Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
85 90 95

Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
100 105 110

Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
115 120 125

Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
130 135 140

Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
145 150 155 160

Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
165 170 175

Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
180 185 190

His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
195 200 205

His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
210 215 220

Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
225 230 235 240

Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
245 250 255

Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr
260 265

<210> 209
<211> 1158
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> RXA00246

<400> 209
ttgcaaggat tgtaatttaa ggcacatcta tgtcggtgtg aaattacatg tgccagaaga 60

gcaatttgcc aagtaatcca agcgagaagg agtgagtttt atg acc act gct gca 115
Met Thr Thr Ala Ala
1 5

ccc caa gaa ttt acc gct gct gtt gtt gaa aaa ttc ggt cat gac gtg 163
Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys Phe Gly His Asp Val
10 15 20

acc gtg aag gat att gac ctt cca aag cca ggg cca cac cag gca ttg 211
Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly Pro His Gln Ala Leu
25 30 35

gtg aag gta ctc acc tcc ggc atc tgc cac acc gac ctc cac gcc ttg 259
Val Lys Val Leu Thr Ser Gly Ile Cys His Thr Asp Leu His Ala Leu
40 45 50

gag ggc gat tgg cca gta aag ccg gaa cca cca ttc gta cca gga cac 307
Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro Phe Val Pro Gly His
55 60 65

gaa ggt gta ggt gaa gtt gtt gag ctc gga cca ggt gaa cac gat gtg 355
Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro Gly Glu His Asp Val
70 75 80 85

aag gtc ggc gat att gtc ggc aat gcg tgg ctc tgg tca gcg tgt ggc 403
Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu Trp Ser Ala Cys Gly
90 95 100

acc tgc gaa tac tgc atc acc ggc agg gaa act cag tgc aac gaa gct 451
Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr Gln Cys Asn Glu Ala
105 110 115

gag tat ggt ggc tac acc caa aat gga tcc ttc ggc cag tac atg ctg 499
Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe Gly Gln Tyr Met Leu
120 125 130

gtg gat acc cgt tac gcc gct cgc atc cca gac ggc gtg gac tac ctc 547
Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp Gly Val Asp Tyr Leu
135 140 145

gaa gca gca cca att ctg tgt gca ggc gtg act gtc tac aag gca ctc 595
Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys Ala Leu
150 155 160 165

aaa gtc tct gaa acc cgc ccg ggc caa ttc atg gtg atc tcc ggt gtc 643
Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met Val Ile Ser Gly Val
170 175 180

ggc gga ctt ggc cac atc gca gtc caa tac gca gcg gcg atg ggc atg 691
Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala Ala Ala Met Gly Met
185 190 195

```
cgt gtc att gcg gta gat att gcc gat gac aag ctg gaa ctt gcc cgt   739
Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys Leu Glu Leu Ala Arg
        200                 205                 210

aag cac ggt gcg gaa ttt acc gtg aat gcg cgt aat gaa gat tca ggc   787
Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg Asn Glu Asp Ser Gly
    215                 220                 225

gaa gct gta cag aag tac acc aac ggt ggc gca cac ggc gtg ctt gtg   835
Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala His Gly Val Leu Val
230                 235                 240                 245

act gca gtt cac gag gca gca ttc ggc cag gca ctg gat atg gct cga   883
Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala Leu Asp Met Ala Arg
                250                 255                 260

cgt gca gga aca att gtg ttc aac ggt ctg cca ccg gga gag ttc cca   931
Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro Pro Gly Glu Phe Pro
            265                 270                 275

gca tcc gtg ttc aac atc gta ttc aag ggc ctg acc atc cgt gga tcc   979
Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu Thr Ile Arg Gly Ser
        280                 285                 290

ctc gtg gga acc cgc caa gac ttg gcc gaa gcg ctc gat ttc ttt gca   1027
Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala Leu Asp Phe Phe Ala
    295                 300                 305

cgc gga cta atc aag cca acc gtg agt gag tgc tcc ctc gat gag gtc   1075
Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys Ser Leu Asp Glu Val
310                 315                 320                 325

aat ggt gtg ctt gac cgc atg cga aac ggc aag atc gat ggt cgt gtg   1123
Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys Ile Asp Gly Arg Val
                330                 335                 340

gcg att cgt ttc taacggattg tgttgaaact gct                        1158
Ala Ile Arg Phe
            345
```

<210> 210
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 210

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Met Thr Thr Ala Ala Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys
  1               5                  10                  15

Phe Gly His Asp Val Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly
            20                  25                  30

Pro His Gln Ala Leu Val Lys Val Leu Thr Ser Gly Ile Cys His Thr
        35                  40                  45

Asp Leu His Ala Leu Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro
    50                  55                  60

Phe Val Pro Gly His Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro
```

65 70 75 80

Gly Glu His Asp Val Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu
85 90 95

Trp Ser Ala Cys Gly Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr
100 105 110

Gln Cys Asn Glu Ala Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe
115 120 125

Gly Gln Tyr Met Leu Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp
130 135 140

Gly Val Asp Tyr Leu Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr
145 150 155 160

Val Tyr Lys Ala Leu Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met
165 170 175

Val Ile Ser Gly Val Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala
180 185 190

Ala Ala Met Gly Met Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys
195 200 205

Leu Glu Leu Ala Arg Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg
210 215 220

Asn Glu Asp Ser Gly Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala
225 230 235 240

His Gly Val Leu Val Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala
245 250 255

Leu Asp Met Ala Arg Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro
260 265 270

Pro Gly Glu Phe Pro Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu
275 280 285

Thr Ile Arg Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala
290 295 300

Leu Asp Phe Phe Ala Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys
305 310 315 320

Ser Leu Asp Glu Val Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys
325 330 335

Ile Asp Gly Arg Val Ala Ile Arg Phe
340 345

<210> 211
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(700)
<223> RXA01571

<400> 211
aaactacctg ctgagagctt tgtaatttac ggtgtggttg tggaggggtg cgtcgagaag 60

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cgctcgtagg cgcttttgat ttttcggtag gctaactggg gtg agt atc tca gta   115
                                          Val Ser Ile Ser Val
                                            1               5

aaa gca cta caa aag tcc ggc cca gaa gca cct ttc gag gtc aag atc   163
Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro Phe Glu Val Lys Ile
                10                  15                  20

att gaa cgc cgt gac cca cgc gca gat gat gtg gtt att gat atc aaa   211
Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val Val Ile Asp Ile Lys
            25                  30                  35

gct gcg ggc atc tgc cac agc gat atc cac acc atc cgc aac gaa tgg   259
Ala Ala Gly Ile Cys His Ser Asp Ile His Thr Ile Arg Asn Glu Trp
        40                  45                  50

ggc gag gcg cac ttc ccg ctc acc gtc ggc cac gaa atc gca ggc gtt   307
Gly Glu Ala His Phe Pro Leu Thr Val Gly His Glu Ile Ala Gly Val
    55                  60                  65

gtc tct gcg gtt gga tcc gat gta acc aaa tgg aaa gtc ggc gac cgc   355
Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp Lys Val Gly Asp Arg
70                  75                  80                  85

gtg ggc gtc ggc tgc ctc gtt aac tcc tgc ggc gaa tgc gaa cag tgc   403
Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly Glu Cys Glu Gln Cys
                90                  95                  100

gtc gca gga ttt gaa aac aac tgc ctt cgc gga aac gtc gga acc tac   451
Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly Asn Val Gly Thr Tyr
            105                 110                 115

aac tct aac gac gtc gac ggc acc atc acc caa ggc ggc tac gct gaa   499
Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln Gly Gly Tyr Ala Glu
        120                 125                 130

aag gta gtg gtc aac gaa cgt ttc ctg tgc agc atc cca gag gaa ctt   547
Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser Ile Pro Glu Glu Leu
    135                 140                 145

aac ttc gat gtc gca gca cca ctg ctg tgc gca ggc atc acc acc tac   595
Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala Gly Ile Thr Thr Tyr
150                 155                 160                 165

tcc cca atc gct cgc tgg aac gtt aaa gaa ggc gac aaa gta gca gtc   643
Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly Asp Lys Val Ala Val
                170                 175                 180

atg ggc ctc ggc ggg act cgg aca cat ggg tgt cca gat cgc tgc agc   691
Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys Pro Asp Arg Cys Ser
            185                 190                 195

caa ggg tgc tgaggttacc gttctgtccc gtt                            723
Gln Gly Cys
        200
```

<210> 212
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 212

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Val Ser Ile Ser Val Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro
  1               5                  10                  15

Phe Glu Val Lys Ile Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val
            20                  25                  30

Val Ile Asp Ile Lys Ala Ala Gly Ile Cys His Ser Asp Ile His Thr
        35                  40                  45

Ile Arg Asn Glu Trp Gly Glu Ala His Phe Pro Leu Thr Val Gly His
    50                  55                  60

Glu Ile Ala Gly Val Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp
65                  70                  75                  80

Lys Val Gly Asp Arg Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly
                85                  90                  95

Glu Cys Glu Gln Cys Val Ala Gly Phe Glu Asn Asn Cys Leu Arg Gly
            100                 105                 110

Asn Val Gly Thr Tyr Asn Ser Asn Asp Val Asp Gly Thr Ile Thr Gln
        115                 120                 125

Gly Gly Tyr Ala Glu Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser
    130                 135                 140

Ile Pro Glu Glu Leu Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala
145                 150                 155                 160

Gly Ile Thr Thr Tyr Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly
                165                 170                 175

Asp Lys Val Ala Val Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys
            180                 185                 190

Pro Asp Arg Cys Ser Gln Gly Cys
        195                 200
```

<210> 213
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXA01572

<400> 213
ctgctgtgcg caggcatcac cacctactcc ccaatcgctc gctggaacgt taaagaaggc 60

```
gacaaagtag cagtcatggg cctcggcggg actcggacac atg ggt gtc cag atc   115
                                             Met Gly Val Gln Ile
                                               1               5

gct gca gcc aag ggt gct gag gtt acc gtt ctg tcc cgt tcc ctg cgc   163
Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu Ser Arg Ser Leu Arg
                 10                  15                  20

aag gca gaa ctt gcc aag gaa ctc ggc gca gct cgc acg ctt gcg act   211
Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala Arg Thr Leu Ala Thr
             25                  30                  35

tct gat gag gat ttc ttc acc gaa cac gcc ggt gaa ttc gac ttc atc   259
Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly Glu Phe Asp Phe Ile
         40                  45                  50

ctc aac acc att agc gca tcc atc cca gtc gac aag tac ctg agc ctt   307
Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp Lys Tyr Leu Ser Leu
     55                  60                  65

ctc aag cca cac ggt gtc atg gct gtt gtc ggt ctg cca cca gag aag   355
Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys
 70                  75                  80                  85

cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc   403
Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr
                 90                  95                 100

gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc   451
Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe
             105                 110                 115

tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac   499
Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn
         120                 125                 130

gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc   547
Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe
     135                 140                 145

cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt       592
Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val
150                 155                 160

taggtttact gaagttcaga ctt                                        615
```

<210> 214
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 214

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Met Gly Val Gln Ile Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu
  1               5                  10                  15

Ser Arg Ser Leu Arg Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala
             20                  25                  30

Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly
         35                  40                  45
```

```
Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp
     50                  55                  60

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly
 65                  70                  75                  80

Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly
                85                  90                  95

Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln
            100                 105                 110

Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu
        115                 120                 125

Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala
    130                 135                 140

Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu
145                 150                 155                 160

Val Glu Ala Val
```

US20050153406A1

<210> 215
<211> 1140
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1117)
<223> RXA01758

<400> 215
ccccccttatt cagagtgatg gtctaccgga gaagtaccca gaccaatagc atcgaccaac 60

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gatagcgcgc tcagaagttc tttagtgaaa gcagaaccaa atg ccc aaa tac att   115
                                            Met Pro Lys Tyr Ile
                                              1               5

gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg   163
Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val
                 10                  15                  20

caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct   211
Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala
             25                  30                  35

agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag   259
Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys
         40                  45                  50

cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc   307
His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile
     55                  60                  65

gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt   355
Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val
```

```
70                  75                  80                  85

gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt   403
Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg
                90                  95                 100

gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct   451
Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser
            105                 110                 115

tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt   499
Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu
        120                 125                 130

gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc   547
Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly
    135                 140                 145

tgc gca ggt gtg aca aca ttc aat gcg ttg cga aac ctg aag ctg gat   595
Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp
150                 155                 160                 165

ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta   643
Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu
                170                 175                 180

gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc   691
Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala
            185                 190                 195

cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac   739
Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His
        200                 205                 210

tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt   787
Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu
    215                 220                 225

ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt   835
Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu
230                 235                 240                 245

tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc   883
Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile
                250                 255                 260

gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg   931
Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met
            265                 270                 275

aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg   979
Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr
        280                 285                 290

gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att   1027
Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile
    295                 300                 305

gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca   1075
Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser
310                 315                 320                 325
```

```
gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca                1117
Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser
                330                 335

taatgccaac agcaagccca att                                             1140
```

<210> 216
<211> 339
<212> PRT
<213> Corynebacterium glutamicum

<400> 216

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Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu
  1               5                  10                  15

Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg
            20                  25                  30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
        35                  40                  45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
    50                  55                  60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
65                  70                  75                  80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
                85                  90                  95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys
            100                 105                 110

Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val
        115                 120                 125

Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu
    130                 135                 140

Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg
145                 150                 155                 160

Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly
                165                 170                 175

Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg
            180                 185                 190

Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln
        195                 200                 205

Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln
    210                 215                 220

Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser
225                 230                 235                 240

Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly
                245                 250                 255
```

```
Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala
           260                 265                 270

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
       275                 280                 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
   290                 295                 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
305                 310                 315                 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
               325                 330                 335

Pro Asn Ser
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<210> 217
<211> 1641
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1618)
<223> RXA02539

<400> 217
ggctgctaag cgtgcgaatg tgcgcgttgt cacaatcgtt gaccaagtgt cacctgacgc 60

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acaggtagtg ctcaggtgga ggtggcccaa aggagaccca atg act gtc tac gca   115
                                            Met Thr Val Tyr Ala
                                              1               5

aat cca gga acc gaa ggc tcg atc gtt aac tat gaa aag cgc tac gag   163
Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr Glu Lys Arg Tyr Glu
                  10                  15                  20

aac tac att ggt ggc aag tgg gtt cca ccg gta gag ggc cag tac ctt   211
Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val Glu Gly Gln Tyr Leu
              25                  30                  35

gag aac att tca cct gtc act ggt gaa gtt ttc tgt gag gtc gca cgt   259
Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe Cys Glu Val Ala Arg
          40                  45                  50

ggc acc gca gcg gac gtg gag ctt gca ctg gat gct gca cat gca gcc   307
Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp Ala Ala His Ala Ala
      55                  60                  65

gct gat gcg tgg ggc aag act tct gtc gct gaa cgt gct ctg atc ctg   355
Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu Arg Ala Leu Ile Leu
  70                  75                  80                  85

cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc gca gtt   403
His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile Ala Val
                  90                  95                 100
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gca gaa acc tgg gag aac ggc aag gca gtc cgt gag act ctt gct gca   451
Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg Glu Thr Leu Ala Ala
            105                 110                 115

gat atc cca ctg gca atc gac cac ttc cgc tac ttt gct ggc gcg atc   499
Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr Phe Ala Gly Ala Ile
        120                 125                 130

cgt gct cag gaa gat cgt tcc tca cag atc gac cac aac act gtt gct   547
Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp His Asn Thr Val Ala
    135                 140                 145

tac cac ttc aac gag cca atc ggt gtt gtt ggt cag atc att cct tgg   595
Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp
150                 155                 160                 165

aac ttc cca atc ctc atg gct acc tgg aag ctc gca ccg gca ctt gct   643
Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala
                170                 175                 180

gca ggt aac gcg atc gtc atg aag cca gct gag cag acc cca gca tcc   691
Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu Gln Thr Pro Ala Ser
            185                 190                 195

att ttg tat ctg att aac atc atc ggc gat ctc atc cca gag ggc gtc   739
Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu Ile Pro Glu Gly Val
        200                 205                 210

ctc aac atc gtc aac gga ctc ggc ggt gaa gca ggc gct gca ctg tcc   787
Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala Gly Ala Ala Leu Ser
    215                 220                 225

ggc tct aat cgg att ggc aag att gct ttc acc ggt tcc acc gag gtc   835
Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr Gly Ser Thr Glu Val
230                 235                 240                 245

ggc aag ctg atc aac cgc gct gca tcc gac aag atc att cct gtc acc   883
Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys Ile Ile Pro Val Thr
                250                 255                 260

ctg gag ctc ggc ggt aag tcc cca tcc atc ttc ttc tcc gat gtt ctg   931
Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe Phe Ser Asp Val Leu
            265                 270                 275

tca cag gat gac gcc ttc gca gag aag gca gtt gaa ggc ttc gcg atg   979
Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val Glu Gly Phe Ala Met
        280                 285                 290

ttc gcc ctc aat cag ggt gaa gtt tgt acc tgt cct tcc cgt gca ctt  1027
Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu
    295                 300                 305

gtt cat gag tcc atc gct gat gaa ttc ctc gag ctt ggc gtg aag cga  1075
Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu Leu Gly Val Lys Arg
310                 315                 320                 325

gtt cag aac atc aag ctg ggt aac cca ctt gat act gaa acc atg atg  1123
Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp Thr Glu Thr Met Met
                330                 335                 340

ggt gct cag gcg tcc cag gag cag atg gac aag atc tcc tcc tac ctg  1171
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Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys Ile Ser Ser Tyr Leu
            345                 350                 355

aag atc ggc cca gaa gaa ggc gct caa acc ctc act ggt ggc aag gtc   1219
Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu Thr Gly Gly Lys Val
        360                 365                 370

aac aag gtt gat ggc atg gag aac ggt tac tac att gag cca acc gtt   1267
Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr Ile Glu Pro Thr Val
    375                 380                 385

ttc cgc ggc acc aac gac atg agg atc ttc cgc gag gaa atc ttc gga   1315
Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg Glu Glu Ile Phe Gly
390                 395                 400                 405

cca gtc ctt tct gtt gct acc ttc agc gac ttc gat gag gcc atc cgt   1363
Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe Asp Glu Ala Ile Arg
                410                 415                 420

att gca aac gac acc aac tac ggc ctc ggc gct ggt gtc tgg agc cgt   1411
Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg
            425                 430                 435

gac caa aac acc att tat cgt gca ggt cgc gca atc cag gct ggt cga   1459
Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala Ile Gln Ala Gly Arg
        440                 445                 450

gtt tgg gtc aac cag tac cac aac tac cca gcg cac tcc gct ttc ggt   1507
Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala His Ser Ala Phe Gly
    455                 460                 465

gga tac aag gag tcc ggc atc ggc cgt gag aac cac ctc atg atg ctg   1555
Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn His Leu Met Met Leu
470                 475                 480                 485

aac cac tac cag cag acc aag aac ctg ttg gtc tcc tac gat cca aac   1603
Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val Ser Tyr Asp Pro Asn
                490                 495                 500

cca acc gga ctg ttc tgatctaagc gttaagtcct aga                    1641
Pro Thr Gly Leu Phe
            505
```

<210> 218
<211> 506
<212> PRT
<213> Corynebacterium glutamicum

<400> 218

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Met Thr Val Tyr Ala Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr
  1               5                  10                  15

Glu Lys Arg Tyr Glu Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val
             20                  25                  30

Glu Gly Gln Tyr Leu Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe
         35                  40                  45

Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp
     50                  55                  60
```

Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu
65 70 75 80

Arg Ala Leu Ile Leu His Arg Ile Ala Asp Arg Met Glu Glu His Leu
85 90 95

Glu Glu Ile Ala Val Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg
100 105 110

Glu Thr Leu Ala Ala Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr
115 120 125

Phe Ala Gly Ala Ile Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp
130 135 140

His Asn Thr Val Ala Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly
145 150 155 160

Gln Ile Ile Pro Trp Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu
165 170 175

Ala Pro Ala Leu Ala Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu
180 185 190

Gln Thr Pro Ala Ser Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu
195 200 205

Ile Pro Glu Gly Val Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala
210 215 220

Gly Ala Ala Leu Ser Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr
225 230 235 240

Gly Ser Thr Glu Val Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys
245 250 255

Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe
260 265 270

Phe Ser Asp Val Leu Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val
275 280 285

Glu Gly Phe Ala Met Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys
290 295 300

Pro Ser Arg Ala Leu Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu
305 310 315 320

Leu Gly Val Lys Arg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp
325 330 335

Thr Glu Thr Met Met Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys
340 345 350

Ile Ser Ser Tyr Leu Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu
355 360 365

Thr Gly Gly Lys Val Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr
370 375 380

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```
Ile Glu Pro Thr Val Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg
385                 390                 395                 400

Glu Glu Ile Phe Gly Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe
                405                 410                 415

Asp Glu Ala Ile Arg Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala
            420                 425                 430

Gly Val Trp Ser Arg Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala
        435                 440                 445

Ile Gln Ala Gly Arg Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala
    450                 455                 460

His Ser Ala Phe Gly Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn
465                 470                 475                 480

His Leu Met Met Leu Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val
                485                 490                 495

Ser Tyr Asp Pro Asn Pro Thr Gly Leu Phe
            500                 505


<210> 219
<211> 430
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(430)
<223> RXN03061

<400> 219
ctgccaccac tggtcattgc agaggacact ctccgtgatg gtcttcaggt gttagtcgca 60

gccctagagc gcgaaaccgc gcaccagaag gtgggctaaa gtg tct ttg acc ttc   115
                                            Val Ser Leu Thr Phe
                                              1               5

cca gta atc aac ccc agc gat ggc tcc acc atc acc gag cta gaa aac   163
Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile Thr Glu Leu Glu Asn
                  10                  15                  20

cac gat tcc acc cag tgg atg tcc gcg ctc tct gat gca gtt gca gct   211
His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser Asp Ala Val Ala Ala
              25                  30                  35

ggt cct tca tgg gct gcg aaa act ccc cgc gaa aga tcc gtg gta ctc   259
Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu Arg Ser Val Val Leu
          40                  45                  50

acc gca atc ttc gaa gca ctg acc gaa cgc gcc caa gaa ctt gca gag   307
Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala Gln Glu Leu Ala Glu
      55                  60                  65

atc atc cac ctg gaa gct gga aaa tcc gat gca gaa gct ctt ggt gaa   355
Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala Glu Ala Leu Gly Glu
  70                  75                  80                  85
```

```
gtc gct tat ggt gca gaa tac ttc cgt tgg ttt gcg gaa gaa gca gtg   403
Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe Ala Glu Glu Ala Val
                 90                  95                 100

cgc ctg ccc ggc cgc tac gga cag tca                              430
Arg Leu Pro Gly Arg Tyr Gly Gln Ser
            105                 110
```

<210> 220
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 220

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Val Ser Leu Thr Phe Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile
  1               5                  10                  15

Thr Glu Leu Glu Asn His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser
            20                  25                  30

Asp Ala Val Ala Ala Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu
         35                  40                  45

Arg Ser Val Val Leu Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala
     50                  55                  60

Gln Glu Leu Ala Glu Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala
 65                  70                  75                  80

Glu Ala Leu Gly Glu Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe
                 85                  90                  95

Ala Glu Glu Ala Val Arg Leu Pro Gly Arg Tyr Gly Gln Ser
            100                 105                 110
```

<210> 221
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXN03150

<400> 221

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tttaacagag tgcgtttcaa tgcctgtagt gttccggcaa ttttgaatgt cgttacggtt 60

acccaaggct gaattcctga gctcaccttg tacaagatca gtg gaa gcc cag ttc   115
                                            Val Glu Ala Gln Phe
                                              1               5

acc tct ccc ctg ctc aac aat ggg caa acc tgt ttc ctt ggt acc cga   163
Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys Phe Leu Gly Thr Arg
                10                  15                  20

atc ctt gct cca aaa tca cgt tac gcg gaa gta gtc gat gca ttc acc   211
Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val Val Asp Ala Phe Thr
```

```
            25                  30                  35

gct ttc gct ggc agc ctg cag gtt gga gtc acg tcc tcc cct gac act   259
Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr Ser Ser Pro Asp Thr
        40                  45                  50

cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc   307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser
    55                  60                  65

tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc   355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly
70                  75                  80                  85

agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg   403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val
                90                  95                  100

ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc   451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe
            105                 110                 115

gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc   499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile
        120                 125                 130

caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg   547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Gly Thr Val Trp Thr
    135                 140                 145

agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga   595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly
150                 155                 160                 165

acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga   643
Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly
                170                 175                 180

ggt gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt   691
Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu
            185                 190                 195

gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata 744
Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
        200                 205

tat                                                               747


<210> 222
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 222
Val Glu Ala Gln Phe Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys
  1               5                  10                  15

Phe Leu Gly Thr Arg Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val
            20                  25                  30
```

09353909.1

```
Val Asp Ala Phe Thr Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr
        35                  40                  45

Ser Ser Pro Asp Thr Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg
    50                  55                  60

Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg
65                  70                  75                  80

Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe
                85                  90                  95

Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala
            100                 105                 110

Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp
        115                 120                 125

Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly
    130                 135                 140

Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg
145                 150                 155                 160

Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro
                165                 170                 175

Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu
            180                 185                 190

Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
        195                 200                 205
```

09502340.1

<210> 223
<211> 881
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(858)
<223> RXN01340

<400> 223

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aaa gtg ggg gag atc atc gcc tcc gtc ttt gat acc ttt aat atc ccg   48
Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
  1               5                  10                  15

cag ggc ttg gtc tca atc atc acc acc act cga gat gca gag cta tcg   96
Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
             20                  25                  30

gca gaa ctc atg gct gat cct cgc ttg gct aaa gtc acc ttc act gga   144
Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
         35                  40                  45

tca acc aac gtg gga cgc atc ctg gtc cgc caa tcc gcg gac cga ctg   192
```

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Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
     50                  55                  60

ctg cgc acc tcc atg gaa ctc ggc gga aat gca gct ttt gtt atc gac   240
Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp
 65                  70                  75                  80

gaa gcc gca gac ctc gac gaa gcc gta tcc ggt gcc atc gcc gca aaa   288
Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys
                85                  90                  95

ctc cgc aac gcc ggc caa gta tgc atc gca gct aac cgt ttc ttg gtt   336
Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
            100                 105                 110

cat gaa tcc cgc gct gcc gaa ttc acc tca aag ctg gcg aca gcc atg   384
His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met
        115                 120                 125

cag aac act ccc att ggg ccg gtg att tct gcc cgc caa cgc gac cgg   432
Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg
    130                 135                 140

atc gca gca cta gtg gat gaa gcc atc acc gac ggc gcc cgc ctc atc   480
Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile
145                 150                 155                 160

atc ggt ggg gag gtc ccc gac ggc tcc ggc ttc ttc tat cca gcc acc   528
Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr
                165                 170                 175

atc ttg gcc gat gtc cct gca cag tca cgg att gtg cat gag gaa atc   576
Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile
            180                 185                 190

ttc gga cct gtg gcc acc att gcc act ttc acc gac ttg gcc gaa ggc   624
Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly
        195                 200                 205

gtt gca caa gca aat tcc acc gaa ttc ggc ctc gca gcc tac gga ttc   672
Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe
    210                 215                 220

agc aac aat gtg aaa gca aca cag tac atg gcg gaa cac ttg gaa gcc   720
Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala
225                 230                 235                 240

gga atg gtc gga atc aac aga ggc gcc atc tct gac cca gca gca cct   768
Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro
                245                 250                 255

ttt ggc ggc atc gga caa tcc ggc ttc ggc aga gaa ggc gga acc gaa   816
Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu
            260                 265                 270

gga atc gaa gaa tat ctc tcc gtg cgt tac ctc gct ttg ccg           858
Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro
        275                 280                 285

tgacacatga gctgtccggt gaa                                        881
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<210> 224
<211> 286
<212> PRT
<213> Corynebacterium glutamicum

<400> 224
Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
1 5 10 15

Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
20 25 30

Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
35 40 45

Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
50 55 60

Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp
65 70 75 80

Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys
85 90 95

Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
100 105 110

His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met
115 120 125

Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg
130 135 140

Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile
145 150 155 160

Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr
165 170 175

Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile
180 185 190

Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly
195 200 205

Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe
210 215 220

Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala
225 230 235 240

Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro
245 250 255

Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu
260 265 270

Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro
275 280 285

<210> 225
<211> 1686
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1663)
<223> RXN01498

<400> 225
cagtggacaa ctacttggcg ggtcttaaat cagctgtgaa ggattctgca taagctgggc 60

accacacgag catcagaacg cgaaacgaag gtaaaagccc atg atc aaa cgt ctt 115
Met Ile Lys Arg Leu
1 5

cct tta ggt ccg ctg cct aaa gaa ctt cat cag act ctg ctt gat ctg 163
Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln Thr Leu Leu Asp Leu
10 15 20

acc gca aat gcc caa gat gcg gcg aaa gtg gag gtt ata gcg cca ttt 211
Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu Val Ile Ala Pro Phe
25 30 35

act ggc gag acc ctc gga ttt ggt ttt gat ggt gat gag caa gac gtc 259
Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly Asp Glu Gln Asp Val
40 45 50

gag cat gct ttt gca ctt tca agg gca gcc cag aaa aag tgg gtg cac 307
Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln Lys Lys Trp Val His
55 60 65

acc acg gca gtg gaa cgg aag aag atc ttc ctg aag gtt cat gat ctg 355
Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu Lys Val His Asp Leu
70 75 80 85

gta ttg aaa aac cgt gag ctg ctc atg gac atc gtg cag ttg gaa aca 403
Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile Val Gln Leu Glu Thr
90 95 100

ggc aaa aat cga gca tcg gct gcc gat gag gtg ttg gac gtt gcg atc 451
Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val Leu Asp Val Ala Ile
105 110 115

acc acc cgc ttc tac gca aac aat gca gga aag ttt tta aat gac aag 499
Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys Phe Leu Asn Asp Lys
120 125 130

aaa cgc ccc ggc gcg ctt ccg atc atc acg aaa aac aca caa cag tat 547
Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys Asn Thr Gln Gln Tyr
135 140 145

gtg ccc aag gga gtg gtc ggg cag atc acg ccg tgg aat tac cct tta 595
Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro Trp Asn Tyr Pro Leu
150 155 160 165

act ttg gga gta tct gat gct gtt ccg gcg ctg ctg gca gga aac gca 643
Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu Leu Ala Gly Asn Ala
170 175 180

```
gtg gtg gct aaa cct gac ctc gcg aca cct ttc tcc tgc ttg atc atg   691
Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe Ser Cys Leu Ile Met
            185                 190                 195

gtg cac ctg ctc att gaa gcc ggt ctg ccg cgt gat ttg atg cag gtt   739
Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg Asp Leu Met Gln Val
        200                 205                 210

gtc acc ggc cct ggc gat att gtt ggc ggt gcg att gca gct cag tgt   787
Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala Ile Ala Ala Gln Cys
    215                 220                 225

gat ttc ctc atg ttc act gga tcc acg gcc acg ggc cgg atc ttg ggt   835
Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr Gly Arg Ile Leu Gly
230                 235                 240                 245

cgg aca atg ggt gag cgt ttg gtg ggt ttc tct gcg gaa tta ggc gga   883
Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser Ala Glu Leu Gly Gly
                250                 255                 260

aag aac cct ctt att gtg gcc aag gat gca gat ctg gac aag gtg gaa   931
Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp Leu Asp Lys Val Glu
            265                 270                 275

gct gag ctt ccg cag gcg tgt ttt tcc aac tcg ggg caa ttg tgt gtc   979
Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser Gly Gln Leu Cys Val
        280                 285                 290

tcc act gaa cgt att tat gtc gag gaa gac gtg tac gag gag gtg att   1027
Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val Tyr Glu Glu Val Ile
    295                 300                 305

gca cgg ttt agc aag gcg gcg aaa gcc atg tcc att ggt gcc gga ttt   1075
Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser Ile Gly Ala Gly Phe
310                 315                 320                 325

gag tgg aaa tat gag atg ggt tcg ttg atc aat cac gcg cag ctg gat   1123
Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn His Ala Gln Leu Asp
                330                 335                 340

cgg gtg agc acc ttt gtt gat cag gct aaa gct gcg ggc gcc acg gtg   1171
Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala Ala Gly Ala Thr Val
            345                 350                 355

ctg tgc ggt ggc aag tca cgc cct gat att ggt ccc ttc ttc tat gag   1219
Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly Pro Phe Phe Tyr Glu
        360                 365                 370

ccc acg gta ttg gcg gat gtc cca gag ggc acc cca ctg ctc acg gag   1267
Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr Pro Leu Leu Thr Glu
    375                 380                 385

gaa gtc ttc ggg ccg gtg gtg ttc atc gaa aag gta gcc aca ctg gaa   1315
Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys Val Ala Thr Leu Glu
390                 395                 400                 405

gaa gcc gtc gat aag gca aat ggc acg ccc tac ggc ctg aat gcg tcc   1363
Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr Gly Leu Asn Ala Ser
                410                 415                 420
```

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```
gtc ttt ggg tcg tcg gaa acc ggc aat ctt gtt gca ggc cag ctg gaa   1411
Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val Ala Gly Gln Leu Glu
            425                 430                 435

gct ggc ggt atc ggt att aat gat ggc tac gcc gcg acg tgg gcg agc   1459
Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala Ala Thr Trp Ala Ser
        440                 445                 450

gtg tcc acg cct ctg ggt ggc atg aag cag tcg ggg ctg ggg cac cgc   1507
Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser Gly Leu Gly His Arg
    455                 460                 465

cat ggt gcg gag gga att aca aaa tat gcg gag atc cga aac atc gcg   1555
His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu Ile Arg Asn Ile Ala
470                 475                 480                 485

gag cag cgc tgg atg tct atg cgt ggg ccg gcc aaa atg ccg cga aag   1603
Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala Lys Met Pro Arg Lys
                490                 495                 500

gtg tac tca gac acc gtg gcc aca gcg cta aag ctg ggc aaa atc ttt   1651
Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys Leu Gly Lys Ile Phe
            505                 510                 515

aaa gtt ttg ccg tagcaaaaag ccggaccctt gct                        1686
Lys Val Leu Pro
        520
```

US-09-925-150-A

<210> 226
<211> 521
<212> PRT
<213> Corynebacterium glutamicum

<400> 226

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Met Ile Lys Arg Leu Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln
  1               5                  10                  15

Thr Leu Leu Asp Leu Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu
             20                  25                  30

Val Ile Ala Pro Phe Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly
         35                  40                  45

Asp Glu Gln Asp Val Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln
     50                  55                  60

Lys Lys Trp Val His Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu
 65                  70                  75                  80

Lys Val His Asp Leu Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile
                 85                  90                  95

Val Gln Leu Glu Thr Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val
            100                 105                 110

Leu Asp Val Ala Ile Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys
        115                 120                 125

Phe Leu Asn Asp Lys Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys
    130                 135                 140
```

```
Asn Thr Gln Gln Tyr Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro
145                 150                 155                 160

Trp Asn Tyr Pro Leu Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu
                165                 170                 175

Leu Ala Gly Asn Ala Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe
            180                 185                 190

Ser Cys Leu Ile Met Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg
        195                 200                 205

Asp Leu Met Gln Val Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala
    210                 215                 220

Ile Ala Ala Gln Cys Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr
225                 230                 235                 240

Gly Arg Ile Leu Gly Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser
                245                 250                 255

Ala Glu Leu Gly Gly Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp
            260                 265                 270

Leu Asp Lys Val Glu Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser
        275                 280                 285

Gly Gln Leu Cys Val Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val
    290                 295                 300

Tyr Glu Glu Val Ile Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser
305                 310                 315                 320

Ile Gly Ala Gly Phe Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn
                325                 330                 335

His Ala Gln Leu Asp Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala
            340                 345                 350

Ala Gly Ala Thr Val Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly
        355                 360                 365

Pro Phe Phe Tyr Glu Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr
    370                 375                 380

Pro Leu Leu Thr Glu Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys
385                 390                 395                 400

Val Ala Thr Leu Glu Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr
                405                 410                 415

Gly Leu Asn Ala Ser Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val
            420                 425                 430

Ala Gly Gln Leu Glu Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala
        435                 440                 445

Ala Thr Trp Ala Ser Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser
    450                 455                 460
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```
Gly Leu Gly His Arg His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu
465                 470                 475                 480

Ile Arg Asn Ile Ala Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala
                485                 490                 495

Lys Met Pro Arg Lys Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys
            500                 505                 510

Leu Gly Lys Ile Phe Lys Val Leu Pro
        515                 520
```

<210> 227
<211> 1575
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1552)
<223> RXN02674

<400> 227

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atcgacctct agggcagcag tgattgattt cataaaaatc acaagtttgt aactaaaggt 60

acagttggtg aagtatccac aatcaacttt aggagacctt gtg act gca aca ttt   115
                                          Val Thr Ala Thr Phe
                                            1               5

gct gga atc gac gcc acc aaa cac ctc atc gga ggt cag tgg gtg gag   163
Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly Gly Gln Trp Val Glu
                  10                  15                  20

gga aac tcg gat cga att tcc acc aat atc aat cct tac gac gat tcc   211
Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn Pro Tyr Asp Asp Ser
              25                  30                  35

gta atc gcc gaa agc aaa caa gct tcc att gct gat gtt gat gcc gcg   259
Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala Asp Val Asp Ala Ala
          40                  45                  50

tat gaa gcc gcg aag aag gcc cag gct gag tgg gca gct acg ccc gct   307
Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp Ala Ala Thr Pro Ala
      55                  60                  65

gcg gaa cga tct gcc atc atc tac cgt gcg gct gaa ctt ctt gaa gag   355
Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala Glu Leu Leu Glu Glu
  70                  75                  80                  85

cac cgg gag gaa atc gtg gaa tgg ctg atc aag gaa tcc ggc tcg acg   403
His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys Glu Ser Gly Ser Thr
                  90                  95                 100

cgt tcc aag gct aat ttg gaa atc act ttg gca gga aac atc act aaa   451
Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala Gly Asn Ile Thr Lys
              105                 110                 115

gaa tcg gct tca ttc cct ggt cgt gtg cat ggt cga att tct cct tcg   499
Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly Arg Ile Ser Pro Ser
          120                 125                 130
```

```
aat act ccg ggc aaa gaa aac cgt gtg tac cgc gta gcc aag ggc gtt   547
Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg Val Ala Lys Gly Val
    135                 140                 145

gtc gga gtg att agt cca tgg aat ttc cca ctg aac ctc tcg atc cgc   595
Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu Asn Leu Ser Ile Arg
150                 155                 160                 165

tcg gtt gct ccg gca cta gcc gtg ggc aac gcc gta gtg att aag cct   643
Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala Val Val Ile Lys Pro
                170                 175                 180

gcg agt gat acc cca gtt act ggt ggt gta att cct gca cga atc ttt   691
Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile Pro Ala Arg Ile Phe
            185                 190                 195

gag gag gcc gga gtt cct gca ggc gtg atc agc acg gtt gcg ggc gca   739
Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser Thr Val Ala Gly Ala
        200                 205                 210

gga tct gaa atc ggt gat cac ttt gtc acc cac gcc gtg cca aag ctg   787
Gly Ser Glu Ile Gly Asp His Phe Val Thr His Ala Val Pro Lys Leu
    215                 220                 225

att tct ttc acc ggt tca acc cca gtc ggt cgt cgt gtc ggt gag ctg   835
Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg Arg Val Gly Glu Leu
230                 235                 240                 245

gca att aat ggt gga cca atg aaa act gtt gca cta gag ctc ggt ggc   883
Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala Leu Glu Leu Gly Gly
                250                 255                 260

aac gcg ccg ttc gtt gtg ctt gcc gac gcc gac atc gac gcc gct gcc   931
Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp Ile Asp Ala Ala Ala
            265                 270                 275

cag gct gcc gca gtt ggc gct ttc cta cac cag gga cag att tgt atg   979
Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln Gly Gln Ile Cys Met
        280                 285                 290

tca atc aac cga gtc att gtt gat gct gca gtt cat gat gaa ttc cta   1027
Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val His Asp Glu Phe Leu
    295                 300                 305

gag aag ttc gtt gaa gca gtg aag aac att cca acc ggc gat cca agc   1075
Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro Thr Gly Asp Pro Ser
310                 315                 320                 325

gca gaa gga acc ctt gtt gga cct gtc att aat gac agt cag ctc agt   1123
Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn Asp Ser Gln Leu Ser
                330                 335                 340

ggt ttg aag gaa aag atc gag ttg gcc aaa aag gaa ggc gca acc gtc   1171
Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys Glu Gly Ala Thr Val
            345                 350                 355

cag gtt gaa ggg cca att gaa ggc cga ctg gtt cat ccg cat gtg ttc   1219
Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val His Pro His Val Phe
        360                 365                 370
```

```
tct gat gtc acc tct gac atg gaa atc gct cgt gag gaa atc ttc gga   1267
Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg Glu Glu Ile Phe Gly
    375                 380                 385

cct ctc atc agc gtg ctg aag gcc gat gat gag gca cac gca gca gag   1315
Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu Ala His Ala Ala Glu
390                 395                 400                 405

ctg gcc aat gct tcc gac ttt ggt ttg agc gcg gca gtg tgg tcg aag   1363
Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala Ala Val Trp Ser Lys
                410                 415                 420

gat att gat cgt gca gcc cag ttt gct ctg cag att gat tcc ggc atg   1411
Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln Ile Asp Ser Gly Met
            425                 430                 435

gtt cac atc aat gac ctc acc gtc aac gat gaa cca cac gtg atg ttc   1459
Val His Ile Asn Asp Leu Thr Val Asn Asp Glu Pro His Val Met Phe
        440                 445                 450

ggt ggt tca aag aac tct ggc ctc ggc cgc ttc aac ggc gat tgg gcg   1507
Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe Asn Gly Asp Trp Ala
    455                 460                 465

atc gag gag ttc acc aca gat cga tgg atc ggc atc aag cgc agc       1552
Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly Ile Lys Arg Ser
470                 475                 480

taattgtttt tcgacgtaac ccc                                        1575
```

<210> 228
<211> 484
<212> PRT
<213> Corynebacterium glutamicum

<400> 228

```
Val Thr Ala Thr Phe Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly
  1               5                  10                  15

Gly Gln Trp Val Glu Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn
            20                  25                  30

Pro Tyr Asp Asp Ser Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala
        35                  40                  45

Asp Val Asp Ala Ala Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp
    50                  55                  60

Ala Ala Thr Pro Ala Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala
65                  70                  75                  80

Glu Leu Leu Glu Glu His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys
                85                  90                  95

Glu Ser Gly Ser Thr Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala
            100                 105                 110

Gly Asn Ile Thr Lys Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly
        115                 120                 125
```

```
Arg Ile Ser Pro Ser Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg
    130                 135                 140

Val Ala Lys Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu
145                 150                 155                 160

Asn Leu Ser Ile Arg Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala
                165                 170                 175

Val Val Ile Lys Pro Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile
            180                 185                 190

Pro Ala Arg Ile Phe Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser
        195                 200                 205

Thr Val Ala Gly Ala Gly Ser Glu Ile Gly Asp His Phe Val Thr His
    210                 215                 220

Ala Val Pro Lys Leu Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg
225                 230                 235                 240

Arg Val Gly Glu Leu Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala
                245                 250                 255

Leu Glu Leu Gly Gly Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp
            260                 265                 270

Ile Asp Ala Ala Ala Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln
        275                 280                 285

Gly Gln Ile Cys Met Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val
    290                 295                 300

His Asp Glu Phe Leu Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro
305                 310                 315                 320

Thr Gly Asp Pro Ser Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn
                325                 330                 335

Asp Ser Gln Leu Ser Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys
            340                 345                 350

Glu Gly Ala Thr Val Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val
        355                 360                 365

His Pro His Val Phe Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg
    370                 375                 380

Glu Glu Ile Phe Gly Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu
385                 390                 395                 400

Ala His Ala Ala Glu Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala
                405                 410                 415

Ala Val Trp Ser Lys Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln
            420                 425                 430

Ile Asp Ser Gly Met Val His Ile Asn Asp Leu Thr Val Asn Asp Glu
        435                 440                 445

Pro His Val Met Phe Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe
```

DO NOT ENTER

```
    450                 455                 460

Asn Gly Asp Trp Ala Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly
465                 470                 475                 480

Ile Lys Arg Ser
```

<210> 229
<211> 2034
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2011)
<223> RXN00868

<400> 229

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cgatgaccca gcgcacgcct gggttcgaga tacatggacc gggcaagcat ttgatgatcg 60

cttgccatat gagaacgcaa acaaggaggg ataaaatttc atg gct gaa acg aag   115
                                            Met Ala Glu Thr Lys
                                              1               5

aga atg aca gtt agc cag gca ctg gtt gaa ttc ctt ggt cac cag tgg   163
Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe Leu Gly His Gln Trp
                 10                  15                  20

act gtc gac ggc gat atc cgc gag cgc acc att cca ggc atg ttc gga   211
Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile Pro Gly Met Phe Gly
             25                  30                  35

att ttc gga cac gga aac gtt gct ggc att ggc cag gca ctc aag cag   259
Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly Gln Ala Leu Lys Gln
         40                  45                  50

tac aac gtt gaa caa cct gag ctc atg ccg tac tac cag gct cgt aat   307
Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr Tyr Gln Ala Arg Asn
     55                  60                  65

gag cag gcg atg gtg cac cag tct gtt gga tat gca cgc atg cac cgc   355
Glu Gln Ala Met Val His Gln Ser Val Gly Tyr Ala Arg Met His Arg
 70                  75                  80                  85

cgt cgt ggc aca tac gca tct gcc gca tct gtt gga ccc ggc gcg acc   403
Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val Gly Pro Gly Ala Thr
                 90                  95                 100

aac ctg tta acc ggt gcg gct ctt gct acc acc aac cgt ttg cca gcg   451
Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr Asn Arg Leu Pro Ala
            105                 110                 115

ttg ctg ctg cct agt gat act ttt gcc acc cgc gtg gcg gat cca gtg   499
Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg Val Ala Asp Pro Val
        120                 125                 130

ttg cag cag ttg gag cag cca tgg gat atc ggg ctg acg gtt aat gat   547
Leu Gln Gln Leu Glu Gln Pro Trp Asp Ile Gly Leu Thr Val Asn Asp
    135                 140                 145
```

```
gct ttc cgc cct gtg tct aag ttc ttt gat cgg gtg cag cgc ccg gag   595
Ala Phe Arg Pro Val Ser Lys Phe Phe Asp Arg Val Gln Arg Pro Glu
150                 155                 160                 165

cag ttg ttc tct att gcg ttg gct gcg atg cgt gtg ttg act gat ccc   643
Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg Val Leu Thr Asp Pro
                170                 175                 180

gca gaa acc ggt gcg gtc acc att gcg ctt cca gaa gat gtg cag gct   691
Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro Glu Asp Val Gln Ala
            185                 190                 195

gaa atg ctc gat gtg ccg gtg gag ttc ttg cag gat cgt gag tgg cac   739
Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln Asp Arg Glu Trp His
        200                 205                 210

att agg cgc cca cgt cca gag cgt gct gcg ttg gct cgt gcg att gaa   787
Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu Ala Arg Ala Ile Glu
    215                 220                 225

gtc atc aaa aac gct aag aat ccg atg atc att gct ggt ggc gga gtg   835
Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile Ala Gly Gly Gly Val
230                 235                 240                 245

ttg tac tcc gat gcg gaa acg cag ctg cag gca ctt gtg gag cag act   883
Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala Leu Val Glu Gln Thr
                250                 255                 260

ggc att cca gtg ggt acc tcc caa gct ggt ggt ggc gtg ttg gcg tgg   931
Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly Gly Val Leu Ala Trp
            265                 270                 275

gat cat gca caa aac tta ggt ggt gtg ggt gcc acc gga acg ttg gct   979
Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala Thr Gly Thr Leu Ala
        280                 285                 290

gcc aac cgc att gcg ggt gat gct gat gtg atc atc ggt atc ggt act  1027
Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile Ile Gly Ile Gly Thr
    295                 300                 305

cgt tac agc gat ttc acc acc gca tct cgc act gcg ttc caa aac cct  1075
Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr Ala Phe Gln Asn Pro
310                 315                 320                 325

gat gtc acc ttc atc aac atc aat gtt gct tcc ttc gat gct tac aag  1123
Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser Phe Asp Ala Tyr Lys
                330                 335                 340

cat ggc act cag ttg cct gtg att gca gat gca cgc gag gca att gtg  1171
His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala Arg Glu Ala Ile Val
            345                 350                 355

gag ctt gct gaa gcc ctg cag gga ttc acc gtg gca gag gat tac gcg  1219
Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val Ala Glu Asp Tyr Ala
        360                 365                 370

cag cgc atc gcg aag gaa aag gct gcg tgg gac gca gaa gta gat aag  1267
Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp Ala Glu Val Asp Lys
    375                 380                 385
```

US 2004/0259190 A1

```
tct ttt gcc ccc tcc ggt ctt gcg ctg cct gga cag ccg gag atc atc   1315
Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly Gln Pro Glu Ile Ile
390                 395                 400                 405

ggc gcg gtg cag gcg tcg aca agc gaa aaa gac gtc att gtg cag gcc   1363
Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp Val Ile Val Gln Ala
                410                 415                 420

gct gga tcc ttg cct ggt gac ctg cac aag ctg tgg cgt gtg cgc gat   1411
Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu Trp Arg Val Arg Asp
            425                 430                 435

gcg ctg ggc tac cac gtg gaa tat gcg ttc tcg tgc atg ggc tat gaa   1459
Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser Cys Met Gly Tyr Glu
        440                 445                 450

atc gcg ggc ggt atc ggc gcg aag cgt gga ctt gat gcc gca ggc gat   1507
Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu Asp Ala Ala Gly Asp
    455                 460                 465

gac cgc gac gtg gtg atc atg gtt ggt gat ggg tcc tac ctc atg ctc   1555
Asp Arg Asp Val Val Ile Met Val Gly Asp Gly Ser Tyr Leu Met Leu
470                 475                 480                 485

aac act gag ctg gtc acg gcc gtg gca gaa ggt atc aag gtg att gtg   1603
Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly Ile Lys Val Ile Val
                490                 495                 500

gtg ctc atc caa aac cac ggt tat gcc tcc atc ggc cac ctg tct gaa   1651
Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile Gly His Leu Ser Glu
            505                 510                 515

act gtc ggt tcg cag cgt ttt ggt act tgg tac cgc gaa tat gac gct   1699
Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr Arg Glu Tyr Asp Ala
        520                 525                 530

gag gcg aaa aac ttc cag ggc gag cag att ctg cct gtt gac ctg gcg   1747
Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu Pro Val Asp Leu Ala
    535                 540                 545

atg aat gca cgc agc tac ggc atg gat gtc att gaa gtg gaa cca agc   1795
Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile Glu Val Glu Pro Ser
550                 555                 560                 565

gcg aat gcg atc gag gat ctc aaa gca gcg atg gca acc gcg aag gct   1843
Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met Ala Thr Ala Lys Ala
                570                 575                 580

tcg gag aaa tcc acc ttc atc cac atc aac agc gat ccg ttg atc tac   1891
Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser Asp Pro Leu Ile Tyr
            585                 590                 595

gca cca gac ggt gct ggt tgg tgg gac gtg ccg gtg tcg gag acg tcc   1939
Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro Val Ser Glu Thr Ser
        600                 605                 610

act ctg gat agc acc aac gcg gct cgt gaa gat tac ctg aaa aac caa   1987
Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp Tyr Leu Lys Asn Gln
    615                 620                 625

gcc ctc cag cgt ccg ctg ctc ggc taaaccagtt ggctaaacca aaa         2034
```

Ala Leu Gln Arg Pro Leu Leu Gly
630 635

<210> 230
<211> 637
<212> PRT
<213> Corynebacterium glutamicum

<400> 230
Met Ala Glu Thr Lys Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe
1 5 10 15

Leu Gly His Gln Trp Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile
20 25 30

Pro Gly Met Phe Gly Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly
35 40 45

Gln Ala Leu Lys Gln Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr
50 55 60

Tyr Gln Ala Arg Asn Glu Gln Ala Met Val His Gln Ser Val Gly Tyr
65 70 75 80

Ala Arg Met His Arg Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val
85 90 95

Gly Pro Gly Ala Thr Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr
100 105 110

Asn Arg Leu Pro Ala Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg
115 120 125

Val Ala Asp Pro Val Leu Gln Gln Leu Glu Gln Pro Trp Asp Ile Gly
130 135 140

Leu Thr Val Asn Asp Ala Phe Arg Pro Val Ser Lys Phe Phe Asp Arg
145 150 155 160

Val Gln Arg Pro Glu Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg
165 170 175

Val Leu Thr Asp Pro Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro
180 185 190

Glu Asp Val Gln Ala Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln
195 200 205

Asp Arg Glu Trp His Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu
210 215 220

Ala Arg Ala Ile Glu Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile
225 230 235 240

Ala Gly Gly Gly Val Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala
245 250 255

Leu Val Glu Gln Thr Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly
260 265 270

09529129.090502

```
Gly Val Leu Ala Trp Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala
        275                 280                 285

Thr Gly Thr Leu Ala Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile
    290                 295                 300

Ile Gly Ile Gly Thr Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr
305                 310                 315                 320

Ala Phe Gln Asn Pro Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser
                325                 330                 335

Phe Asp Ala Tyr Lys His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala
            340                 345                 350

Arg Glu Ala Ile Val Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val
        355                 360                 365

Ala Glu Asp Tyr Ala Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp
    370                 375                 380

Ala Glu Val Asp Lys Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly
385                 390                 395                 400

Gln Pro Glu Ile Ile Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp
                405                 410                 415

Val Ile Val Gln Ala Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu
            420                 425                 430

Trp Arg Val Arg Asp Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser
        435                 440                 445

Cys Met Gly Tyr Glu Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu
    450                 455                 460

Asp Ala Ala Gly Asp Asp Arg Asp Val Val Ile Met Val Gly Asp Gly
465                 470                 475                 480

Ser Tyr Leu Met Leu Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly
                485                 490                 495

Ile Lys Val Ile Val Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile
            500                 505                 510

Gly His Leu Ser Glu Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr
        515                 520                 525

Arg Glu Tyr Asp Ala Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu
    530                 535                 540

Pro Val Asp Leu Ala Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile
545                 550                 555                 560

Glu Val Glu Pro Ser Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met
                565                 570                 575

Ala Thr Ala Lys Ala Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser
            580                 585                 590

Asp Pro Leu Ile Tyr Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro
```

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595 600 605

Val Ser Glu Thr Ser Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp
610 615 620

Tyr Leu Lys Asn Gln Ala Leu Gln Arg Pro Leu Leu Gly
625 630 635

<210> 231
<211> 1142
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1119)
<223> RXN01143

<400> 231

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atc cca gtt gtc acc acc ttg atg gct ttg ggt act ttc cca gag tct   48
Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser
  1               5                  10                  15

cac gag ctg cac atg ggt atg cca ggc atg cat ggc act gtg tcc gct   96
His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
            20                  25                  30

gtt ggt gca ctg cag cgc agc gac ctg ctg att gct atc ggc tcc cgc   144
Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
        35                  40                  45

ttt gat gac cgc gtc acc ggt gac gtt gac acc ttc gcg cct gac gcc   192
Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
    50                  55                  60

aag atc att cac gcc gac att gat cct gcc gaa atc ggc aag atc aag   240
Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
65                  70                  75                  80

cag gtt gag gtt cca atc gtg ggc gat gcc cgc gaa gtt ctt gct cgt   288
Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
                85                  90                  95

ctg ctg gaa acc acc aag gca agc aag gca gag acc gag gac atc tcc   336
Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
            100                 105                 110

gag tgg gtt gac tac ctc aag ggc ctc aag gca cgt ttc ccg cgt ggc   384
Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
        115                 120                 125

tac gac gag cag cca ggc gat ctg ctg gca cca cag ttt gtc att gaa   432
Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
    130                 135                 140

acc ctg tcc aag gaa gtt ggc ccc gac gca att tac tgc gcc ggc gtt   480
Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
145                 150                 155                 160

ggc cag cac caa atg tgg gca gct cag ttc gtt gac ttt gaa aag cca   528
```

```
Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
                165                 170                 175

cgc acc tgg ctc aac tcc ggt gga ctg ggc acc atg ggc tac gca gtt   576
Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val
            180                 185                 190

cct gcg gcc ctt gga gca aag gct ggc gca cct gac aag gaa gtc tgg   624
Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp
        195                 200                 205

gct atc gac ggc gac ggc tgt ttc cag atg acc aac cag gaa ctc acc   672
Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr
    210                 215                 220

acc gcc gca gtt gaa ggt ttc ccc att aag atc gca cta atc aac aac   720
Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn
225                 230                 235                 240

gga aaa cct ggg gca tgg gtt cgc caa tgg cag acc cta ttc tat gaa   768
Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu
                245                 250                 255

gga cgg tac tca aat act aaa ctt cgt aac cag ggc gag tac atg ccc   816
Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro
            260                 265                 270

gac ttt gtt acc ctt tct gag gga ctt ggc tgt gtt gcc atc cgc gtc   864
Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val
        275                 280                 285

acc aaa gcg gag gaa gta ctg cca gcc atc caa aag gct cga gag atc   912
Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile
    290                 295                 300

aac gac cgc cca gta gtc atc gac ttc atc gtc ggt gaa gac gca cag   960
Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln
305                 310                 315                 320

gta tgg cca atg gtg tct gct gga tca tcc aac tcc gat atc cag tac  1008
Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr
                325                 330                 335

gca ctc gga ttg cgc cca ttc ttt gat ggt gat gaa tct gca gca gaa  1056
Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu
            340                 345                 350

gat cct gcc gac att cac gaa gcc gtc agc gac att gat gcc gcc gtt  1104
Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val
        355                 360                 365

gaa tcg acc gag gca taaggagaga cccaagatgg cta                   1142
Glu Ser Thr Glu Ala
    370
```

<210> 232
<211> 373
<212> PRT
<213> Corynebacterium glutamicum

<400> 232

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Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser
 1               5                  10                  15

His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
            20                  25                  30

Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
        35                  40                  45

Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
    50                  55                  60

Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
65                  70                  75                  80

Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
                85                  90                  95

Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
            100                 105                 110

Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
        115                 120                 125

Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
    130                 135                 140

Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
145                 150                 155                 160

Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro
                165                 170                 175

Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val
            180                 185                 190

Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp
        195                 200                 205

Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr
    210                 215                 220

Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn
225                 230                 235                 240

Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu
                245                 250                 255

Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro
            260                 265                 270

Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val
        275                 280                 285

Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile
    290                 295                 300

Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln
305                 310                 315                 320
```

Replacement Sheet

```
Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr
                325                 330                 335

Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu
            340                 345                 350

Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val
        355                 360                 365

Glu Ser Thr Glu Ala
    370
```

<210> 233
<211> 793
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXN01146

<400> 233

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tatttagtaa aggagccaga aagtcgtgaa tgtggcagct tctcaacagc ccactcccgc 60

cacggttgca agccgtggtc gatccgccgc ccctgagcgg atg aca ggt gca aag   115
                                              Met Thr Gly Ala Lys
                                                1               5

gca att gtt cga tcg ctc gag gag ctt aac gcc gac atc gtg ttc ggt   163
Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala Asp Ile Val Phe Gly
                10                  15                  20

att cct ggt ggt gcg gtg cta ccg gtg tat gac ccg ctc tat tcc tcc   211
Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp Pro Leu Tyr Ser Ser
            25                  30                  35

aca aag gtg cgc cac gtc ttg gtg cgc cac gag cag ggc gca ggc cac   259
Thr Lys Val Arg His Val Leu Val Arg His Glu Gln Gly Ala Gly His
        40                  45                  50

gca gca acc ggc tac gcg cag gtt act gga cgc gtt ggc gtc tgc att   307
Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg Val Gly Val Cys Ile
    55                  60                  65

gca acc tct ggc cca gga gca acc aac ttg gtt acc cca atc gct gat   355
Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Pro Ile Ala Asp
70                  75                  80                  85

gca aac ttg gac tcc gtt ccc atg gtt gcc atc acc ggc cag gtc gga   403
Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile Thr Gly Gln Val Gly
                90                  95                  100

agt ggc ctg ctg ggt acc gac gct ttc cag gaa gcc gat atc cgc ggc   451
Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu Ala Asp Ile Arg Gly
            105                 110                 115

atc acc atg cca gtg acc aag cac aac ttc atg gtc acc aac cct aac   499
Ile Thr Met Pro Val Thr Lys His Asn Phe Met Val Thr Asn Pro Asn
        120                 125                 130
```

```
gac att cca cag gca ttg gct gag gca ttc cac ctc gcg att act ggt   547
Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His Leu Ala Ile Thr Gly
    135                 140                 145

cgc cct ggc cct gtt ctg gtg gat att cct aag gat gtc cag aac gct   595
Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys Asp Val Gln Asn Ala
150                 155                 160                 165

gaa ttg gat ttc gtc tgg cca cca aag atc gac ctg cca ggc tac cgc   643
Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp Leu Pro Gly Tyr Arg
                170                 175                 180

cca gtt tca aca cca cat gct cgc cag atc gag cag gca gtc aag ctg   691
Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu Gln Ala Val Lys Leu
            185                 190                 195

atc ggt gag gcc aag aag ccc gtc ctt tac gtt ggt ggt ggc gta atc   739
Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val Gly Gly Gly Val Ile
        200                 205                 210

aag gct gac gca cac gaa gag ctt cgt gcg ttc gct gag tac acc ggc   787
Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe Ala Glu Tyr Thr Gly
    215                 220                 225

atc cca                                                          793
Ile Pro
230
```

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<210> 234
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 234

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Met Thr Gly Ala Lys Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala
  1               5                  10                  15

Asp Ile Val Phe Gly Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp
            20                  25                  30

Pro Leu Tyr Ser Ser Thr Lys Val Arg His Val Leu Val Arg His Glu
        35                  40                  45

Gln Gly Ala Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg
    50                  55                  60

Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
65                  70                  75                  80

Thr Pro Ile Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
                85                  90                  95

Thr Gly Gln Val Gly Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu
            100                 105                 110

Ala Asp Ile Arg Gly Ile Thr Met Pro Val Thr Lys His Asn Phe Met
        115                 120                 125

Val Thr Asn Pro Asn Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His
```

```
    130                 135                 140

Leu Ala Ile Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys
145                 150                 155                 160

Asp Val Gln Asn Ala Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp
                165                 170                 175

Leu Pro Gly Tyr Arg Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu
            180                 185                 190

Gln Ala Val Lys Leu Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val
        195                 200                 205

Gly Gly Gly Val Ile Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe
    210                 215                 220

Ala Glu Tyr Thr Gly Ile Pro
225                 230
```

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<210> 235
<211> 639
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(616)
<223> RXN01144

<400> 235

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ggtgatgaat ctgcagcaga agatcctgcc gacattcacg aagccgtcag cgacattgat 60

gccgccgttg aatcgaccga ggcataagga gagacccaag atg gct aat tct gac   115
                                              Met Ala Asn Ser Asp
                                                1               5

gtc acc cgc cac atc ctg tcc gta ctc gtt cag gac gta gac gga atc   163
Val Thr Arg His Ile Leu Ser Val Leu Val Gln Asp Val Asp Gly Ile
                10                  15                  20

att tcc cgc gta tca ggt atg ttc acc cga cgc gca ttc aac ctc gtg   211
Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg Ala Phe Asn Leu Val
            25                  30                  35

ttc ctc gtg tct gca aag acc gaa aca cac ggc atc aac cgc atc acg   259
Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly Ile Asn Arg Ile Thr
        40                  45                  50

gtt gtt gtc gac gcc gac gag ctc aac att gag cag atc acc aag cag   307
Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu Gln Ile Thr Lys Gln
    55                  60                  65

ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg cga ctt gat gaa gag   355
Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val Arg Leu Asp Glu Glu
70                  75                  80                  85

acc act atc gcc cgc gca atc atg ctg gtt aag gtc tct gcg gac agc   403
Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys Val Ser Ala Asp Ser
                90                  95                  100
```

```
acc aac cgt ccg cag atc gtc gac gcc gcg aac atc ttc cgc gcc cga   451
Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn Ile Phe Arg Ala Arg
            105                 110                 115

gtc gtc gac gtg gct cca gac tct gtg gtt att gaa tcc aca ggc acc   499
Val Val Asp Val Ala Pro Asp Ser Val Val Ile Glu Ser Thr Gly Thr
        120                 125                 130

cca ggc aag ctc cgc gca ctg ctt gac gtg atg gaa cca ttc gga atc   547
Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met Glu Pro Phe Gly Ile
    135                 140                 145

cgc gaa ctg atc caa tcc gga cag att gca ctc aac cgc ggt ccg aag   595
Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu Asn Arg Gly Pro Lys
150                 155                 160                 165

acc atg gct ccg gcc aag atc taaacagcaa ttaatctgat tgc             639
Thr Met Ala Pro Ala Lys Ile
                170
```

SEQUENCE LISTING

<210> 236
<211> 172
<212> PRT
<213> Corynebacterium glutamicum

<400> 236

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Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
  1               5                  10                  15

Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg
            20                  25                  30

Ala Phe Asn Leu Val Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly
        35                  40                  45

Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
    50                  55                  60

Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
65                  70                  75                  80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
                85                  90                  95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
            100                 105                 110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
        115                 120                 125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
    130                 135                 140

Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
145                 150                 155                 160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
                165                 170
```

<210> 237
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXA02474

<400> 237
tgctggtcta ttgtggcgac cgagggcctt tgaaggttcg acaaactgta taaggccttg 60

aatcttgaga atttattttg aggaagcaag aggaagtgtc atg agc aaa gtt gca 115
Met Ser Lys Val Ala
1 5

atg gtt acc ggt ggt gca caa ggc atc ggt cgt gga att tca gag aag 163
Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg Gly Ile Ser Glu Lys
10 15 20

ctg gca gca gat ggt ttc gat att gcc gta gcc gac ctg cca caa cag 211
Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala Asp Leu Pro Gln Gln
25 30 35

gaa gaa caa gct gca gag acc atc aag ttg att gaa gct gca ggt caa 259
Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile Glu Ala Ala Gly Gln
40 45 50

aag gct gta ttc gtt gga tta gat gtc acc gat aag gct aat ttc gac 307
Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp Lys Ala Asn Phe Asp
55 60 65

agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta 355
Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu
70 75 80 85

gta aac aac gcc ggc atc gca caa att aag cca ctt ctg gaa gtc acc 403
Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro Leu Leu Glu Val Thr
90 95 100

gaa gaa gac cta aag cag atc tac tcc gtg aac gtt ttt agc gta ttt 451
Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn Val Phe Ser Val Phe
105 110 115

ttt ggt att caa gca gca tcc cga aag ttc gat gag ctt ggc gta aaa 499
Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys
120 125 130

ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca 547
Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro
135 140 145

atc ttg agc gcc tac tcc acc acc aaa ttc gcg gtt cgt ggc ctc acc 595
Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr
150 155 160 165

cag gct gct gcg caa gaa ctc gca ccc aag ggt cac acc gtg aat gcc 643
Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly His Thr Val Asn Ala
170 175 180

```
tac gca cct ggc atc gtg ggc acc gga atg tgg gag caa atc gat gcc   691
Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp Glu Gln Ile Asp Ala
            185                 190                 195

gag ctt tcc aag atc aac ggc aag cca atc ggt gag aac ttc aag gag   739
Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu
        200                 205                 210

tac tcc tcc tca atc gca ttg ggc cga cca tca gta cct gag gat gta   787
Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser Val Pro Glu Asp Val
    215                 220                 225

gcc ggt ctg gtt tcg ttc ctg gct tct gaa aac tcc aac tac atc acc   835
Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn Ser Asn Tyr Ile Thr
230                 235                 240                 245

gga cag gtc atg ctt gtc gac ggc ggc atg ctc tac aac taggggttgc   884
Gly Gln Val Met Leu Val Asp Gly Gly Met Leu Tyr Asn
                250                 255

tttcccgcac tca                                                  897
```

<210> 238
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 238

```
Met Ser Lys Val Ala Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg
  1               5                  10                  15

Gly Ile Ser Glu Lys Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala
            20                  25                  30

Asp Leu Pro Gln Gln Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile
        35                  40                  45

Glu Ala Ala Gly Gln Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp
    50                  55                  60

Lys Ala Asn Phe Asp Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly
65                  70                  75                  80

Gly Phe Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro
                85                  90                  95

Leu Leu Glu Val Thr Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn
            100                 105                 110

Val Phe Ser Val Phe Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp
        115                 120                 125

Glu Leu Gly Val Lys Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala
    130                 135                 140

Ile Gln Gly Phe Pro Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala
145                 150                 155                 160

Val Arg Gly Leu Thr Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly
```

```
                165                 170                 175

His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp
            180                 185                 190

Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly
        195                 200                 205

Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser
    210                 215                 220

Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn
225                 230                 235                 240

Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu
                245                 250                 255

Tyr Asn
```

US 2009/0246842 A1

<210> 239
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXA02453

<400> 239

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aaccaacaaa ggtcatctca accggcttaa gaaaattctg ccagctttct gctgattgaa 60

tcgtgccagc tcagggcata tctcacctaa agtaaacacc atg aaa tca atc ttc   115
                                            Met Lys Ser Ile Phe
                                              1               5

att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt   163
Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe
                10                  15                  20

ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc   211
Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr
            25                  30                  35

tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc   259
Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser
        40                  45                  50

gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc   307
Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly
    55                  60                  65

acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg   355
Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro
70                  75                  80                  85

ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac   403
Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn
                90                  95                  100
```

```
gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg   451
Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala
            105                 110                 115

cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg   499
Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val
        120                 125                 130

tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc   547
Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val
    135                 140                 145

gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att   595
Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile
150                 155                 160                 165

cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac   643
Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn
                170                 175                 180

ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg   691
Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro
            185                 190                 195

gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct cgg   739
Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg
        200                 205                 210

tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg   787
Trp Ala Lys Gly Lys Val His His Gly Val Ser Lys Leu Asp Lys Ala
    215                 220                 225

ctg tat ctc atg aaa tct ctg tcg cct gat cgg gta gcg atg tgt ttt   835
Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe
230                 235                 240                 245

gcg cga cta atc gcc gga taaatgaatt gattatttta ggc                876
Ala Arg Leu Ile Ala Gly
                250
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<210> 240
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 240

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Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala
  1               5                  10                  15

Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp
             20                  25                  30

Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu
         35                  40                  45

Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala
     50                  55                  60

Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val
```

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 65                  70                  75                  80

Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys
                85                  90                  95

Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala
            100                 105                 110

His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser
        115                 120                 125

Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala
    130                 135                 140

Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp
145                 150                 155                 160

Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys
                165                 170                 175

Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly
            180                 185                 190

Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val
        195                 200                 205

His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser
    210                 215                 220

Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg
225                 230                 235                 240

Val Ala Met Cys Phe Ala Arg Leu Ile Ala Gly
                245                 250
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09525450.090306

<210> 241
<211> 1140
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1117)
<223> RXS01758

<400> 241
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ccccccttatt cagagtgatg gtctaccgga gaagtaccca gaccaatagc atcgaccaac 60

gatagcgcgc tcagaagttc tttagtgaaa gcagaaccaa atg ccc aaa tac att   115
                                            Met Pro Lys Tyr Ile
                                              1               5

gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg   163
Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val
                  10                  15                  20

caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct   211
Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala
             25                  30                  35
```

```
agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag   259
Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys
         40                  45                  50

cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc   307
His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile
     55                  60                  65

gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt   355
Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val
 70                  75                  80                  85

gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt   403
Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg
                 90                  95                 100

gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct   451
Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser
            105                 110                 115

tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt   499
Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu
        120                 125                 130

gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc   547
Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly
    135                 140                 145

tgc gca ggt gtg aca aca ttc aat gcg ttg cga aac ctg aag ctg gat   595
Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp
150                 155                 160                 165

ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta   643
Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu
                170                 175                 180

gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc   691
Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala
            185                 190                 195

cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac   739
Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His
        200                 205                 210

tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt   787
Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu
    215                 220                 225

ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt   835
Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu
230                 235                 240                 245

tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc   883
Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile
                250                 255                 260

gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg   931
Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met
            265                 270                 275

aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg   979
```

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Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr
        280                 285                 290

gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att   1027
Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile
    295                 300                 305

gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca   1075
Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser
310                 315                 320                 325

gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca           1117
Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser
                330                 335

taatgccaac agcaagccca att                                        1140


<210> 242
<211> 339
<212> PRT
<213> Corynebacterium glutamicum

<400> 242
Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu
  1               5                  10                  15

Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg
             20                  25                  30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
         35                  40                  45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
     50                  55                  60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
 65                  70                  75                  80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
                 85                  90                  95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys
            100                 105                 110

Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val
        115                 120                 125

Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu
    130                 135                 140

Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg
145                 150                 155                 160

Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly
                165                 170                 175

Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg
            180                 185                 190

Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln
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```
        195                 200                 205

Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln
    210                 215                 220

Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser
225                 230                 235                 240

Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly
                245                 250                 255

Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala
            260                 265                 270

Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
        275                 280                 285

Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
    290                 295                 300

Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
305                 310                 315                 320

Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
                325                 330                 335

Pro Asn Ser



<210> 243
<211> 1665
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1642)
<223> RXA02737

<400> 243
agcacgctgc atcagtaacg gcgacatgaa atcgaattag ttcgatctta tgtggccgtt 60

acacatcttt cattaaagaa aggatcgtga cactaccatc gtg agc aca aac acg   115
                                            Val Ser Thr Asn Thr
                                              1               5

acc ccc tcc agc tgg aca aac cca ctg cgc gac ccg cag gat aaa cga   163
Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp Pro Gln Asp Lys Arg
                10                  15                  20

ctc ccc cgc atc gct ggc cct tcc ggc atg gtg atc ttc ggt gtc act   211
Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val Ile Phe Gly Val Thr
            25                  30                  35

ggc gac ttg gct cga aag aag ctg ctc ccc gcc att tat gat cta gca   259
Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala Ile Tyr Asp Leu Ala
        40                  45                  50

aac cgc gga ttg ctg ccc cca gga ttc tcg ttg gta ggt tac ggc cgc   307
Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu Val Gly Tyr Gly Arg
```

```
     55                  60                  65

cgc gaa tgg tcc aaa gaa gac ttt gaa aaa tac gta cgc gat gcc gca   355
Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr Val Arg Asp Ala Ala
 70                  75                  80                  85

agt gct ggt gct cgt acg gaa ttc cgt gaa aat gtt tgg gag cgc ctc   403
Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn Val Trp Glu Arg Leu
                 90                  95                 100

gcc gag ggt atg gaa ttt gtt cgc ggc aac ttt gat gat gat gca gct   451
Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe Asp Asp Asp Ala Ala
            105                 110                 115

ttc gac aac ctc gct gca aca ctc aag cgc atc gac aaa acc cgc ggc   499
Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile Asp Lys Thr Arg Gly
        120                 125                 130

acc gcc ggc aac tgg gct tac tac ctg tcc att cca cca gat tcc ttc   547
Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile Pro Pro Asp Ser Phe
    135                 140                 145

aca gcg gtc tgc cac cag ctg gag cgt tcc ggc atg gct gaa tcc acc   595
Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly Met Ala Glu Ser Thr
150                 155                 160                 165

gaa gaa gca tgg cgc cgc gtg atc atc gag aag cct ttc ggc cac aac   643
Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys Pro Phe Gly His Asn
                170                 175                 180

ctc gaa tcc gca cac gag ctc aac cag ctg gtc aac gca gtc ttc cca   691
Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val Asn Ala Val Phe Pro
            185                 190                 195

gaa tct tct gtg ttc cgc atc gac cac tat ttg ggc aag gaa aca gtt   739
Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu Gly Lys Glu Thr Val
        200                 205                 210

caa aac atc ctg gct ctg cgt ttt gct aac cag ctg ttt gag cca ctg   787
Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln Leu Phe Glu Pro Leu
    215                 220                 225

tgg aac tcc aac tac gtt gac cac gtc cag atc acc atg gct gaa gat   835
Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile Thr Met Ala Glu Asp
230                 235                 240                 245

att ggc ttg ggt gga cgt gct ggt tac tac gac ggc atc ggc gca gcc   883
Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp Gly Ile Gly Ala Ala
                250                 255                 260

cgc gac gtc atc cag aac cac ctg atc cag ctc ttg gct ctg gtt gcc   931
Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu Leu Ala Leu Val Ala
            265                 270                 275

atg gaa gaa cca att tct ttc gtg cca gcg cag ctg cag gca gaa aag   979
Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln Leu Gln Ala Glu Lys
        280                 285                 290

atc aag gtg ctc tct gcg aca aag ccg tgc tac cca ttg gat aaa acc  1027
Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr Pro Leu Asp Lys Thr
    295                 300                 305
```

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```
tcc gct cgt ggt cag tac gct gcc ggt tgg cag ggc tct gag tta gtc   1075
Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln Gly Ser Glu Leu Val
310                 315                 320                 325

aag gga ctt cgc gaa gaa gat ggc ttc aac cct gag tcc acc act gag   1123
Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro Glu Ser Thr Thr Glu
                330                 335                 340

act ttt gcg gct tgt acc tta gag atc acg tct cgt cgc tgg gct ggt   1171
Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser Arg Arg Trp Ala Gly
            345                 350                 355

gtg ccg ttc tac ctg cgc acc ggt aag cgt ctt ggt cgc cgt gtt act   1219
Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu Gly Arg Arg Val Thr
        360                 365                 370

gag att gcc gtg gtg ttt aaa gac gca cca cac cag cct ttc gac ggc   1267
Glu Ile Ala Val Val Phe Lys Asp Ala Pro His Gln Pro Phe Asp Gly
    375                 380                 385

gac atg act gta tcc ctt ggc caa aac gcc atc gtg att cgc gtg cag   1315
Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile Val Ile Arg Val Gln
390                 395                 400                 405

cct gat gaa ggt gtg ctc atc cgc ttc ggt tcc aag gtt cca ggt tct   1363
Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser Lys Val Pro Gly Ser
                410                 415                 420

gcc atg gaa gtc cgt gac gtc aac atg gac ttc tcc tac tca gaa tcc   1411
Ala Met Glu Val Arg Asp Val Asn Met Asp Phe Ser Tyr Ser Glu Ser
            425                 430                 435

ttc act gaa gaa tca cct gaa gca tac gag cgc ctc att ttg gat gcg   1459
Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg Leu Ile Leu Asp Ala
        440                 445                 450

ctg tta gat gaa tcc agc ctc ttc cct acc aac gag gaa gtg gaa ctg   1507
Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn Glu Glu Val Glu Leu
    455                 460                 465

agc tgg aag att ctg gat cca att ctt gaa gca tgg gat gcc gat gga   1555
Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala Trp Asp Ala Asp Gly
470                 475                 480                 485

gaa cca gag gat tac cca gcg ggt acg tgg ggt cca aag agc gct gat   1603
Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly Pro Lys Ser Ala Asp
                490                 495                 500

gaa atg ctt tcc cgc aac ggt cac acc tgg cgc agg cca taatttaggg    1652
Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg Arg Pro
            505                 510

gcaaaaaatg atc                                                   1665
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<210> 244
<211> 514
<212> PRT
<213> Corynebacterium glutamicum

<400> 244

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Val Ser Thr Asn Thr Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp
  1               5                  10                  15

Pro Gln Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val
             20                  25                  30

Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala
         35                  40                  45

Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu
     50                  55                  60

Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr
 65                  70                  75                  80

Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn
                 85                  90                  95

Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe
            100                 105                 110

Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile
        115                 120                 125

Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile
    130                 135                 140

Pro Pro Asp Ser Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
145                 150                 155                 160

Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys
                165                 170                 175

Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val
            180                 185                 190

Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu
        195                 200                 205

Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln
    210                 215                 220

Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile
225                 230                 235                 240

Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp
                245                 250                 255

Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu
            260                 265                 270

Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln
        275                 280                 285

Leu Gln Ala Glu Lys Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr
    290                 295                 300

Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln
305                 310                 315                 320
```

```
Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro
                325                 330                 335

Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser
            340                 345                 350

Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu
        355                 360                 365

Gly Arg Arg Val Thr Glu Ile Ala Val Val Phe Lys Asp Ala Pro His
    370                 375                 380

Gln Pro Phe Asp Gly Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile
385                 390                 395                 400

Val Ile Arg Val Gln Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser
                405                 410                 415

Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe
            420                 425                 430

Ser Tyr Ser Glu Ser Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg
        435                 440                 445

Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn
    450                 455                 460

Glu Glu Val Glu Leu Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala
465                 470                 475                 480

Trp Asp Ala Asp Gly Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly
                485                 490                 495

Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg
            500                 505                 510

Arg Pro
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DO NOT ENTER ABOVE THIS LINE

<210> 245
<211> 1203
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1180)
<223> RXA02738

<400> 245
ttgttgttaa tcggtacaaa gggtcttaag cacatccctt acttgcctgc tctccttgag 60

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cacagttcaa gaacaattct tttaaggaaa atttagtttc atg tct cac att gat   115
                                              Met Ser His Ile Asp
                                                1               5

gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac ctc tcc cgc   163
Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp Leu Ser Arg
                10                  15                  20
```

```
gag cgc att act tcc ggc aat ctc agc cag gtt att gag gaa aag tct   211
Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu Glu Lys Ser
             25                  30                  35

gta gtc ggt gtc acc acc aac cca gct att ttc gca gca gca atg tcc   259
Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala Ala Met Ser
         40                  45                  50

aag ggc gat tcc tac gac gct cag atc gca gag ctc aag gcc gct ggc   307
Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys Ala Ala Gly
     55                  60                  65

gca tct gtt gac cag gct gtt tac gcc atg agc atc gac gac gtt cgc   355
Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp Asp Val Arg
 70                  75                  80                  85

aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc aac ggc tac   403
Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser Asn Gly Tyr
                 90                  95                 100

gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct gct gac cgc   451
Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser Ala Asp Arg
            105                 110                 115

gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag gtt gat cgt   499
Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys Val Asp Arg
        120                 125                 130

cca aac gtc atg atc aag atc cct gca acc cca ggt tct ttg cca gca   547
Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser Leu Pro Ala
    135                 140                 145

atc acc gac gct ttg gct gag ggc atc agc gtt aac gtc acc ttg atc   595
Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val Thr Leu Ile
150                 155                 160                 165

ttc tcc gtt gct cgc tac cgc gag gtc atc gct gcg ttc atc gag ggc   643
Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Phe Ile Glu Gly
                170                 175                 180

atc aag cag gct gct gca aac ggc cac gac gtc tcc aag atc cac tct   691
Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val Ser Lys Ile His Ser
            185                 190                 195

gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt gag atc gac aag cgc   739
Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile Asp Lys Arg
        200                 205                 210

ctc gag gca atc gga tcc gat gag gct ttg gct ctg cgc ggc aag gca   787
Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Leu Arg Gly Lys Ala
    215                 220                 225

ggc gtt gcc aac gct cag cgc gct tac gct gtg tac aag gag ctt ttc   835
Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val Tyr Lys Glu Leu Phe
230                 235                 240                 245

gac gcc gcc gag ctg cct gaa ggt gcc aac act cag cgc cca ctg tgg   883
Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg Pro Leu Trp
                250                 255                 260

gca tcc acc ggc gtg aag aac cct gcg tac gct gca act ctt tac gtt   931
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US 2006/0234360 A1

```
Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala Ala Thr Leu Tyr Val
            265                 270                 275

tcc gag ctg gct ggt cca aac acc gtc aac acc atg cca gaa ggc acc   979
Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro Glu Gly Thr
        280                 285                 290

atc gac gcg gtt ctg gag cag ggc aac ctg cac ggt gac acc ctg tcc   1027
Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His Gly Asp Thr Leu Ser
    295                 300                 305

aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt gag gct ctg   1075
Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser Gln Leu Glu Ala Leu
310                 315                 320                 325

ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc gag ggt gtg   1123
Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr Glu Gly Val
                330                 335                 340

gac aag ttc gtt gct tct tgg agc gaa ctg ctt gag tcc atg gaa gct   1171
Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser Met Glu Ala
            345                 350                 355

cgc ctg aag tagaatcagc acgctgcatc agt                            1203
Arg Leu Lys
        360
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US 2005/0153417 A1

<210> 246
<211> 360
<212> PRT
<213> Corynebacterium glutamicum

<400> 246

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Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu
  1               5                  10                  15

Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val
             20                  25                  30

Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe
         35                  40                  45

Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
     50                  55                  60

Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
 65                  70                  75                  80

Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
                 85                  90                  95

Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
            100                 105                 110

Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
        115                 120                 125

Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
    130                 135                 140
```

```
Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
145                 150                 155                 160

Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala
                165                 170                 175

Ala Phe Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val
            180                 185                 190

Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val
        195                 200                 205

Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala
    210                 215                 220

Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val
225                 230                 235                 240

Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr
                245                 250                 255

Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala
            260                 265                 270

Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr
        275                 280                 285

Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His
    290                 295                 300

Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
305                 310                 315                 320

Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
                325                 330                 335

Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu
            340                 345                 350

Glu Ser Met Glu Ala Arg Leu Lys
        355                 360


<210> 247
<211> 2223
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2200)
<223> RXA02739

<400> 247
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aacgaaccaa aactttggtc ccggtttaac ccaggaagga ttg acc acc ttg acg   115
                                                Leu Thr Thr Leu Thr
                                                  1               5

ctg tca cct gaa ctt cag gcg ctc act gta cgc aat tac ccc tct gat   163
```

```
Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg Asn Tyr Pro Ser Asp
                10                  15                  20

tgg tcc gat gtg gac acc aag gct gta gac act gtt cgt gtc ctc gct   211
Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr Val Arg Val Leu Ala
            25                  30                  35

gca gac gct gta gaa aac tgt ggc tcc ggc cac cca ggc acc gca atg   259
Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His Pro Gly Thr Ala Met
        40                  45                  50

agc ctg gct ccc ctt gca tac acc ttg tac cag cgg gtt atg aac gta   307
Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln Arg Val Met Asn Val
    55                  60                  65

gat cca cag gac acc aac tgg gca ggc cgt gac cgc ttc gtt ctt tct   355
Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp Arg Phe Val Leu Ser
70                  75                  80                  85

tgt ggc cac tcc tct ttg acc cag tac atc cag ctt tac ttg ggt gga   403
Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln Leu Tyr Leu Gly Gly
                90                  95                  100

ttc ggc ctt gag atg gat gac ctg aag gct ctg cgc acc tgg gat tcc   451
Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu Arg Thr Trp Asp Ser
            105                 110                 115

ttg acc cca gga cac cct gag tac cgc cac acc aag ggc gtt gag atc   499
Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr Lys Gly Val Glu Ile
        120                 125                 130

acc act ggc cct ctt ggc cag ggt ctt gca tct gca gtt ggt atg gcc   547
Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser Ala Val Gly Met Ala
    135                 140                 145

atg gct gct cgt cgt gag cgt ggc cta ttc gac cca acc gct gct gag   595
Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp Pro Thr Ala Ala Glu
150                 155                 160                 165

ggc gaa tcc cca ttc gac cac cac atc tac gtc att gct tct gat ggt   643
Gly Glu Ser Pro Phe Asp His His Ile Tyr Val Ile Ala Ser Asp Gly
                170                 175                 180

gac ctg cag gaa ggt gtc acc tct gag gca tcc tcc atc gct ggc acc   691
Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser Ser Ile Ala Gly Thr
            185                 190                 195

cag cag ctg ggc aac ctc atc gtg ttc tgg gat gac aac cgc atc tcc   739
Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp Asp Asn Arg Ile Ser
        200                 205                 210

atc gaa gac aac act gag atc gct ttc aac gag gac gtt gtt gct cgt   787
Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu Asp Val Val Ala Arg
    215                 220                 225

tac aag gct tac ggc tgg cag acc att gag gtt gag gct ggc gag gac   835
Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val Glu Ala Gly Glu Asp
230                 235                 240                 245

gtt gca gca atc gaa gct gca gtg gct gag gct aag aag gac acc aag   883
Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala Lys Lys Asp Thr Lys
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                250                 255                 260

cga cct acc ttc atc cgc gtt cgc acc atc atc ggc ttc cca gct cca   931
Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile Gly Phe Pro Ala Pro
            265                 270                 275

act atg atg aac acc ggt gct gtg cac ggt gct gct ctt ggc gca gct   979
Thr Met Met Asn Thr Gly Ala Val His Gly Ala Ala Leu Gly Ala Ala
        280                 285                 290

gag gtt gca gca acc aag act gag ctt gga ttc gat cct gag gct cac   1027
Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe Asp Pro Glu Ala His
    295                 300                 305

ttc gcg atc gac gat gag gtt atc gct cac acc cgc tcc ctc gca gag   1075
Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr Arg Ser Leu Ala Glu
310                 315                 320                 325

cgc gct gca cag aag aag gct gca tgg cag gtc aag ttc gat gag tgg   1123
Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val Lys Phe Asp Glu Trp
                330                 335                 340

gca gct gcc aac cct gag aac aag gct ctg ttc gat cgc ctg aac tcc   1171
Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe Asp Arg Leu Asn Ser
            345                 350                 355

cgt gag ctt cca gcg ggc tac gct gac gag ctc cca aca tgg gat gca   1219
Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu Pro Thr Trp Asp Ala
        360                 365                 370

gat gag aag ggc gtc gca act cgt aag gct tcc gag gct gca ctt cag   1267
Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser Glu Ala Ala Leu Gln
    375                 380                 385

gca ctg ggc aag acc ctt cct gag ctg tgg ggc ggt tcc gct gac ctc   1315
Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly Gly Ser Ala Asp Leu
390                 395                 400                 405

gca ggt tcc aac aac acc gtg atc aag ggc tcc cct tcc ttc ggc cct   1363
Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser Pro Ser Phe Gly Pro
                410                 415                 420

gag tcc atc tcc acc gag acc tgg tct gct gag cct tac ggc cgt aac   1411
Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu Pro Tyr Gly Arg Asn
            425                 430                 435

ctg cac ttc ggt atc cgt gag cac gct atg gga tcc atc ctc aac ggc   1459
Leu His Phe Gly Ile Arg Glu His Ala Met Gly Ser Ile Leu Asn Gly
        440                 445                 450

att tcc ctc cac ggt ggc acc cgc cca tac ggc gga acc ttc ctc atc   1507
Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly Gly Thr Phe Leu Ile
    455                 460                 465

ttc tcc gac tac atg cgt cct gca gtt cgt ctt gca gct ctc atg gag   1555
Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu Ala Ala Leu Met Glu
470                 475                 480                 485

acc gac gct tac tac gtc tgg acc cac gac tcc atc ggt ctg ggc gaa   1603
Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser Ile Gly Leu Gly Glu
                490                 495                 500
```

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gat ggc cca acc cac cag cct gtt gaa acc ttg gct gca ctg cgc gcc   1651
Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu Ala Ala Leu Arg Ala
            505                 510                 515

atc cca ggt ctg tcc gtc ctg cgt cct gca gat gcg aac gag acc gcc   1699
Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp Ala Asn Glu Thr Ala
        520                 525                 530

cag gct tgg gct gca gca ctt gag tac aag gaa ggc cct aag ggt ctt   1747
Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu Gly Pro Lys Gly Leu
    535                 540                 545

gca ctg acc cgc cag aac gtt cct gtt ctg gaa ggc acc aag gag aag   1795
Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu Gly Thr Lys Glu Lys
550                 555                 560                 565

gct gct gaa ggc gtt cgc cgc ggt ggc tac gtc ctg gtt gag ggt tcc   1843
Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val Leu Val Glu Gly Ser
                570                 575                 580

aag gaa acc cca gat gtg atc ctc atg ggc tcc ggc tcc gag gtt cag   1891
Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser Gly Ser Glu Val Gln
            585                 590                 595

ctt gca gtt aac gct gcg aag gct ctg gaa gct gag ggc gtt gca gct   1939
Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala Glu Gly Val Ala Ala
        600                 605                 610

cgc gtt gtt tcc gtt cct tgc atg gat tgg ttc cag gag cag gac gca   1987
Arg Val Val Ser Val Pro Cys Met Asp Trp Phe Gln Glu Gln Asp Ala
    615                 620                 625

gag tac atc gag tcc gtt ctg cct gca gct gtg acc gct cgt gtg tct   2035
Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val Thr Ala Arg Val Ser
630                 635                 640                 645

gtt gaa gct ggc atc gca atg cct tgg tac cgc ttc ttg ggc acc cag   2083
Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg Phe Leu Gly Thr Gln
                650                 655                 660

ggc cgt gct gtc tcc ctt gag cac ttc ggt gct tct gcg gat tac cag   2131
Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala Ser Ala Asp Tyr Gln
            665                 670                 675

acc ctg ttt gag aag ttc ggc atc acc acc gat gca gtc gtg gca gcg   2179
Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp Ala Val Val Ala Ala
        680                 685                 690

gcc aag gac tcc att aac ggt taattgccct gctgttttta gct            2223
Ala Lys Asp Ser Ile Asn Gly
    695                 700
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<210> 248
<211> 700
<212> PRT
<213> Corynebacterium glutamicum

<400> 248
Leu Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg

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  1               5                  10                  15

Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr
            20                  25                  30

Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His
        35                  40                  45

Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln
    50                  55                  60

Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp
65                  70                  75                  80

Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln
                85                  90                  95

Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu
            100                 105                 110

Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr
        115                 120                 125

Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser
    130                 135                 140

Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp
145                 150                 155                 160

Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val
                165                 170                 175

Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser
            180                 185                 190

Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp
        195                 200                 205

Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu
    210                 215                 220

Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val
225                 230                 235                 240

Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala
                245                 250                 255

Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile
            260                 265                 270

Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala
        275                 280                 285

Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe
    290                 295                 300

Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr
305                 310                 315                 320

Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val
                325                 330                 335
```

Pegnfo-pegnfo

Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe
340 345 350

Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu
355 360 365

Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser
370 375 380

Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly
385 390 395 400

Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser
405 410 415

Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu
420 425 430

Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly
435 440 445

Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly
450 455 460

Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu
465 470 475 480

Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser
485 490 495

Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu
500 505 510

Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp
515 520 525

Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu
530 535 540

Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu
545 550 555 560

Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val
565 570 575

Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser
580 585 590

Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala
595 600 605

Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met Asp Trp Phe
610 615 620

Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val
625 630 635 640

Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg
645 650 655

Replacement Sheet

```
Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala
            660                 665                 670

Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp
        675                 680                 685

Ala Val Val Ala Ala Ala Lys Asp Ser Ile Asn Gly
    690                 695                 700


<210> 249
<211> 793
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (48)..(770)
<223> RXA00965

<400> 249
agattgcggg cctcggcttc attgaaaaca agacggtgtt tgaataaatg aca act    56
                                                    Met Thr Thr
                                                      1

ttc cac gat ctt ccg ctg gag gag cgg ctg aca ctg gcc agg ttg ggc   104
Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala Arg Leu Gly
      5                  10                  15

aca tcc cac tac tcc cgt cag ctc tcc ctc gtg gac aac gct gag ttc   152
Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn Ala Glu Phe
 20                  25                  30                  35

ggc gag cat tcc ctg cta gaa ggg tgg act cgt tcc cac ctc att gcc   200
Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His Leu Ile Ala
                 40                  45                  50

cac gtg gca tac aac gcc atc gca ctg tgc aac ctc atg cac tgg gca   248
His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met His Trp Ala
             55                  60                  65

aat act ggt gag gaa acc cca atg tac gtg tcg cca gaa gcg cgc aac   296
Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu Ala Arg Asn
         70                  75                  80

gag gaa att gcc tac ggt tcc acg ctc aat ccc gat gcg ttg cgt aac   344
Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala Leu Arg Asn
     85                  90                  95

ctg cat gaa cac tcc gtc gca cgc ctg gac gtg gct tgg cgt gaa acg   392
Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp Arg Glu Thr
100                 105                 110                 115

tct gaa gat gct tgg tca cac gag gtt ctg aca gct cag gga cgc act   440
Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln Gly Arg Thr
                120                 125                 130

gtc cca gct agt gaa aca ttg tgg atg cgt tcc cgc gaa gtc tgg atc   488
Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu Val Trp Ile
            135                 140                 145
```

```
cac gca gtt gac ctc ggt gca gtg gca acc ttt ggc gac atc cca gag   536
His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp Ile Pro Glu
        150                 155                 160

gtc atc ctg cgc acc tta gct gca gaa atc aca caa aag tgg aca agc   584
Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys Trp Thr Ser
    165                 170                 175

caa gga gcc ggc gag gga ctt gtg ctt ctc gac gag ccc tcc agc act   632
Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro Ser Ser Thr
180                 185                 190                 195

cgc tac ccc gcc gcc cca ggg cag gac gag gta gta gtg tcc ggt agc   680
Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val Ser Gly Ser
                200                 205                 210

ctt gca ggc att gtt cgc tac gcc gct ggc cgc ggt tcc gat gga gtc   728
Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser Asp Gly Val
            215                 220                 225

act tct tcc act gga gag gtt cca gag cca ccg cgc tgg ctg           770
Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp Leu
        230                 235                 240

tagtttccac acattcttaa atg                                        793


<210> 250
<211> 241
<212> PRT
<213> Corynebacterium glutamicum

<400> 250
Met Thr Thr Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala
  1               5                  10                  15

Arg Leu Gly Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn
             20                  25                  30

Ala Glu Phe Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His
         35                  40                  45

Leu Ile Ala His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met
     50                  55                  60

His Trp Ala Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu
 65                  70                  75                  80

Ala Arg Asn Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala
                 85                  90                  95

Leu Arg Asn Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp
            100                 105                 110

Arg Glu Thr Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln
        115                 120                 125

Gly Arg Thr Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu
    130                 135                 140

Val Trp Ile His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp
```

```
145                 150                 155                 160

Ile Pro Glu Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys
                165                 170                 175

Trp Thr Ser Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro
            180                 185                 190

Ser Ser Thr Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val
        195                 200                 205

Ser Gly Ser Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser
    210                 215                 220

Asp Gly Val Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp
225                 230                 235                 240

Leu
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09025160.1090205

<210> 251
<211> 1575
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1552)
<223> RXN00999

<400> 251
cctcctgtga cctggtaaaa tcgccactac ccccaaatgg tcacaccttt taggccgatt 60

ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115
Met Thr Asn Gly Asp
1 5

aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163
Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
10 15 20

ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211
Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
25 30 35

cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259
Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
40 45 50

ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307
Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
55 60 65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355
Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
70 75 80 85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403
Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
90 95 100

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atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag   451
Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
            105                 110                 115

aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc   499
Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser
        120                 125                 130

ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc   547
Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly
    135                 140                 145

cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct   595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala
150                 155                 160                 165

gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc   643
Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly
                170                 175                 180

gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac   691
Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp
            185                 190                 195

atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc   739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly
        200                 205                 210

atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc   787
Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly
    215                 220                 225

gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag   835
Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln
230                 235                 240                 245

gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct   883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala
                250                 255                 260

gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat   931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp
            265                 270                 275

ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca   979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala
        280                 285                 290

ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct   1027
Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro
    295                 300                 305

gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag   1075
Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln
310                 315                 320                 325

ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct   1123
Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala
                330                 335                 340
```

```
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac   1171
Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn
            345                 350                 355

tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc   1219
Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys
        360                 365                 370

atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca   1267
Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
    375                 380                 385

aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag   1315
Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
390                 395                 400                 405

ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc   1363
Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
                410                 415                 420

cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac   1411
Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
            425                 430                 435

gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag   1459
Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
        440                 445                 450

cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc   1507
Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
    455                 460                 465

tcc ttc cac acc gag tgg tcc ggc gac cgc tcc gag gtt gaa gct       1552
Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser Glu Val Glu Ala
470                 475                 480

taaaggctct ccttttaaca caa                                        1575
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09250210.090502

<210> 252
<211> 484
<212> PRT
<213> Corynebacterium glutamicum

<400> 252

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Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
  1               5                  10                  15

Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr
            20                  25                  30

Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
        35                  40                  45

Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
    50                  55                  60

Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
65                  70                  75                  80

Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
```

```
                85                  90                  95

Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
            100                 105                 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
        115                 120                 125

Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
    130                 135                 140

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
145                 150                 155                 160

Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
                165                 170                 175

Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
            180                 185                 190

Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
        195                 200                 205

Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
    210                 215                 220

Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
225                 230                 235                 240

Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
                245                 250                 255

Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
            260                 265                 270

Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
        275                 280                 285

Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
    290                 295                 300

Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
305                 310                 315                 320

Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
                325                 330                 335

Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
            340                 345                 350

Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
        355                 360                 365

Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
    370                 375                 380

Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
385                 390                 395                 400

Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
                405                 410                 415
```

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```
Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
            420                 425                 430

Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
        435                 440                 445

Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
    450                 455                 460

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser
465                 470                 475                 480

Glu Val Glu Ala
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<210> 253
<211> 1537
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1537)
<223> FRXA00999

<400> 253

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cctcctgtga cctggtaaaa tcgccactac ccccaaatgg tcacaccttt taggccgatt 60

ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat   115
                                          Met Thr Asn Gly Asp
                                            1               5

aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac   163
Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn
                10                  15                  20

ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac   211
Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn
            25                  30                  35

cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa   259
Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu
        40                  45                  50

ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg   307
Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu
    55                  60                  65

gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc   355
Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr
70                  75                  80                  85

gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc   403
Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile
                90                  95                  100

atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag   451
Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu
            105                 110                 115
```

```
aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc   499
Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser
        120                 125                 130

ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc   547
Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly
    135                 140                 145

cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct   595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala
150                 155                 160                 165

gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc   643
Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly
                170                 175                 180

gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac   691
Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp
            185                 190                 195

atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc   739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly
        200                 205                 210

atg cag cca gct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc   787
Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly
    215                 220                 225

gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag   835
Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln
230                 235                 240                 245

gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct   883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala
                250                 255                 260

gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat   931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp
            265                 270                 275

ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca   979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala
        280                 285                 290

ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct   1027
Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro
    295                 300                 305

gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag   1075
Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln
310                 315                 320                 325

ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct   1123
Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala
                330                 335                 340

tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac   1171
Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn
            345                 350                 355
```

```
tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc   1219
Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys
        360                 365                 370

atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca   1267
Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala
    375                 380                 385

aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag   1315
Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu
390                 395                 400                 405

ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc   1363
Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr
                410                 415                 420

cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac   1411
Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr
            425                 430                 435

gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag   1459
Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln
        440                 445                 450

cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc   1507
Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly
    455                 460                 465

tcc ttc cac acc gag tgg tcc ggc gac cgc                          1537
Ser Phe His Thr Glu Trp Ser Gly Asp Arg
470                 475
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<210> 254
<211> 479
<212> PRT
<213> Corynebacterium glutamicum

<400> 254

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Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala
  1               5                  10                  15

Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr
             20                  25                  30

Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
         35                  40                  45

Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
     50                  55                  60

Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65                  70                  75                  80

Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
                 85                  90                  95

Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
            100                 105                 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
```

```
        115                 120                 125

Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
    130                 135                 140

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
145                 150                 155                 160

Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
                165                 170                 175

Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
            180                 185                 190

Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
        195                 200                 205

Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
    210                 215                 220

Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
225                 230                 235                 240

Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
                245                 250                 255

Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
            260                 265                 270

Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
        275                 280                 285

Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
    290                 295                 300

Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
305                 310                 315                 320

Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
                325                 330                 335

Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
            340                 345                 350

Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
        355                 360                 365

Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
    370                 375                 380

Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
385                 390                 395                 400

Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
                405                 410                 415

Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
            420                 425                 430

Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
        435                 440                 445
```

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```
Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
    450                 455                 460

Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg
465                 470                 475


<210> 255
<211> 1326
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1303)
<223> RXN02596

<400> 255
aaggtatctg ggtgtggata tgccctgcta actggagaaa cttggcccga tcgggtgtct 60

gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa   115
                                        Met Thr Glu Ser Lys
                                          1               5

aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg   163
Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
                 10                  15                  20

gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa   211
Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
             25                  30                  35

cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag   259
Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
         40                  45                  50

acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc   307
Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser
     55                  60                  65

aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc   355
Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly
 70                  75                  80                  85

tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc   403
Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe
                 90                  95                 100

ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc   451
Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser
            105                 110                 115

cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat   499
Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp
        120                 125                 130

tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt   547
Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly
    135                 140                 145
```

```
cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg   595
Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp
150                 155                 160                 165

cag act gat cca aag aac ctc cca gcc ggc aac atc acc cgc ctg cca   643
Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn Ile Thr Arg Leu Pro
                170                 175                 180

gtt cgc tac aac ttc aac aac cgc tat ttc aac gac acc tac gaa ggc   691
Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn Asp Thr Tyr Glu Gly
            185                 190                 195

ctt ccc aca gac ggc tac gcg gca tgg ttg gaa aag atg gca gag cat   739
Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu Lys Met Ala Glu His
        200                 205                 210

gag ctt atc gac gtc cgc ctc gac acc gac tgg ttc gac gtt cgc gat   787
Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp Phe Asp Val Arg Asp
    215                 220                 225

gac ctc cgc gca agc aac ccc gac gca cct gtg gtc tac acc ggc cca   835
Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val Val Tyr Thr Gly Pro
230                 235                 240                 245

ctc gac ctc tac ttc aac tac gca gag ggc aag ctg gga tgg cgc acc   883
Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys Leu Gly Trp Arg Thr
                250                 255                 260

ctc gac ttt gaa acc gaa gta gta gaa acc ggt gac ttc caa gga acc   931
Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly Asp Phe Gln Gly Thr
            265                 270                 275

cca gtg atg aac tac aac gat gcg gac gta cct ttc acc cgc atc cac   979
Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro Phe Thr Arg Ile His
        280                 285                 290

gag ttc cgt cac ttc cac cca gag cgt gat gac agt tac ccc aag gat   1027
Glu Phe Arg His Phe His Pro Glu Arg Asp Asp Ser Tyr Pro Lys Asp
    295                 300                 305

aag acc gtc atc atg cgc gag ttc tcc cgt ttc gca gat aac gag gat   1075
Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe Ala Asp Asn Glu Asp
310                 315                 320                 325

gag cct tat tac cca atc aac act cca gac gac cga gac atg ctg aag   1123
Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp Arg Asp Met Leu Lys
                330                 335                 340

cag tac cgc ctt ctg gct gct gaa gag gct gct aat aat aag gtg ctg   1171
Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala Asn Asn Lys Val Leu
            345                 350                 355

ttc ggc ggt cga ctg ggc acg tac cag tac ctc gac atg cac atg gct   1219
Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu Asp Met His Met Ala
        360                 365                 370

atc ggt tct gcg ctg agc atg ttt gac aac aag ctg gtg ccg ttc ttt   1267
Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys Leu Val Pro Phe Phe
    375                 380                 385

gaa gaa ggc aca ccg cta gag cag gaa cgc gga cac taaaaggaag        1313
```

```
Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly His
390                 395                 400

ggcatctccc aca                                                    1326


<210> 256
<211> 401
<212> PRT
<213> Corynebacterium glutamicum

<400> 256
Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu
  1               5                  10                  15

Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys
             20                  25                  30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
         35                  40                  45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
     50                  55                  60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65                  70                  75                  80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
                 85                  90                  95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
            100                 105                 110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
        115                 120                 125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
    130                 135                 140

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
145                 150                 155                 160

Thr Ala Lys Gln Trp Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn
                165                 170                 175

Ile Thr Arg Leu Pro Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn
            180                 185                 190

Asp Thr Tyr Glu Gly Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu
        195                 200                 205

Lys Met Ala Glu His Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp
    210                 215                 220

Phe Asp Val Arg Asp Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val
225                 230                 235                 240

Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys
                245                 250                 255

Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly
```

```
            260                 265                 270

Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro
        275                 280                 285

Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg Asp Asp
    290                 295                 300

Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe
305                 310                 315                 320

Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp
                325                 330                 335

Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala
            340                 345                 350

Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu
        355                 360                 365

Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys
    370                 375                 380

Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly
385                 390                 395                 400

His
```

<210> 257
<211> 512
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(489)
<223> FRXA02596

<400> 257

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cct gtg gtc tac acc ggc cca ctc gac ctc tac ttc aac tac gca gag   48
Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu
  1               5                  10                  15

ggc aag ctg gga tgg cgc acc ctc gac ttt gaa acc gaa gta gta gaa   96
Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
             20                  25                  30

acc ggt gac ttc caa gga acc cca gtg atg aac tac aac gat gcg gac   144
Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
         35                  40                  45

gta cct ttc acc cgc atc cac gag ttc cgt cac ttc cac cca gag cgt   192
Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
     50                  55                  60

gat gac agt tac ccc aag gat aag acc gtc atc atg cgc gag ttc tcc   240
Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
 65                  70                  75                  80
```

```
cgt ttc gca gat aac gag gat gag cct tat tac cca atc aac act cca   288
Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
                 85                  90                  95

gac gac cga gac atg ctg aag cag tac cgc ctt ctg gct gct gaa gag   336
Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
            100                 105                 110

gct gct aat aat aag gtg ctg ttc ggc ggt cga ctg ggc acg tac cag   384
Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
        115                 120                 125

tac ctc gac atg cac atg gct atc ggt tct gcg ctg agc atg ttt gac   432
Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
    130                 135                 140

aac aag ctg gtg ccg ttc ttt gaa gaa ggc aca ccg cta gag cag gaa   480
Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
145                 150                 155                 160

cgc gga cac taaaaggaag ggcatctccc aca                            512
Arg Gly His
```

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<210> 258
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 258

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Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu
  1               5                  10                  15

Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
             20                  25                  30

Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
         35                  40                  45

Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
     50                  55                  60

Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
 65                  70                  75                  80

Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
                 85                  90                  95

Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
            100                 105                 110

Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
        115                 120                 125

Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
    130                 135                 140

Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
145                 150                 155                 160
```

Arg Gly His

<210> 259
<211> 598
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> FRXA02642

<400> 259
aaggtatctg ggtgtggata tgccctgcta actggagaaa cttggcccga tcgggtgtct 60

gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa 115
Met Thr Glu Ser Lys
1 5

aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
10 15 20

gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
25 30 35

cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259
Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
40 45 50

acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307
Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser
55 60 65

aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355
Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly
70 75 80 85

tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403
Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe
90 95 100

ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451
Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser
105 110 115

cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499
Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp
120 125 130

tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547
Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly
135 140 145

cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595
Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp
150 155 160 165

cag 598
Gln

<210> 260
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 260
Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu
1 5 10 15

Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys
20 25 30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
35 40 45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
50 55 60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
65 70 75 80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
85 90 95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
100 105 110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
115 120 125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
130 135 140

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
145 150 155 160

Thr Ala Lys Gln Trp Gln
165

<210> 261
<211> 668
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(645)
<223> RXA02572

<400> 261
gcg gtc gct gag att tgc gag ccg acc ggc gcc gat gcg gtt gcg ctt 48
Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu
1 5 10 15

gtg gat gcc atc ggt cac gac gat cgt atc ggc cga aag ttc tta ggc 96

```
Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly
             20                  25                  30

gcg ggc ctg gga ttc ggt ggc ggt tgt ttg cct aaa gac atc cgc gct   144
Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala
         35                  40                  45

ttc atg gca cgc gcg ggc gaa ttg ggt gct gac cag gca tta acg ttc   192
Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe
     50                  55                  60

ttg cgt gag gtc gat tcc atc aat atg cgt cgt cgc gac cgt gtg gtg   240
Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val
 65                  70                  75                  80

cag ctg gcc aaa gag atg tgt ggc ggt tcg ctg ctg ggc aag cgg gtt   288
Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val
                 85                  90                  95

aca gtg ctc ggc gcc gca ttc aaa ccc aac tcg gac gat gtc cgc gat   336
Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp
            100                 105                 110

tct ccg gcg ctg tcg gtc gcg ggt tcg ctg tcg ctc cag ggt gcg gcg   384
Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala
        115                 120                 125

gtc tcg gtc tac gac ccg gaa gct atg gac aac gct cga cgc gtc ttc   432
Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe
    130                 135                 140

ccg acg ctc agc tat gcg tcc agc act aaa gag gcg ctt atc gac gcc   480
Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala
145                 150                 155                 160

cac ctc gtc gtt ctt gcc act gaa tgg caa gaa ttc cgc gac ctt gac   528
His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp
                165                 170                 175

ccc gaa gtg gcg gga ggg gtc gtc gag aag cgc gct att att gat ggc   576
Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly
            180                 185                 190

cga aac gtc ctc gat gtt gcc aaa tgg aag gcc gcc ggt tgg gaa atg   624
Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met
        195                 200                 205

gaa gcg ctc ggc cgc aac ctt tagtgcggtg gatcaggcgg ggc            668
Glu Ala Leu Gly Arg Asn Leu
    210                 215
```

<210> 262
<211> 215
<212> PRT
<213> Corynebacterium glutamicum

<400> 262

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Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu
  1               5                  10                  15
```

```
Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly
             20                  25                  30

Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala
         35                  40                  45

Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe
     50                  55                  60

Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val
 65                  70                  75                  80

Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val
                 85                  90                  95

Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp
            100                 105                 110

Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala
        115                 120                 125

Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe
    130                 135                 140

Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala
145                 150                 155                 160

His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp
                165                 170                 175

Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly
            180                 185                 190

Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met
        195                 200                 205

Glu Ala Leu Gly Arg Asn Leu
    210                 215
```

09525760.090905

<210> 263
<211> 1224
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1201)
<223> RXA02485

<400> 263

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cggtggtcag tgcttggtgc accttgccga cgggctgatt gatcgtaatg gtgttttctg 60

tacgcgttgc catgaggata agactaccgt tagtggggtg ttg gat tca tcg cta   115
                                              Leu Asp Ser Ser Leu
                                                1               5

gcc cag gaa atc gcc gcg atc gac ggc gtc gaa ctc gat tcg gaa gtc   163
Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu Leu Asp Ser Glu Val
                10                  15                  20
```

```
act ttc gcc gat ctg acg acc ctc cgc atc ggc gga aaa ccc cgc agc   211
Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly Gly Lys Pro Arg Ser
             25                  30                  35

gcc gta cgt tgc cag acc acg gag gcg ctg gtc agc gcc ata aaa ttg   259
Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val Ser Ala Ile Lys Leu
         40                  45                  50

ctt gac gac gcc tcc ctc ccc ctc ctc att gtc ggc ggc ggg tcc aat   307
Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val Gly Gly Gly Ser Asn
     55                  60                  65

ctc gtc gtg gcc gac ggc gat ctg gat gtt att gcc gtc atc atc gaa   355
Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile Ala Val Ile Ile Glu
 70                  75                  80                  85

acc gac gac gtc tcc atc aac ctc acc gac ggt ctc ctc acc gcc gat   403
Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly Leu Leu Thr Ala Asp
                 90                  95                 100

gca ggc gct gtt tgg gac gat gtt gtc cac ctt tcg gtg gat gcc ggc   451
Ala Gly Ala Val Trp Asp Asp Val Val His Leu Ser Val Asp Ala Gly
            105                 110                 115

ctc ggt gga att gaa tgc ctc tcc gga atc ccc ggc tcc gcc ggc gcc   499
Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro Gly Ser Ala Gly Ala
        120                 125                 130

acc cca gtc caa aac gtg ggc gcc tac ggc acg gaa gtt tcc gat gta   547
Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr Glu Val Ser Asp Val
    135                 140                 145

ctc acc cgc gtc cag ctt ctc gac cgc acc acc cac caa gtc tcc tgg   595
Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr His Gln Val Ser Trp
150                 155                 160                 165

gtc gac gcc tcc gaa ctc gac ctc tct tac cga tac tcc aat ctc aaa   643
Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg Tyr Ser Asn Leu Lys
                170                 175                 180

ttc acc aac cgc gca gtc gtc ttg gcg atc gaa ctc cag ctc ctc acc   691
Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu Leu Gln Leu Leu Thr
            185                 190                 195

gac gga ttg tcc gcg ccg cta cgt ttt ggt gaa ttg gga cgt cga tta   739
Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu Leu Gly Arg Arg Leu
        200                 205                 210

gcg atc tcc gag gcc gaa ccc cac cca cgt cgc ccc gtc cgc atg gtc   787
Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg Pro Val Arg Met Val
    215                 220                 225

cgc gac gcc gtc cta gaa ctc cgc cgc gcc aaa ggc atg gtc gtg gaa   835
Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys Gly Met Val Val Glu
230                 235                 240                 245

cac acc gac cac gac acc tgg tcc gcc gga tcc ttc ttc acc aac cca   883
His Thr Asp His Asp Thr Trp Ser Ala Gly Ser Phe Phe Thr Asn Pro
                250                 255                 260

atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa   931
```

```
Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu
            265                 270                 275

ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc   979
Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser
        280                 285                 290

gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc   1027
Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly
    295                 300                 305

gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc   1075
Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr
310                 315                 320                 325

aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa   1123
Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu
                330                 335                 340

atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa   1171
Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu
            345                 350                 355

ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg     1221
Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
        360                 365

gca                                                               1224


<210> 264
<211> 367
<212> PRT
<213> Corynebacterium glutamicum

<400> 264
Leu Asp Ser Ser Leu Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu
  1               5                  10                  15

Leu Asp Ser Glu Val Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly
             20                  25                  30

Gly Lys Pro Arg Ser Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val
         35                  40                  45

Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val
     50                  55                  60

Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile
 65                  70                  75                  80

Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly
                 85                  90                  95

Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu
            100                 105                 110

Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro
        115                 120                 125

Gly Ser Ala Gly Ala Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr
```

```
    130                 135                 140

Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr
145                 150                 155                 160

His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg
                165                 170                 175

Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu
            180                 185                 190

Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu
        195                 200                 205

Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg
    210                 215                 220

Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys
225                 230                 235                 240

Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser
                245                 250                 255

Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe
            260                 265                 270

Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly
        275                 280                 285

Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys
    290                 295                 300

Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His
305                 310                 315                 320

Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val
                325                 330                 335

Ala Leu Ala Lys Glu Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val
            340                 345                 350

Thr Leu Val Pro Glu Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
        355                 360                 365


<210> 265
<211> 1124
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1101)
<223> RXA01216

<400> 265
acc gac cac act ctg tct gca ctg ctg gat gca cac gtg gaa gtt cca   48
Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro
  1               5                  10                  15

acc gct gtc acc gtg ttg acc atg cgt ctg gat gac ccc acc ggc tac   96
```

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```
Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr
            20                  25                  30

ggc cgc atc gtg cgc aac gaa gaa ggc gaa gtc acc gcc atc gtt gag   144
Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu
        35                  40                  45

caa aaa gat gct tca gca gaa gtc caa gcc atc gat gag gtc aac tcc   192
Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser
    50                  55                  60

ggt gtc ttt gct ttc gac gcc gcc atc ttg cgt tcc gca ctg gct gaa   240
Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu
65                  70                  75                  80

ctg aag tcc gac aac gct cag ggc gag ctg tac ctg acc gac gtt ttg   288
Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu
                85                  90                  95

ggc att gct cgt ggc gag ggc cac cca gtg cgc gcc cac acc gcc gcc   336
Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala
            100                 105                 110

gat gct cgt gaa ctc gcc ggc gtc aac gat cgt gtg cag ctc gca gaa   384
Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu
        115                 120                 125

gcc ggc gcc gaa cta aac cgt cgc acc gtc atc gcc gct atg cgt ggt   432
Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly
    130                 135                 140

ggc gca acc atc gtt gat cca gca acc acc tgg atc gat gtg gag gtt   480
Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val
145                 150                 155                 160

tct atc gga cgc gac gtg atc atc cac cct ggc acc cag ctc aag ggc   528
Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly
                165                 170                 175

gaa act gtc atc gga gac cgc gtt gaa gtt ggt cca gac acc acc ttg   576
Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu
            180                 185                 190

acc aac atg acc atc ggc gac ggc gca tcc gta atc cgc acc cac ggt   624
Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly
        195                 200                 205

ttc gac tcc acc atc ggt gaa aac gcc acc gtt ggc ccc ttc acc tac   672
Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr
    210                 215                 220

atc cgc cca gga acc aca ctg gga cca gaa ggc aag ctc ggt ggc ttc   720
Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe
225                 230                 235                 240

gta gaa acc aag aag gcc aca atc ggc cgt ggc tcc aag gtt cca cac   768
Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His
                245                 250                 255

ctc acc tat gtc ggc gac gcc acc atc ggc gag gaa tcc aac atc gga   816
Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly
```

```
            260                 265                 270

gcc tcc tct gtc ttc gtg aac tac gac ggt gaa aac aag cac cac acc   864
Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr
        275                 280                 285

acc atc ggc agc cac gtt cgc act ggt tct gac acc atg ttt atc gct   912
Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala
    290                 295                 300

cca gtg acc gtg ggt gac gga gcg tat tcc gga gcc ggt aca gta att   960
Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile
305                 310                 315                 320

aaa gac gat gtt ccg cca gga gcc ctt gcc gtg tcc ggc gga cgc caa  1008
Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln
                325                 330                 335

cga aac atc gaa ggc tgg gtg caa aag aag cgc cct gga acc gct gca  1056
Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala
            340                 345                 350

gca caa gcc gca gaa gcc gcc caa aac gtc cac aac cag gaa ggc      1101
Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly
        355                 360                 365

taagcaggat cctcatgact gct                                       1124


<210> 266
<211> 367
<212> PRT
<213> Corynebacterium glutamicum

<400> 266
Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro
  1               5                  10                  15

Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr
             20                  25                  30

Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu
         35                  40                  45

Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser
     50                  55                  60

Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu
 65                  70                  75                  80

Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu
                 85                  90                  95

Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala
            100                 105                 110

Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu
        115                 120                 125

Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly
    130                 135                 140
```

```
Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val
145                 150                 155                 160

Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly
                165                 170                 175

Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu
            180                 185                 190

Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly
        195                 200                 205

Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr
    210                 215                 220

Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe
225                 230                 235                 240

Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His
                245                 250                 255

Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly
            260                 265                 270

Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr
        275                 280                 285

Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala
    290                 295                 300

Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile
305                 310                 315                 320

Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln
                325                 330                 335

Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala
            340                 345                 350

Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly
        355                 360                 365
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<210> 267
<211> 981
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(958)
<223> RXA01259

<400> 267
aagagaatta tttctaaaat tcggtatcgt ctaagaaatg agtttgccaa tagctcagca 60

tcaaaatgct gtaaaaactg tcgtggtacc agctgcagga atg gga aca cgg ttc 115
Met Gly Thr Arg Phe
1 5

```
ctt cct gca acg aag aca att cca aag gag ctt ctt cct gta gtt gat   163
Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu Leu Pro Val Val Asp
                10                  15                  20

acc ccg ggt att gaa ctt gtt gcc aaa gag gct gct gat ctt ggt gca   211
Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala Ala Asp Leu Gly Ala
            25                  30                  35

act cgg tta gca att atc act gct ccg aac aaa gac gga att ctt aaa   259
Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys Asp Gly Ile Leu Lys
        40                  45                  50

cac ttc gag gag ttc cct gag ctt gag gca act ctt gag gct cgc ggt   307
His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr Leu Glu Ala Arg Gly
    55                  60                  65

aag act gat caa ctg aat aaa gtt cga gca gct cga gaa ttg att gca   355
Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala Arg Glu Leu Ile Ala
70                  75                  80                  85

aca gtt cca gtg gtt caa gaa aag cca ttg ggg ctt ggt cac gct gtt   403
Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly Leu Gly His Ala Val
                90                  95                  100

ggc ctt gct gag tct gtg ctc gat gat gat gaa gat gtt gtg gct gtc   451
Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu Asp Val Val Ala Val
            105                 110                 115

atg ctg cca gac gat ttg gtg ctg cca ttt ggt gtg acc gag aga atg   499
Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly Val Thr Glu Arg Met
        120                 125                 130

gca gaa gtt cgc gct aag ttt ggc gga tct gtt ctt gca gca att gag   547
Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val Leu Ala Ala Ile Glu
    135                 140                 145

gtg gct gaa gat gaa gtc tca aat tac gga gta ttt aag ctc ggt gaa   595
Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val Phe Lys Leu Gly Glu
150                 155                 160                 165

ctc gat gca gag tcc gaa agt gaa ggc att agg cgt gtt gta gga atg   643
Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg Arg Val Val Gly Met
                170                 175                 180

gtt gaa aag cct gcg cct gaa gat gca cca tca agg ttt gcc gca acg   691
Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Arg Phe Ala Ala Thr
            185                 190                 195

ggc cgt tat cta ctt gat cga gct att ttt gat gca ctg cgt cga att   739
Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp Ala Leu Arg Arg Ile
        200                 205                 210

gag cct ggt gct ggt gga gaa ctg caa tta aca gat gcc atc gca tta   787
Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr Asp Ala Ile Ala Leu
    215                 220                 225

ttg atc gaa gaa ggc cat ccg gta cac att gtg gtt cat gaa gga aag   835
Leu Ile Glu Glu Gly His Pro Val His Ile Val Val His Glu Gly Lys
230                 235                 240                 245

cgc cat gac ctt ggt aat cca gct ggg tac att cct gct gtt gtg tac   883
```

```
Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile Pro Ala Val Val Tyr
                250                 255                 260

ttc gga ctt cgt cat gca gag tac ggt tcc aag att cac cgt gcg gtg   931
Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys Ile His Arg Ala Val
            265                 270                 275

aag gaa ata ctc gct gag ttt gaa tct taaaaaggaa accgccttcc         978
Lys Glu Ile Leu Ala Glu Phe Glu Ser
        280                 285

aca                                                               981
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<210> 268
<211> 286
<212> PRT
<213> Corynebacterium glutamicum

<400> 268

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Met Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu
  1               5                  10                  15

Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala
            20                  25                  30

Ala Asp Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
        35                  40                  45

Asp Gly Ile Leu Lys His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr
    50                  55                  60

Leu Glu Ala Arg Gly Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala
65                  70                  75                  80

Arg Glu Leu Ile Ala Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly
                85                  90                  95

Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
            100                 105                 110

Asp Val Val Ala Val Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly
        115                 120                 125

Val Thr Glu Arg Met Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val
    130                 135                 140

Leu Ala Ala Ile Glu Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val
145                 150                 155                 160

Phe Lys Leu Gly Glu Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg
                165                 170                 175

Arg Val Val Gly Met Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser
            180                 185                 190

Arg Phe Ala Ala Thr Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp
        195                 200                 205

Ala Leu Arg Arg Ile Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr
    210                 215                 220
```

```
Asp Ala Ile Ala Leu Leu Ile Glu Glu Gly His Pro Val His Ile Val
225                 230                 235                 240

Val His Glu Gly Lys Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile
                245                 250                 255

Pro Ala Val Val Tyr Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys
            260                 265                 270

Ile His Arg Ala Val Lys Glu Ile Leu Ala Glu Phe Glu Ser
        275                 280                 285


<210> 269
<211> 526
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(526)
<223> RXA02028

<400> 269
tgcgcagttc ctgcttagtt tggctcataa atctaaggat aaccgttatt ttcggagggg 60

tacgacgatt ggggttgcgg gggcaggtac tcttggttcc atg agt ttg cct atc   115
                                        Met Ser Leu Pro Ile
                                          1               5

gat gag cac gtg aac gcg gtt aaa acc gtc gta gtg cct gct gca gga   163
Asp Glu His Val Asn Ala Val Lys Thr Val Val Val Pro Ala Ala Gly
                  10                  15                  20

ctg gga acc cga ttc ctt ccg gcc acc aaa acc gta ccc aag gag ttg   211
Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Val Pro Lys Glu Leu
              25                  30                  35

ctg ccg gtt gtc gat acc cca ggt att gag ctg att gct gct gag gct   259
Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Ile Ala Ala Glu Ala
          40                  45                  50

gcc gaa ctt ggt gcg acc agg ctg gcg atc atc act gcg cca aac aaa   307
Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
      55                  60                  65

gct ggg gta ctt gca cac ttt gag cgt tct tct gaa ttg gaa gaa acg   355
Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser Glu Leu Glu Glu Thr
  70                  75                  80                  85

ctg atg gag cgt ggc aag act gac cag gtg gag ata atc cgc cgc gcc   403
Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu Ile Ile Arg Arg Ala
                  90                  95                 100

gcc gat tta atc aag gca gtt cca gta acc cag gac aag ccg ctg ggg   451
Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln Asp Lys Pro Leu Gly
              105                 110                 115

cta ggt cat gct gtt ggt ttg gct gag tct gtg ttg gat gat gat gaa   499
Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
```

```
        120                 125                 130

gat gtc gta gcg gtg atg ttg ccg cac                                    526
Asp Val Val Ala Val Met Leu Pro His
    135                 140


<210> 270
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 270
Met Ser Leu Pro Ile Asp Glu His Val Asn Ala Val Lys Thr Val Val
  1               5                  10                  15

Val Pro Ala Ala Gly Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr
             20                  25                  30

Val Pro Lys Glu Leu Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu
         35                  40                  45

Ile Ala Ala Glu Ala Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile
     50                  55                  60

Thr Ala Pro Asn Lys Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser
 65                  70                  75                  80

Glu Leu Glu Glu Thr Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu
                 85                  90                  95

Ile Ile Arg Arg Ala Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln
            100                 105                 110

Asp Lys Pro Leu Gly Leu Gly His Ala Val Gly Leu Ala Glu Ser Val
        115                 120                 125

Leu Asp Asp Asp Glu Asp Val Val Ala Val Met Leu Pro His
    130                 135                 140


<210> 271
<211> 1284
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1261)
<223> RXA01262

<400> 271
tatactcgtc aagggccttc gataaaacaa agacaatttt cccccgacgg gacaatctga 60

aaacttgctg tatcaataaa acacgaaaag gaatactttt atg aaa att gcc gtc   115
                                               Met Lys Ile Ala Val
                                                 1               5

gca ggg ctc gga tat gtt ggg ctt tca aat gca gct ctc ctc tct aaa   163
Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala Ala Leu Leu Ser Lys
                10                  15                  20
```

```
aat cat aaa gtt gtt gca gtt gac att gat gaa gaa cga gtg aaa cta   211
Asn His Lys Val Val Ala Val Asp Ile Asp Glu Glu Arg Val Lys Leu
            25                  30                  35

gtt caa gaa ttt cgt tcg cca att gtc gat agc gat ctc gaa gaa tat   259
Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser Asp Leu Glu Glu Tyr
        40                  45                  50

ctg tcc act aag cct caa aac tta act gcc aca acg gac gcc gaa gcc   307
Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr Thr Asp Ala Glu Ala
    55                  60                  65

gct tac aaa ggc gca gat ttt att gtt att gca acg cca act aat tac   355
Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala Thr Pro Thr Asn Tyr
70                  75                  80                  85

gac cca gag tca aac ttt ttt gat act tcc agc gtt gag tcc gta att   403
Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser Val Glu Ser Val Ile
                90                  95                  100

gag ata gtc ctt aag gtt tct cct gga tcc aca atc gta att aaa tcg   451
Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr Ile Val Ile Lys Ser
            105                 110                 115

act atc cct gtt ggt ttt aca tcg gaa cta cgc att aag cat cca gaa   499
Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg Ile Lys His Pro Glu
        120                 125                 130

gct tcg att att ttt tca cct gag ttc ctg cgt gaa ggc cga gca ttc   547
Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg Glu Gly Arg Ala Phe
    135                 140                 145

tac gac aat ctc tac cca tcc aga gtt gtc gtt ggt gat cgc agt cct   595
Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val Gly Asp Arg Ser Pro
150                 155                 160                 165

ctg ggg gaa gaa ttt gcg act ctg tta gct gag ggg gca aaa gaa aag   643
Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu Gly Ala Lys Glu Lys
                170                 175                 180

cct ccg att cta ctt acg gac tca act gag gca gag gcg att aaa tta   691
Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala Glu Ala Ile Lys Leu
            185                 190                 195

ttt tct aat aca tat ctt gca ctg cga gtt gct ttt ttc aac gaa ctg   739
Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala Phe Phe Asn Glu Leu
        200                 205                 210

gat act tat gcg tct gtt cga agc ttg gat act aag cag att att gaa   787
Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr Lys Gln Ile Ile Glu
    215                 220                 225

ggg gta ggg ctc gat cca cgt att gga tct cat tac aat aat cct tca   835
Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His Tyr Asn Asn Pro Ser
230                 235                 240                 245

ttt gga tat ggc gga tat tgt ctt ccg aaa gat acg aaa cag ctt ctc   883
Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp Thr Lys Gln Leu Leu
                250                 255                 260
```

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```
gcc aac tat aag gat gtc ccg cag aat cta atc tct gca gta gtc caa   931
Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile Ser Ala Val Val Gln
            265                 270                 275

gca aat aag act cgt aag gac ttt att gca gag gat atc ctc agt aaa   979
Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu Asp Ile Leu Ser Lys
        280                 285                 290

tca cct act gta gtt gga att tac cgc ctt gta atg aag tct gga tca   1027
Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val Met Lys Ser Gly Ser
    295                 300                 305

gat aac ttt cgt tct tct tct att caa gga gtc atg aaa cga att aag   1075
Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val Met Lys Arg Ile Lys
310                 315                 320                 325

gcc aag gga atc gaa att gta gta ttt gaa ccg aat ctc gga gaa gaa   1123
Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro Asn Leu Gly Glu Glu
                330                 335                 340

act ttc tac aat tcg aag atc ctt aat gac atc gaa gag ttt aag gat   1171
Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile Glu Glu Phe Lys Asp
            345                 350                 355

tac tgc gac atc att att gca aat cgt cca acc gat gag ctt tct gat   1219
Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr Asp Glu Leu Ser Asp
        360                 365                 370

gta cca gaa aaa gtt tat aca cgt gat att ttc cag cgt gac           1261
Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe Gln Arg Asp
    375                 380                 385

taagtggaaa gaatcttttg ttg                                        1284
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<210> 272
<211> 387
<212> PRT
<213> Corynebacterium glutamicum

<400> 272

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Met Lys Ile Ala Val Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala
  1               5                  10                  15

Ala Leu Leu Ser Lys Asn His Lys Val Val Ala Val Asp Ile Asp Glu
            20                  25                  30

Glu Arg Val Lys Leu Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser
        35                  40                  45

Asp Leu Glu Glu Tyr Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr
    50                  55                  60

Thr Asp Ala Glu Ala Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala
65                  70                  75                  80

Thr Pro Thr Asn Tyr Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser
                85                  90                  95

Val Glu Ser Val Ile Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr
            100                 105                 110
```

```
Ile Val Ile Lys Ser Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg
        115                 120                 125

Ile Lys His Pro Glu Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg
    130                 135                 140

Glu Gly Arg Ala Phe Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val
145                 150                 155                 160

Gly Asp Arg Ser Pro Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu
                165                 170                 175

Gly Ala Lys Glu Lys Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala
            180                 185                 190

Glu Ala Ile Lys Leu Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala
        195                 200                 205

Phe Phe Asn Glu Leu Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr
    210                 215                 220

Lys Gln Ile Ile Glu Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His
225                 230                 235                 240

Tyr Asn Asn Pro Ser Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp
                245                 250                 255

Thr Lys Gln Leu Leu Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile
            260                 265                 270

Ser Ala Val Val Gln Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu
        275                 280                 285

Asp Ile Leu Ser Lys Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val
    290                 295                 300

Met Lys Ser Gly Ser Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val
305                 310                 315                 320

Met Lys Arg Ile Lys Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro
                325                 330                 335

Asn Leu Gly Glu Glu Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile
            340                 345                 350

Glu Glu Phe Lys Asp Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr
        355                 360                 365

Asp Glu Leu Ser Asp Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe
    370                 375                 380

Gln Arg Asp
385
```

<210> 273
<211> 1209
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1186)
<223> RXA01377

<400> 273
tgaaatggat ttgctgcggc cccggaatta ccctttcgc ggccgtcatc aaatttgtac 60

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ccccttaaag acaccctaaa cacgagtgaa ataggaacac atg act tta act gac   115
                                          Met Thr Leu Thr Asp
                                            1               5

aac agc aaa aac gtt gat gct gtc atc ttg gtc ggt ggc aaa ggt acc   163
Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val Gly Gly Lys Gly Thr
                10                  15                  20

cga ctg cgc ccc ctg acc gtc aat act cca aag cca atg ctg cca act   211
Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys Pro Met Leu Pro Thr
            25                  30                  35

gct ggc cac cca ttc ttg acc cac ctt ttg gcc cgc atc aag gcc gca   259
Ala Gly His Pro Phe Leu Thr His Leu Leu Ala Arg Ile Lys Ala Ala
        40                  45                  50

ggc atc aca cac gtc gtg ctg gga acg tca ttc aaa gct gaa gtc ttc   307
Gly Ile Thr His Val Val Leu Gly Thr Ser Phe Lys Ala Glu Val Phe
    55                  60                  65

gag gaa tac ttc gga gat ggc tcc gaa atg ggc ttg gaa att gaa tat   355
Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly Leu Glu Ile Glu Tyr
70                  75                  80                  85

gtc gtc gag gat cag cct ttg ggc act ggt ggt ggc atc cga aac gtc   403
Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly Gly Ile Arg Asn Val
                90                  95                  100

tac gac aag ctg cgt cac gat act gcg att gtg ttc aac ggc gat gtg   451
Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val Phe Asn Gly Asp Val
            105                 110                 115

ctc tcc ggt gcg gat ctc aac agc att ctg gac acc cac cgc gaa aag   499
Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp Thr His Arg Glu Lys
        120                 125                 130

gac gca gat ctg acc atg cat ctc gtg cgc gta gct aac cct cgt gcg   547
Asp Ala Asp Leu Thr Met His Leu Val Arg Val Ala Asn Pro Arg Ala
    135                 140                 145

ttt ggt tgc gtc ccc acc gat gag gat ggt cgc gtc agc gaa ttc ctt   595
Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg Val Ser Glu Phe Leu
150                 155                 160                 165

gaa aag acc gaa gat cca cca acc gat cag atc aac gcc ggc tgc tac   643
Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile Asn Ala Gly Cys Tyr
                170                 175                 180

gtg ttc aag aag gaa ctc atc gag cag atc ccg gca ggc cga gca gtt   691
Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro Ala Gly Arg Ala Val
            185                 190                 195

tcc gtc gag cgc gaa acc ttc cct cag ctg ttg gaa gaa ggc aag cga   739
```

```
Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu Glu Glu Gly Lys Arg
        200                 205                 210

gtc ttc ggc cac gtc gac gct tcc tac tgg cgc gac atg ggc acc cca   787
Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg Asp Met Gly Thr Pro
    215                 220                 225

agc gac ttc gtc cgc ggc tcg gct gac ctg gtc cgc ggc att gcg tac   835
Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val Arg Gly Ile Ala Tyr
230                 235                 240                 245

tcc cca ttg ctc gaa ggc aaa aca gga gag tcg ctt gtc gac gcc tcc   883
Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser Leu Val Asp Ala Ser
                250                 255                 260

gcc ggc gtt cgc gac ggc gtc ctg ctg ctc ggc gga acc gta gtc ggc   931
Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly Gly Thr Val Val Gly
            265                 270                 275

cgc ggc act gag atc ggt gcc ggc tgc cgc gtt gac aac act gtt att   979
Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val Asp Asn Thr Val Ile
        280                 285                 290

ttc gac ggc gtc acc att gaa cca ggt gcg gtc att gaa aat tcc atc   1027
Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val Ile Glu Asn Ser Ile
    295                 300                 305

att tcc tcg gga gca cgc atc ggt gct aat gcg cac atc tcc ggt tgc   1075
Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala His Ile Ser Gly Cys
310                 315                 320                 325

atc att ggc gag ggc gca cag gtt ggt gct cgg tgt gaa ctc aac gca   1123
Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg Cys Glu Leu Asn Ala
                330                 335                 340

ggg atg cgc gtc ttc cca ggc gtt gtg atc cca gac agc gga att cgt   1171
Gly Met Arg Val Phe Pro Gly Val Val Ile Pro Asp Ser Gly Ile Arg
            345                 350                 355

ttt tcg tct gat cag taggcatttt tagccctttt gga                    1209
Phe Ser Ser Asp Gln
        360
```

<210> 274
<211> 362
<212> PRT
<213> Corynebacterium glutamicum

<400> 274

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Met Thr Leu Thr Asp Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val
  1               5                  10                  15

Gly Gly Lys Gly Thr Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys
             20                  25                  30

Pro Met Leu Pro Thr Ala Gly His Pro Phe Leu Thr His Leu Leu Ala
         35                  40                  45

Arg Ile Lys Ala Ala Gly Ile Thr His Val Val Leu Gly Thr Ser Phe
     50                  55                  60
```

Lys Ala Glu Val Phe Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly
65 70 75 80

Leu Glu Ile Glu Tyr Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly
85 90 95

Gly Ile Arg Asn Val Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val
100 105 110

Phe Asn Gly Asp Val Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp
115 120 125

Thr His Arg Glu Lys Asp Ala Asp Leu Thr Met His Leu Val Arg Val
130 135 140

Ala Asn Pro Arg Ala Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg
145 150 155 160

Val Ser Glu Phe Leu Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile
165 170 175

Asn Ala Gly Cys Tyr Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro
180 185 190

Ala Gly Arg Ala Val Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu
195 200 205

Glu Glu Gly Lys Arg Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg
210 215 220

Asp Met Gly Thr Pro Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val
225 230 235 240

Arg Gly Ile Ala Tyr Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser
245 250 255

Leu Val Asp Ala Ser Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly
260 265 270

Gly Thr Val Val Gly Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val
275 280 285

Asp Asn Thr Val Ile Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val
290 295 300

Ile Glu Asn Ser Ile Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala
305 310 315 320

His Ile Ser Gly Cys Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg
325 330 335

Cys Glu Leu Asn Ala Gly Met Arg Val Phe Pro Gly Val Val Ile Pro
340 345 350

Asp Ser Gly Ile Arg Phe Ser Ser Asp Gln
355 360

<210> 275
<211> 1350

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1327)
<223> RXA02063

<400> 275
accgaaatgg gggcattaaa aggggctatc attcggaccc caaaacgatg tttagacaat 60

ttgttaccca gctttcatgc gggatagtta ttttgccttt atg gtt aag ggt gtg 115
Met Val Lys Gly Val
1 5

aag ggt aga cca aat gtt cta gca atc gtt ctc gca ggt ggc gag ggc 163
Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu Ala Gly Gly Glu Gly
10 15 20

aaa cga ctt ttt ccg ttg acg gag gac cga gct aag cct gcg gtc cca 211
Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala Lys Pro Ala Val Pro
25 30 35

ttc ggc gga act tac aga ttg atc gac ttt gtt ttg tcg aac ctg gtg 259
Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val Leu Ser Asn Leu Val
40 45 50

aac tcc gga ttc ctc aag atc gcg gta ctg act cag tac aag tcg cat 307
Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr Gln Tyr Lys Ser His
55 60 65

tca ttg gat agg cat att tca ttg tcg tgg aac gtg tct ggt cca acg 355
Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn Val Ser Gly Pro Thr
70 75 80 85

ggg cag tac att gct tct gtt cct gcg cag cag cgc ctg ggc aag cga 403
Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln Arg Leu Gly Lys Arg
90 95 100

tgg ttc act ggt tcc gcg gat gca att ttg cag tct ctg aac ttg atc 451
Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln Ser Leu Asn Leu Ile
105 110 115

tct gat gag aaa ccg gat tat gtc atc gtt ttc ggc gcg gac cac gtg 499
Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe Gly Ala Asp His Val
120 125 130

tat cgc atg gac cca agc cag atg cta gat gag cac att gca tct ggt 547
Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu His Ile Ala Ser Gly
135 140 145

cgc gcg gtg tct gtg gca ggt att cgc gtt cca cgt gag gaa gca act 595
Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro Arg Glu Glu Ala Thr
150 155 160 165

gcg ttt ggt tgc atc cag tcc gat gtc gac ggc aac ata acc gag ttc 643
Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly Asn Ile Thr Glu Phe
170 175 180

ttg gaa aag cca gct gac cct ccg gga acc cct gat gat cct gac atg 691
Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro Asp Asp Pro Asp Met

```
            185                 190                 195

act tac gcg tcg atg ggt aac tac att ttc acc act gaa gcc ctg atc   739
Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr Thr Glu Ala Leu Ile
        200                 205                 210

cag gcg ctg aaa gat gat gaa aat aac gag aac agt gat cat gac atg   787
Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn Ser Asp His Asp Met
    215                 220                 225

ggc gga gac atc att ccg tac ttc gtc tct cgc aat gat gcg cat gtt   835
Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg Asn Asp Ala His Val
230                 235                 240                 245

tat gat ttc tcc gga aac att gtt cct ggc gca act gag cgt gac aag   883
Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala Thr Glu Arg Asp Lys
                250                 255                 260

ggc tac tgg cgc gac gtc ggt acc att gat gcg ttc tac gag tgc cac   931
Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Phe Tyr Glu Cys His
            265                 270                 275

atg gac ctg att tcc gtg cac cca atc ttc aat ctg tat aac tct gag   979
Met Asp Leu Ile Ser Val His Pro Ile Phe Asn Leu Tyr Asn Ser Glu
        280                 285                 290

tgg cca atc cac acg acc tct gaa ggt aac ttg cct ccg gct aag ttc  1027
Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu Pro Pro Ala Lys Phe
    295                 300                 305

gtt cgg ggc ggt atc gcg cag tcg tcg atg gtg tct tca ggt tcc atc  1075
Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val Ser Ser Gly Ser Ile
310                 315                 320                 325

att tct gct ggg act gtt cgc aac tcc gtg ctg tcc aac aac gtt gtc  1123
Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu Ser Asn Asn Val Val
                330                 335                 340

gtc gaa gag ggc gca acg gtg gaa ggt gca gtg ctg atg cca ggc gtg  1171
Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val Leu Met Pro Gly Val
            345                 350                 355

cgc atc ggt aag ggt gct gtt gtc cgc cat gcg att ctg gac aag aac  1219
Arg Ile Gly Lys Gly Ala Val Val Arg His Ala Ile Leu Asp Lys Asn
        360                 365                 370

gtg gtt gtc cgc gac gga gag ctc atc ggt gtc gac caa gtg cgc gat  1267
Val Val Val Arg Asp Gly Glu Leu Ile Gly Val Asp Gln Val Arg Asp
    375                 380                 385

gcg cag cgc ttc aag gtg agc gcc ggc ggc gtc gtg gtt gtc ggt aag  1315
Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val Val Val Val Gly Lys
390                 395                 400                 405

aac cag gta gtc taaacgggaa agggacctta aaa                        1350
Asn Gln Val Val
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<210> 276
<211> 409

<212> PRT
<213> Corynebacterium glutamicum

<400> 276

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Met Val Lys Gly Val Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu
 1               5                  10                  15

Ala Gly Gly Glu Gly Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala
            20                  25                  30

Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val
        35                  40                  45

Leu Ser Asn Leu Val Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr
    50                  55                  60

Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn
65                  70                  75                  80

Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln
                85                  90                  95

Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln
            100                 105                 110

Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe
        115                 120                 125

Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu
    130                 135                 140

His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro
145                 150                 155                 160

Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly
                165                 170                 175

Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro
            180                 185                 190

Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr
        195                 200                 205

Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn
    210                 215                 220

Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg
225                 230                 235                 240

Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala
                245                 250                 255

Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala
            260                 265                 270

Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn
        275                 280                 285

Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu
    290                 295                 300
```

```
Pro Pro Ala Lys Phe Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val
305                 310                 315                 320

Ser Ser Gly Ser Ile Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu
                325                 330                 335

Ser Asn Asn Val Val Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val
            340                 345                 350

Leu Met Pro Gly Val Arg Ile Gly Lys Gly Ala Val Val Arg His Ala
        355                 360                 365

Ile Leu Asp Lys Asn Val Val Val Arg Asp Gly Glu Leu Ile Gly Val
    370                 375                 380

Asp Gln Val Arg Asp Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val
385                 390                 395                 400

Val Val Val Gly Lys Asn Gln Val Val
                405
```

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```
<210> 277
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
<223> RXN00014

<400> 277
catcaaagtg accgccggcg gcgtcgaatg gtccgttgca ggaaacgcgg aagcagttag 60

tgagatctcc gaaactttaa gcgcactaga ctaacaacac atg agc aaa tat gca   115
                                            Met Ser Lys Tyr Ala
                                              1               5

gac gat tta gcc tta gcc ctc gaa ctt gcc gaa ctt gcc gat tcc atc   163
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile
                  10                  15                  20

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca   211
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro
              25                  30                  35

gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc   259
Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu
          40                  45                  50

cgt gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa   307
Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu
      55                  60                  65

gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac   355
Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp
  70                  75                  80                  85

ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca   403
Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala
```

```
                90                  95                  100

acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc   451
Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile
            105                 110                 115

tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc   499
Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly
        120                 125                 130

gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc   547
Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser
    135                 140                 145

cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc   595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser
150                 155                 160                 165

ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat   643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp
                170                 175                 180

acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc   691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu
            185                 190                 195

gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc   739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu
        200                 205                 210

tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag   787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys
    215                 220                 225

ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta   835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val
230                 235                 240                 245

gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa       880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys
                250                 255                 260

tagactcccg ggttttgctt ggt                                        903


<210> 278
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 278
Met Ser Lys Tyr Ala Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu
  1               5                  10                  15

Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu
            20                  25                  30

Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala
        35                  40                  45

Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp
```

```
     50                  55                  60

Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg
 65                  70                  75                  80

Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly
                 85                  90                  95

Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro
            100                 105                 110

Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala
        115                 120                 125

Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg
    130                 135                 140

Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser
145                 150                 155                 160

Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe
                165                 170                 175

Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe
            180                 185                 190

Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu
        195                 200                 205

Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr
    210                 215                 220

Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His
225                 230                 235                 240

Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu
                245                 250                 255

Asp Arg Leu Lys
            260
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09252010.08.2010

<210> 279
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(880)
<223> FRXA00014

<400> 279
catcaaagtg accgccggcg gcgtcgaatg gtccgttgca ggaaacgcgg aagcagttag 60

tgagatctcc gaaactttaa gcgcactaga ctagcaacac atg agc aaa tat gca 115
                                                Met Ser Lys Tyr Ala
                                                  1   5

gac gat tta gcc tta gcc ctc gaa ctc gcc gaa ctt gcc gat tcc atc 163
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile

```
                10                  15                  20

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca   211
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro
            25                  30                  35

gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc   259
Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu
        40                  45                  50

cgc gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa   307
Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu
    55                  60                  65

gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac   355
Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp
70                  75                  80                  85

ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca   403
Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala
                90                  95                  100

acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc   451
Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile
            105                 110                 115

tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc   499
Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly
        120                 125                 130

gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc   547
Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser
    135                 140                 145

cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc   595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser
150                 155                 160                 165

ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat   643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp
                170                 175                 180

acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc   691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu
            185                 190                 195

gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc   739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu
        200                 205                 210

tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag   787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys
    215                 220                 225

ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta   835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val
230                 235                 240                 245

gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa       880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys
                250                 255                 260
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tagactcccg ggttttgctt ggt 903

<210> 280
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 280
Met Ser Lys Tyr Ala Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu
1 5 10 15

Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu
20 25 30

Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala
35 40 45

Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp
50 55 60

Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg
65 70 75 80

Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly
85 90 95

Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro
100 105 110

Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala
115 120 125

Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg
130 135 140

Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser
145 150 155 160

Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe
165 170 175

Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe
180 185 190

Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu
195 200 205

Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr
210 215 220

Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His
225 230 235 240

Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu
245 250 255

Asp Arg Leu Lys
260

<210> 281
<211> 978
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(955)
<223> RXA01570

<400> 281
cactgaactc cgttttggat ctcggcaaaa tcgaagccac cggatttagc gcaccgacct 60

ggcagacccg cctcaacgac tacctcaagg aactctcaaa gtg aaa ggc atc atc 115
Val Lys Gly Ile Ile
1 5

ctc gca ggt ggc tcc ggc acc cgg ctc tac ccc atc acc aag ggc atc 163
Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro Ile Thr Lys Gly Ile
10 15 20

tcc aag caa ctg atg ccg att tac gac aaa ccc atg gtc tac tac cca 211
Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro Met Val Tyr Tyr Pro
25 30 35

ctg acc acg ctc att cag gcc ggc atc aaa gac atc ctg att atc acc 259
Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp Ile Leu Ile Ile Thr
40 45 50

acc cct gaa gac agc gcc tcc ttt gaa cgc ttg ctt ggc gac ggc tcc 307
Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu Leu Gly Asp Gly Ser
55 60 65

tcc tgg ggc atc aac ctc acc tac gcc gtc caa ccc tcc ccc gac gga 355
Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln Pro Ser Pro Asp Gly
70 75 80 85

cta gcc caa gca ttc atc atc ggc gag gaa ttc atc ggt gac gac gac 403
Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe Ile Gly Asp Asp Asp
90 95 100

gtc gcg ttg gtg ctt ggc gat aac atc ttc gac ggc gca caa ctt ggc 451
Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp Gly Ala Gln Leu Gly
105 110 115

cac gca cta aag cag tgc tcc aac ccc gac ggt ggc att gtc ttt gct 499
His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly Gly Ile Val Phe Ala
120 125 130

tat gag gtc tcc gat cct gag cgt tat ggc gtg gtg gaa ttt gat gct 547
Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val Val Glu Phe Asp Ala
135 140 145

gct aat aag gcg gtg tct att gaa gaa aag ccc acc gcg cca aaa tcc 595
Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro Thr Ala Pro Lys Ser
150 155 160 165

aac ttt gcc gtg gta gga cta tat ttc tac gac aat cgc gtg gtg gac 643
Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp Asn Arg Val Val Asp
170 175 180

```
atc gcc aag tca atc aag cct tcc tcg cgt ggc gaa ctg gaa atc acc   691
Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly Glu Leu Glu Ile Thr
            185                 190                 195

tcc gtt aac gat gcc tac ctc cag caa ggt gct tta act gtg cag cgc   739
Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala Leu Thr Val Gln Arg
        200                 205                 210

ctg gac cgt ggc gat gtc tgg tta gat acc ggc aca atc gat tcc atg   787
Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly Thr Ile Asp Ser Met
    215                 220                 225

tcc gag gcg tct tcc tat gtt gag gtc ctg caa aaa cgt acc ggc aac   835
Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln Lys Arg Thr Gly Asn
230                 235                 240                 245

atc atc gga tcc ccc gaa gtc gct gcg tac cgc gaa ggt ttc atc aca   883
Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg Glu Gly Phe Ile Thr
                250                 255                 260

gct gaa gaa ctc aca gtg ctt ggt gag gaa ctg aag aaa tca ggc tac   931
Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu Lys Lys Ser Gly Tyr
            265                 270                 275

gga aac tac ctg ctg aga gct ttg taatttacgg tgtggttgtg gag         978
Gly Asn Tyr Leu Leu Arg Ala Leu
        280                 285
```

<210> 282
<211> 285
<212> PRT
<213> Corynebacterium glutamicum

<400> 282

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Val Lys Gly Ile Ile Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro
  1               5                  10                  15

Ile Thr Lys Gly Ile Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro
             20                  25                  30

Met Val Tyr Tyr Pro Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp
         35                  40                  45

Ile Leu Ile Ile Thr Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu
     50                  55                  60

Leu Gly Asp Gly Ser Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln
 65                  70                  75                  80

Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe
                 85                  90                  95

Ile Gly Asp Asp Asp Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp
            100                 105                 110

Gly Ala Gln Leu Gly His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly
        115                 120                 125

Gly Ile Val Phe Ala Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val
```

```
    130                 135                 140

Val Glu Phe Asp Ala Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro
145                 150                 155                 160

Thr Ala Pro Lys Ser Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp
                165                 170                 175

Asn Arg Val Val Asp Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly
            180                 185                 190

Glu Leu Glu Ile Thr Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala
        195                 200                 205

Leu Thr Val Gln Arg Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly
    210                 215                 220

Thr Ile Asp Ser Met Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln
225                 230                 235                 240

Lys Arg Thr Gly Asn Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg
                245                 250                 255

Glu Gly Phe Ile Thr Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu
            260                 265                 270

Lys Lys Ser Gly Tyr Gly Asn Tyr Leu Leu Arg Ala Leu
        275                 280                 285


<210> 283
<211> 891
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(868)
<223> RXA02666

<400> 283
gctcggcgac gaggaagaga agaaggacgc attcgacgac ttcgacgatt ccgacgtgga 60

tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga   115
                                            Met Ser Ser Thr Arg
                                              1               5

atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc   163
Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly Arg Gly Thr Arg Leu
                10                  15                  20

ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt   211
Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu
            25                  30                  35

tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa   259
Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu
        40                  45                  50

atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg   307
Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu
```

```
     55                  60                  65

ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg   355
Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg
 70                  75                  80                  85

ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt   403
Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu
                90                  95                 100

cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc   451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile
            105                 110                 115

cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg   499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val
        120                 125                 130

gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca   547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro
    135                 140                 145

gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc   595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val
150                 155                 160                 165

gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc   643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly
                170                 175                 180

ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac   691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp
            185                 190                 195

ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg   739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp
        200                 205                 210

tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa   787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys
    215                 220                 225

gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa   835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu
230                 235                 240                 245

gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atcccccgcg 888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp
                250                 255

tag                                                               891


<210> 284
<211> 256
<212> PRT
<213> Corynebacterium glutamicum

<400> 284
Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly
  1               5                  10                  15
```

```
Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu
            20                  25                  30

Arg Glu Arg Thr Leu Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser
        35                  40                  45

Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr
    50                  55                  60

Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu
65                  70                  75                  80

Gly Val Arg Val Arg Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser
                85                  90                  95

Val Trp Ala Gly Leu Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp
            100                 105                 110

Ala Ile Val Leu Ile His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly
        115                 120                 125

Met Ile Ala Arg Val Val Arg Lys Val His Glu Gly Ala Thr Ala Val
    130                 135                 140

Ile Pro Val Leu Pro Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp
145                 150                 155                 160

Gly Gly Val Val Val Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val
                165                 170                 175

Gln Thr Pro Gln Gly Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu
            180                 185                 190

Lys Phe Phe Ala Asp Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala
        195                 200                 205

Ser Leu Met Glu Trp Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp
    210                 215                 220

Pro Met Ala Phe Lys Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln
225                 230                 235                 240

Arg Ile Thr Asp Glu Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp
                245                 250                 255
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<210> 285
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXA00825

<400> 285

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cccgttcatg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60

tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt   115
                                            Met Arg Thr Val Val
                                              1               5

acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc   163
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile
                 10                  15                  20

aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc   211
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg
             25                  30                  35

ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg   259
Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val
         40                  45                  50

gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac   307
Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His
     55                  60                  65

aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac   355
Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His
 70                  75                  80                  85

tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc   403
Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr
                 90                  95                 100

atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc   451
Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val
            105                 110                 115

ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca   499
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro
        120                 125                 130

gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc   547
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser
    135                 140                 145

aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc   595
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly
150                 155                 160                 165

tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa   643
Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln
                170                 175                 180

gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt   691
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu
            185                 190                 195

ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc   739
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg
        200                 205                 210

gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct   787
Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser
    215                 220                 225
```

```
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa   835
Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu
230                 235                 240                 245

acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc   883
Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser
                250                 255                 260

aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc   931
Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg
            265                 270                 275

agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct   979
Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro
        280                 285                 290

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc   1027
Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg
    295                 300                 305

act cac taggggaaaa tccaccacaa atc                                1056
Thr His
310
```

<210> 286
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 286

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Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu
  1               5                  10                  15

Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn
             20                  25                  30

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly
         35                  40                  45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
     50                  55                  60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
 65                  70                  75                  80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
                 85                  90                  95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
            100                 105                 110

Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu
        115                 120                 125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
    130                 135                 140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
145                 150                 155                 160
```

```
Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
                165                 170                 175

Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile
            180                 185                 190

Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp
        195                 200                 205

Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala
    210                 215                 220

Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile
225                 230                 235                 240

Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala
                245                 250                 255

Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu
            260                 265                 270

Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val
        275                 280                 285

Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr
    290                 295                 300

Val Glu Tyr Phe Arg Thr His
305                 310


<210> 287
<211> 1134
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1111)
<223> RXA01887

<400> 287
catctttaca ggaaacccct tgacggcatc aatgggtggt atctagtatc tactagaacg 60

ttatagtaga acgttctagt aaaacttgga aggatgaaaa atg tca gtc aaa ctt   115
                                        Met Ser Val Lys Leu
                                          1               5

gcc ctc atc ggt gct gga cgc atc gga tca aat cac gca cgc ctg atc   163
Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn His Ala Arg Leu Ile
                  10                  15                  20

aca aac cac gtg atc ggc tct gaa ctg gtc gcc gtc gtt gac cca act   211
Thr Asn His Val Ile Gly Ser Glu Leu Val Ala Val Val Asp Pro Thr
              25                  30                  35

ccc aac gca gaa acc ctc gct gat gaa ttg ggc gcc gtt gcg ttc tct   259
Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly Ala Val Ala Phe Ser
          40                  45                  50
```

```
aac cca gat gac gtc ctg acc cgc gat gac att gac gcg gtt ttg att   307
Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile Asp Ala Val Leu Ile
     55                  60                  65

gct aca cca gca cga acc cac gcg gat ctc gtg gtc aaa gca gcg gca   355
Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val Val Lys Ala Ala Ala
 70                  75                  80                  85

gcg ggc aag cac gtg ttt gtg gaa aag ccc atg gcc gtc acc ctc gag   403
Ala Gly Lys His Val Phe Val Glu Lys Pro Met Ala Val Thr Leu Glu
                 90                  95                 100

gac gca gat cgt gcc atc aac gca gca cgc gaa gca aac act gtc ctg   451
Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu Ala Asn Thr Val Leu
            105                 110                 115

cag gtg ggc ttc aat cgt cgt ttc gcg gca ggt ttc gct gca gca cgc   499
Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly Phe Ala Ala Ala Arg
        120                 125                 130

gca cgc att gac gca ggc gat atc ggc acc cca cag ctg ctt cgt tcc   547
Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro Gln Leu Leu Arg Ser
    135                 140                 145

gtg acc cgc gat cca gga cca ttc acc gct gac ccc aac aag atc cct   595
Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp Pro Asn Lys Ile Pro
150                 155                 160                 165

cag tgg acc atc ttc ctg gaa acc ctc atc cac gat ttc gat gcg ctg   643
Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His Asp Phe Asp Ala Leu
                170                 175                 180

tgc tac ctc aac cca ggc gca acc cca gtg gaa gta acc gct cac gct   691
Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu Val Thr Ala His Ala
            185                 190                 195

gat tgc ctc gtc gtt cca gaa gct gct ggc act ggc ttc ctc gac acc   739
Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr Gly Phe Leu Asp Thr
        200                 205                 210

gca gtg gtg act gtc cgt ttt gat aac gga gca att ggt act gca gaa   787
Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala Ile Gly Thr Ala Glu
    215                 220                 225

gca agc ttc agc gca gcc tat ggt tat gac gtt cgc ggt gaa gtc ttc   835
Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val Arg Gly Glu Val Phe
230                 235                 240                 245

gga tcc aag ggc atg atg acc gca ggc gac gcg cgc gca acc aac atg   883
Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala Arg Ala Thr Asn Met
                250                 255                 260

act ttc tac ggc gct gag ggc atc gcg gct gcc acc tca cgc gcg gat   931
Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala Thr Ser Arg Ala Asp
            265                 270                 275

acc gat ctg ctc tcc gat gct tac cga gct gaa ttc caa gct ttc gtc   979
Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu Phe Gln Ala Phe Val
        280                 285                 290

gac tcc atc cgt acc aac acc cct tcc aag gtt cca ggc gaa gct gca  1027
```

```
Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val Pro Gly Glu Ala Ala
    295                 300                 305

cgc acc gca cta ctc atc gca ctc ggc gcc atc cga agc gta gaa acc   1075
Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile Arg Ser Val Glu Thr
310                 315                 320                 325

ggc gca acc atc aac ctt gct gaa agc atc gag gtt taaccatgac        1121
Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu Val
                330                 335

ttttaaactc gca                                                   1134
```

<210> 288
<211> 337
<212> PRT
<213> Corynebacterium glutamicum

<400> 288

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Met Ser Val Lys Leu Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn
  1               5                  10                  15

His Ala Arg Leu Ile Thr Asn His Val Ile Gly Ser Glu Leu Val Ala
            20                  25                  30

Val Val Asp Pro Thr Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly
        35                  40                  45

Ala Val Ala Phe Ser Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile
    50                  55                  60

Asp Ala Val Leu Ile Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val
65                  70                  75                  80

Val Lys Ala Ala Ala Ala Gly Lys His Val Phe Val Glu Lys Pro Met
                85                  90                  95

Ala Val Thr Leu Glu Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu
            100                 105                 110

Ala Asn Thr Val Leu Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly
        115                 120                 125

Phe Ala Ala Ala Arg Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro
    130                 135                 140

Gln Leu Leu Arg Ser Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp
145                 150                 155                 160

Pro Asn Lys Ile Pro Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His
                165                 170                 175

Asp Phe Asp Ala Leu Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu
            180                 185                 190

Val Thr Ala His Ala Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr
        195                 200                 205

Gly Phe Leu Asp Thr Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala
    210                 215                 220
```

```
Ile Gly Thr Ala Glu Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val
225                 230                 235                 240

Arg Gly Glu Val Phe Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala
                245                 250                 255

Arg Ala Thr Asn Met Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala
            260                 265                 270

Thr Ser Arg Ala Asp Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu
        275                 280                 285

Phe Gln Ala Phe Val Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val
    290                 295                 300

Pro Gly Glu Ala Ala Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile
305                 310                 315                 320

Arg Ser Val Glu Thr Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu
                325                 330                 335

Val
```

US20070015265A1

<210> 289
<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> RXN00013

<400> 289

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ctgcagaaaa ttcgggacgc atgattgcac atattacccg caccgattgt gattcttaga 60

acgccacctt attcagcaca cttggccgac ggcatgcaca atg gaa ggc atg act   115
                                                Met Glu Gly Met Thr
                                                  1               5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa   163
Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys
                  10                  15                  20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag   211
Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu
              25                  30                  35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc   259
His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg
          40                  45                  50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat   307
Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp
      55                  60                  65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt   355
Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val
```

```
 70                  75                  80                  85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg   403
Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala
                 90                  95                 100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat   451
Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp
            105                 110                 115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc   499
Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu
        120                 125                 130

gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc   547
Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly
    135                 140                 145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga   595
Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly
150                 155                 160                 165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc   643
Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala
                170                 175                 180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc   691
Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile
            185                 190                 195

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct   739
Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro
        200                 205                 210

gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc   787
Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile
    215                 220                 225

gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg   835
Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp
230                 235                 240                 245

gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gca tgc   883
Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys
                250                 255                 260

atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg   931
Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala
            265                 270                 275

gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac           973
Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp
        280                 285                 290

taacaacaca tgagcaaata tgc                                        996
```

<210> 290
<211> 291
<212> PRT
<213> Corynebacterium glutamicum

<400> 290

```
Met Glu Gly Met Thr Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu
 1               5                  10                  15

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
            20                  25                  30

Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
        35                  40                  45

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
    50                  55                  60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
65                  70                  75                  80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
                85                  90                  95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
            100                 105                 110

Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
        115                 120                 125

Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
    130                 135                 140

Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
145                 150                 155                 160

Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp
                165                 170                 175

Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile
            180                 185                 190

His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser
        195                 200                 205

Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile
    210                 215                 220

Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His
225                 230                 235                 240

Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly
                245                 250                 255

Val Gly Gly Ala Cys Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser
            260                 265                 270

Val Ala Gly Asn Ala Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser
        275                 280                 285

Ala Leu Asp
    290
```

<210> 291

<211> 996
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(973)
<223> FRXA00013

<400> 291
ctgcagaaaa ttcgggacgc atgattgcac atattacccg caccgattgt gattcttaga 60

```
acgccacctt attcagcaca cttggccgac ggcatgcaca atg gaa ggc atg act   115
                                              Met Glu Gly Met Thr
                                                1               5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa   163
Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys
                  10                  15                  20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag   211
Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu
              25                  30                  35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc   259
His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg
          40                  45                  50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat   307
Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp
      55                  60                  65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt   355
Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val
  70                  75                  80                  85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg   403
Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala
                  90                  95                 100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat   451
Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp
             105                 110                 115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc   499
Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu
         120                 125                 130

gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc   547
Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly
     135                 140                 145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga   595
Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly
150                 155                 160                 165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc   643
Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala
                170                 175                 180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc   691
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```
Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile
            185                 190                 195

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct   739
Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro
        200                 205                 210

gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc   787
Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile
    215                 220                 225

gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg   835
Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp
230                 235                 240                 245

gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gcg tgc   883
Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys
                250                 255                 260

atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg   931
Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala
            265                 270                 275

gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac          973
Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp
        280                 285                 290

tagcaacaca tgagcaaata tgc                                       996


<210> 292
<211> 291
<212> PRT
<213> Corynebacterium glutamicum

<400> 292
Met Glu Gly Met Thr Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu
  1               5                  10                  15

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
             20                  25                  30

Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
         35                  40                  45

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
     50                  55                  60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65                  70                  75                  80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
                 85                  90                  95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
            100                 105                 110

Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
        115                 120                 125

Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
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    130                 135                 140

Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
145                 150                 155                 160

Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp
                165                 170                 175

Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile
            180                 185                 190

His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser
        195                 200                 205

Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile
    210                 215                 220

Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His
225                 230                 235                 240

Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly
                245                 250                 255

Val Gly Gly Ala Cys Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser
            260                 265                 270

Val Ala Gly Asn Ala Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser
        275                 280                 285

Ala Leu Asp
    290


<210> 293
<211> 948
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(925)
<223> RXA01099

<400> 293
ggatgagggc attgattccg tcatcattgg caaggcactt tatgagcaca agttcaccct 60

cgaagaggct ttggctgcag tagaaaagct cggttaatac atg gat gct cgt ggg   115
                                            Met Asp Ala Arg Gly
                                              1               5

atg ttg gcc att gcg gag gcc gtt gta gat gat gcc gaa gcc ctc ttc   163
Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp Ala Glu Ala Leu Phe
                  10                  15                  20

atg cag ggc ttc gga gct gca cct gcc cat atg aaa tcc ccg ggg gat   211
Met Gln Gly Phe Gly Ala Ala Pro Ala His Met Lys Ser Pro Gly Asp
              25                  30                  35

ttt gcc acg gaa gtg gat atg gcc atc gaa tcc cat atg cgt tcg atg   259
Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser His Met Arg Ser Met
          40                  45                  50
```

```
ctg aac atg atg aca ggc att gct gtc atc ggt gaa gaa ggt ggc ggt   307
Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly Glu Glu Gly Gly Gly
     55                  60                  65

gcg acc tcc ggc acg cgc tgg gtg att gat ccc atc gac ggc acc gcc   355
Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro Ile Asp Gly Thr Ala
 70                  75                  80                  85

aac ttc gcg gcg tcc aac ccg atg agc gcg atc ctg gtg tct ttg ctt   403
Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile Leu Val Ser Leu Leu
                 90                  95                 100

gtc gac gac cag ccc gtc ctg ggt att acc tcc atg ccc atg ctg ggt   451
Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser Met Pro Met Leu Gly
            105                 110                 115

aaa cgc ctc acc gct ttt gaa ggt tca ccg ctg atg atc aac ggt gaa   499
Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu Met Ile Asn Gly Glu
        120                 125                 130

cct cag gaa cca ttg caa gaa caa tcc agt ttg gta tcc cac att ggt   547
Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu Val Ser His Ile Gly
    135                 140                 145

ttt agt tcc atg gcc tcc ccg cgc aat aca gcg ttt cct gtg gag ttg   595
Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala Phe Pro Val Glu Leu
150                 155                 160                 165

cgt cgg gat ctt ctg acc gag ctc acg gaa tcg tat ctt cgt ccc cgc   643
Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser Tyr Leu Arg Pro Arg
                170                 175                 180

att aca ggt tcg gtg ggt gtt gat ctc gcg ttc act gcg cag ggc att   691
Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe Thr Ala Gln Gly Ile
            185                 190                 195

ttt gga gca tgc gta tcg ttt agt cct cat gtt tgg gac aat tcc gca   739
Phe Gly Ala Cys Val Ser Phe Ser Pro His Val Trp Asp Asn Ser Ala
        200                 205                 210

ggc gtg atg ttg atg cgc gct gct ggt gca caa gtt act gac acc gaa   787
Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln Val Thr Asp Thr Glu
    215                 220                 225

ggc cat ccg tgg gca cca ggt agg gga gtc gtg gcc gga aca aaa agg   835
Gly His Pro Trp Ala Pro Gly Arg Gly Val Val Ala Gly Thr Lys Arg
230                 235                 240                 245

gct cac gat gtg ctg tta agt aag att gaa aaa gtt cgg ttg atg cat   883
Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys Val Arg Leu Met His
                250                 255                 260

gca gat gca ggt aat gac cag tcg tta aat gag gag tac aag           925
Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu Glu Tyr Lys
            265                 270                 275

taaaatgggc gtggcaattc gag                                        948
```

<210> 294

<211> 275
<212> PRT
<213> Corynebacterium glutamicum

<400> 294

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Met Asp Ala Arg Gly Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp
  1               5                  10                  15

Ala Glu Ala Leu Phe Met Gln Gly Phe Gly Ala Ala Pro Ala His Met
             20                  25                  30

Lys Ser Pro Gly Asp Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser
         35                  40                  45

His Met Arg Ser Met Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly
     50                  55                  60

Glu Glu Gly Gly Gly Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro
 65                  70                  75                  80

Ile Asp Gly Thr Ala Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile
                 85                  90                  95

Leu Val Ser Leu Leu Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser
            100                 105                 110

Met Pro Met Leu Gly Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu
        115                 120                 125

Met Ile Asn Gly Glu Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu
    130                 135                 140

Val Ser His Ile Gly Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala
145                 150                 155                 160

Phe Pro Val Glu Leu Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser
                165                 170                 175

Tyr Leu Arg Pro Arg Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe
            180                 185                 190

Thr Ala Gln Gly Ile Phe Gly Ala Cys Val Ser Phe Ser Pro His Val
        195                 200                 205

Trp Asp Asn Ser Ala Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln
    210                 215                 220

Val Thr Asp Thr Glu Gly His Pro Trp Ala Pro Gly Arg Gly Val Val
225                 230                 235                 240

Ala Gly Thr Lys Arg Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys
                245                 250                 255

Val Arg Leu Met His Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu
            260                 265                 270

Glu Tyr Lys
        275
```

<210> 295

<211> 576
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(576)
<223> RXN01332

<400> 295

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cac atc tct gcc att att gag ccc gac gca gca cgt gcc gct gca gct   48
His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala
  1               5                  10                  15

gca gaa gac gcg ccg ggt gca cag gcc ttc act cgc att gaa gat gct   96
Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala
             20                  25                  30

atc gca gcc gat gct gtc gac gca gtg ctg atc gcc gta cca ggt cag   144
Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln
         35                  40                  45

ttc cat gag cca gta ctt gtc cca gca cta gaa gca ggc ctt ccc atc   192
Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
     50                  55                  60

ctg tgt gaa aag cca ctg acc cca gat tct gaa tcc tca ctg cgc atc   240
Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
 65                  70                  75                  80

gtc gag ctg gag cag aag ctg gac aag cca cac atc cag gtt ggt ttc   288
Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
                 85                  90                  95

atg cgc cgc ttc gac cct gag tac aac aac ttg cgc aaa ttg gtg gaa   336
Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
            100                 105                 110

tcc ggc gaa gct ggc gaa ctg ctc atg ctc cgc ggc ctg cac cgc aac   384
Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
        115                 120                 125

cca agt gtt ggt gag agc tac acc cag tcc atg ctg atc acc gac tcc   432
Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
    130                 135                 140

gtc gtc cac gaa ttc gat gtc atc cca tgg ctc gca ggc tcc cga gtt   480
Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
145                 150                 155                 160

gtc tcc gtt gaa gtg aag tac cca aag acc tcc tca ctg gcg cac tcc   528
Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser
                165                 170                 175

ggc ctc aag gaa cca atc ctg gtg atc atg gag ctc gaa aac ggc gtg   576
Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val
            180                 185                 190
```

<210> 296
<211> 192

<212> PRT
<213> Corynebacterium glutamicum

<400> 296
His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala
1 5 10 15

Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala
20 25 30

Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln
35 40 45

Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
50 55 60

Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
65 70 75 80

Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
85 90 95

Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
100 105 110

Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
115 120 125

Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
130 135 140

Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
145 150 155 160

Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser
165 170 175

Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val
180 185 190

<210> 297
<211> 549
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(549)
<223> FRXA01332

<400> 297
gca gca cgt gcc gct gca gct gca gaa gac gcg ccg ggt gca cag gcc 48
Ala Ala Arg Ala Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala
1 5 10 15

ttc act cgc att gaa gat gct atc gca gcc gat gct gtc gac gca gtg 96
Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val

```
            20                  25                  30

ctg atc gcc gta cca ggt cag ttc cat gag cca gta ctt gtc cca gca   144
Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala
        35                  40                  45

cta gaa gca ggc ctt ccc atc ctg tgt gaa aag cca ctg acc cca gat   192
Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp
    50                  55                  60

tct gaa tcc tca ctg cgc atc gtc gag ctg gag cag aag ctg gac aag   240
Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys
65                  70                  75                  80

cca cac atc cag gtt ggt ttc atg cgc cgc ttc gac cct gag tac aac   288
Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn
                85                  90                  95

aac ttg cgc aaa ttg gtg gaa tcc ggc gaa gct ggc gaa ctg ctc atg   336
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met
            100                 105                 110

ctc cgc ggc ctg cac cgc aac cca agt gtt ggt gag agc tac acc cag   384
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln
        115                 120                 125

tcc atg ctg atc acc gac tcc gtc gtc cac gaa ttc gat gtc atc cca   432
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro
    130                 135                 140

tgg ctc gca ggc tcc cga gtt gtc tcc gtt gaa gtg aag tac cca aag   480
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys
145                 150                 155                 160

acc tcc tca ctg gcg cac tcc ggc ctc aag gaa cca atc ctg gtg atc   528
Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile
                165                 170                 175

atg gag ctc gaa aac ggc gtg                                      549
Met Glu Leu Glu Asn Gly Val
            180
```

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<210> 298
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 298

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Ala Ala Arg Ala Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala
  1               5                  10                  15

Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val
            20                  25                  30

Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala
        35                  40                  45

Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp
    50                  55                  60
```

```
Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys
 65                  70                  75                  80

Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn
                85                  90                  95

Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met
            100                 105                 110

Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln
        115                 120                 125

Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro
    130                 135                 140

Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys
145                 150                 155                 160

Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile
                165                 170                 175

Met Glu Leu Glu Asn Gly Val
            180
```

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<210> 299
<211> 1128
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1105)
<223> RXA01632

<400> 299

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aagggctgca acgtgctttc gacaccacca tcgcagcgtt tgaacaagct gctcgtctcg 60

ccccctccac taactgatct ttgaaaggct gaaaaaactc atg act ctt cgt atc   115
                                            Met Thr Leu Arg Ile
                                              1               5

gcc ctt ttc ggc gct ggc cgc atc ggt cac gtc cac gct gcc aac att   163
Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val His Ala Ala Asn Ile
                10                  15                  20

gct gca aac cct gat ctt gaa ctc gtt gtt atc gcc gat cct ttc att   211
Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile Ala Asp Pro Phe Ile
            25                  30                  35

gaa ggc gca cag cgt ttg gca gaa gcc aat ggg gca gaa gcg gtt gca   259
Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly Ala Glu Ala Val Ala
        40                  45                  50

tca cca gat gag gtg ttc gcc cgc gat gat atc gat ggc atc gtg atc   307
Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile Asp Gly Ile Val Ile
    55                  60                  65

ggt tca cca acc agc acc cac gtt gat ctg atc acc cgc gcc gtg gaa   355
Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile Thr Arg Ala Val Glu
70                  75                  80                  85
```

```
cgt ggc att cct gca ctg tgc gaa aaa ccc att gat tta gac att gaa   403
Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile Asp Leu Asp Ile Glu
                 90                  95                 100

atg gtg cgt gcc tgc aaa gag aag atc ggc gac ggc gct tcc aag gtg   451
Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp Gly Ala Ser Lys Val
            105                 110                 115

atg ctg ggg ttt aac cga cgc ttc gat cct tct ttc gct gcc atc aat   499
Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser Phe Ala Ala Ile Asn
        120                 125                 130

gcg cga gtg gca aac cag gag atc ggc aac ctg gag cag ttg gtg atc   547
Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu Glu Gln Leu Val Ile
    135                 140                 145

atc agc cgc gat cca gcg ccc gca ccg aag gac tac atc gca ggt tcc   595
Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp Tyr Ile Ala Gly Ser
150                 155                 160                 165

ggt gga atc ttc cgc gat atg acc atc cac gat ctg gat atg gcg cgt   643
Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp Leu Asp Met Ala Arg
                170                 175                 180

ttc ttt gtg ccc aat atc gtg gaa gtg act gca acc ggc gcc aat gtt   691
Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala Thr Gly Ala Asn Val
            185                 190                 195

ttc agc cag gaa atc gcg gag ttc aat gac tac gac cag gtt atc gtc   739
Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr Asp Gln Val Ile Val
        200                 205                 210

acg ctt cgt ggc tca aag ggc gag ttg atc aac atc gtg aac tcc cgc   787
Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn Ile Val Asn Ser Arg
    215                 220                 225

cac tgc tcc tac ggc tac gac cag cga ctt gag gct ttc ggc tct aag   835
His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu Ala Phe Gly Ser Lys
230                 235                 240                 245

ggc atg ctc gcc gcc gac aac atc agg ccc acc acg gtg cgc aag cac   883
Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr Thr Val Arg Lys His
                250                 255                 260

aat gcg gaa agc acc gag cag gca gat ccg att ttc aac ttc ttc ctc   931
Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile Phe Asn Phe Phe Leu
            265                 270                 275

gag cgc tac gac gcc gct tac aag gca gag ctc gca act ttt gct caa   979
Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu Ala Thr Phe Ala Gln
        280                 285                 290

gga atc cgc gac ggc caa ggc ttc tca cca aac ttc gag gac ggc gtc   1027
Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn Phe Glu Asp Gly Val
    295                 300                 305

atc gcc ctt gaa cta gcg aat gca tgc ctt gaa tca gct caa acc ggc   1075
Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu Ser Ala Gln Thr Gly
310                 315                 320                 325
```

```
cgc acc gtc acc ctc aac cct gcc aac gtt tagtcaacgt ctagttaatg      1125
Arg Thr Val Thr Leu Asn Pro Ala Asn Val
                330                 335

cct                                                               1128
```

<210> 300
<211> 335
<212> PRT
<213> Corynebacterium glutamicum

<400> 300

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Met Thr Leu Arg Ile Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val
  1               5                  10                  15

His Ala Ala Asn Ile Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile
            20                  25                  30

Ala Asp Pro Phe Ile Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly
        35                  40                  45

Ala Glu Ala Val Ala Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile
    50                  55                  60

Asp Gly Ile Val Ile Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile
65                  70                  75                  80

Thr Arg Ala Val Glu Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile
                85                  90                  95

Asp Leu Asp Ile Glu Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp
            100                 105                 110

Gly Ala Ser Lys Val Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser
        115                 120                 125

Phe Ala Ala Ile Asn Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu
    130                 135                 140

Glu Gln Leu Val Ile Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp
145                 150                 155                 160

Tyr Ile Ala Gly Ser Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp
                165                 170                 175

Leu Asp Met Ala Arg Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala
            180                 185                 190

Thr Gly Ala Asn Val Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr
        195                 200                 205

Asp Gln Val Ile Val Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn
    210                 215                 220

Ile Val Asn Ser Arg His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu
225                 230                 235                 240

Ala Phe Gly Ser Lys Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr
                245                 250                 255
```

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```
Thr Val Arg Lys His Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile
            260                 265                 270

Phe Asn Phe Phe Leu Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu
        275                 280                 285

Ala Thr Phe Ala Gln Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn
    290                 295                 300

Phe Glu Asp Gly Val Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu
305                 310                 315                 320

Ser Ala Gln Thr Gly Arg Thr Val Thr Leu Asn Pro Ala Asn Val
                325                 330                 335


<210> 301
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> RXA01633

<400> 301
gcgaatgcat gccttgaatc agctcaaacc ggccgcaccg tcaccctcaa ccctgccaac 60

gtttagtcaa cgtctagtta atgcctaagg agaaaacctc atg aaa aac atc acc   115
                                            Met Lys Asn Ile Thr
                                              1               5

atc gga atg gtc ggc gtc ggc cgc att ggc cgc atg cac gtc gcc aac   163
Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg Met His Val Ala Asn
                  10                  15                  20

atg ctt gcc gtt gct gaa act ttg aag gaa cgc gac ctc aac att gag   211
Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg Asp Leu Asn Ile Glu
              25                  30                  35

atc gtg ctc gca gac gca atg ccc ggt ttt gcg gag cag gtg ggc gcg   259
Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala Glu Gln Val Gly Ala
          40                  45                  50

gac atg ggc gtg aag gcg gcg gca agc gtc gat aag ctt att gag gac   307
Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp Lys Leu Ile Glu Asp
      55                  60                  65

ggg gtg gat gcc ctt ttc att gcc acc agc acc gct ggc cac gtc gat   355
Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr Ala Gly His Val Asp
  70                  75                  80                  85

gtt ttg cgc aag ggc atc gcg gca aag ctg ccg atg ttc tgc gag aag   403
Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro Met Phe Cys Glu Lys
                  90                  95                 100

ccg atc gcg tcg gat gtg cct gag tcg ctg aac atc atc cgc gaa att   451
Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn Ile Ile Arg Glu Ile
              105                 110                 115
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gat gcg gct ggc gcg acg gtt cag gtc ggc cac cag cgc cgt ttt gac   499
Asp Ala Ala Gly Ala Thr Val Gln Val Gly His Gln Arg Arg Phe Asp
        120                 125                 130

ctc ggt tac cag gaa gct aaa cga cgc cta gat gca ggc gac ctc ggc   547
Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp Ala Gly Asp Leu Gly
    135                 140                 145

tgg ctt cat tcg ctc aag gcc gta tcg agc gat gcg ttt ccg cca ccg   595
Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp Ala Phe Pro Pro Pro
150                 155                 160                 165

gtg tcc tac tgc gct acc tct ggt gga ctt ttc cgc gat gtg tcg ctg   643
Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe Arg Asp Val Ser Leu
                170                 175                 180

cac gat ttc gac atc att cgc tgg ctg acc ggc cag gat att gtc gag   691
His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly Gln Asp Ile Val Glu
            185                 190                 195

gtg tac gcc aag ggc agc aac aac ggc gac cca gaa atc ggc gca gtc   739
Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro Glu Ile Gly Ala Val
        200                 205                 210

ggt gac atc gat acc gga gcg gcc cta ctc acg ctt gcc gac ggc acc   787
Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr Leu Ala Asp Gly Thr
    215                 220                 225

ctc gcc acc gcc atc gcc act cgt tac aac ggt gca ggc cac gac gtt   835
Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly Ala Gly His Asp Val
230                 235                 240                 245

cgc ctc gat gtt atg ggc tct aaa gat tcc acg atc gtt ggc ctg gat   883
Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr Ile Val Gly Leu Asp
                250                 255                 260

gaa aag tct gcg ttc gct tct gcg gag gag ggc atc gat ttc cca acc   931
Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly Ile Asp Phe Pro Thr
            265                 270                 275

ggc gaa tcg cac cca acg ttt gcc gag cgc ttc gcc gac gca tac aag   979
Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe Ala Asp Ala Tyr Lys
        280                 285                 290

aat gag tgc att gcg ttc gtg gag ttg atc ctg gga gag cgg gaa aac   1027
Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu Gly Glu Arg Glu Asn
    295                 300                 305

cct tgt acc cct gca gac gct gtg gct gcg gcg att gtt gcc gat gca   1075
Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ala Ile Val Ala Asp Ala
310                 315                 320                 325

gct cag ctg tcg ctg gtc act ggc gag cca gtg aag att cct act gta   1123
Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val Lys Ile Pro Thr Val
                330                 335                 340

cgg gaa att ctt gaa ggt tct gcg cag cca gtt gag gtg cgt gcg ctg   1171
Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val Glu Val Arg Ala Leu
            345                 350                 355

gtt cca tct gct taaaacctta ctgcttatct aaa                        1206
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Val Pro Ser Ala
360

<210> 302
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 302
Met Lys Asn Ile Thr Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg
1 5 10 15

Met His Val Ala Asn Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg
20 25 30

Asp Leu Asn Ile Glu Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala
35 40 45

Glu Gln Val Gly Ala Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp
50 55 60

Lys Leu Ile Glu Asp Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr
65 70 75 80

Ala Gly His Val Asp Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro
85 90 95

Met Phe Cys Glu Lys Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn
100 105 110

Ile Ile Arg Glu Ile Asp Ala Ala Gly Ala Thr Val Gln Val Gly His
115 120 125

Gln Arg Arg Phe Asp Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp
130 135 140

Ala Gly Asp Leu Gly Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp
145 150 155 160

Ala Phe Pro Pro Pro Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe
165 170 175

Arg Asp Val Ser Leu His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly
180 185 190

Gln Asp Ile Val Glu Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro
195 200 205

Glu Ile Gly Ala Val Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr
210 215 220

Leu Ala Asp Gly Thr Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly
225 230 235 240

Ala Gly His Asp Val Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr
245 250 255

Ile Val Gly Leu Asp Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly
260 265 270

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Ile Asp Phe Pro Thr Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe
        275                 280                 285

Ala Asp Ala Tyr Lys Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu
    290                 295                 300

Gly Glu Arg Glu Asn Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ala
305                 310                 315                 320

Ile Val Ala Asp Ala Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val
                325                 330                 335

Lys Ile Pro Thr Val Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val
            340                 345                 350

Glu Val Arg Ala Leu Val Pro Ser Ala
        355                 360


<210> 303
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> RXN01406

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ttcctcctct tagaaaccca cttctgaaag gtataaaaac atg act att cga atc   115
                                            Met Thr Ile Arg Ile
                                              1               5

gga ctc gtt ggc tac ggt gtc ggc ggc agg ctc ttt cac acc cct tac   163
Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu Phe His Thr Pro Tyr
                  10                  15                  20

atc caa gct tct acg cac tgc gaa tta gta ggc gta gtt gct cgt tcc   211
Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly Val Val Ala Arg Ser
              25                  30                  35

gaa ggc acc aaa gca gcc gtt gca gaa gat ctt cca gat gtt gcc atc   259
Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu Pro Asp Val Ala Ile
          40                  45                  50

gtg gga tcg ctg aca gaa ctc ctc gaa ctg ggc gtc gat gca gtg gtg   307
Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly Val Asp Ala Val Val
      55                  60                  65

atc tcc acc cct cca gcc acg cgc cgg gaa ctg gcc ttg gaa gca atc   355
Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu Ala Leu Glu Ala Ile
  70                  75                  80                  85

aac gca ggt gtc gca gtg gtt gcc gat aaa ccg ttt gca cca tca gcc   403
Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro Phe Ala Pro Ser Ala
                  90                  95                 100

gca gat gcc atg gaa ctt gtc gaa gcc gcc gaa aag gct gga gtg ctg   451
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Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu Lys Ala Gly Val Leu
            105                 110                 115

ctc aac gtc ttc cac aac agg cgc aac gac acc cac att gtc acg gca   499
Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr His Ile Val Thr Ala
        120                 125                 130

ctg gga atc caa gaa gaa ctt ggt gcg atg cgt gga ctg gac ctg cga   547
Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg Gly Leu Asp Leu Arg
    135                 140                 145

cta gac ctg atc gaa cct gat tcc ttg gag gca ggt cct gaa ggt ggt   595
Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala Gly Pro Glu Gly Gly
150                 155                 160                 165

ttg ctg cgc gat ctg ggc tca cac gta gtc gat cag acc ctg gtt ctc   643
Leu Leu Arg Asp Leu Gly Ser His Val Val Asp Gln Thr Leu Val Leu
                170                 175                 180

atg ggg ccg gct acc tct gtc acc gcc caa ctt gga tcc atc gac ctt   691
Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu Gly Ser Ile Asp Leu
            185                 190                 195

cca gaa ggc cca acc aac gca agg ttc cgc atc gtg ttg gaa cat gaa   739
Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile Val Leu Glu His Glu
        200                 205                 210

tcg ggc gcc gta tcg cac att tct gcc agc aag att gac cgc ttg gag   787
Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys Ile Asp Arg Leu Glu
    215                 220                 225

tcc tgg gaa atc cgc ttg gtg ggc gag cgc ggc tcc tac gta tcc aac   835
Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly Ser Tyr Val Ser Asn
230                 235                 240                 245

tac acc gac gtg cag acc gtg gcg atc aaa cag gga ctt cga cca acc   883
Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln Gly Leu Arg Pro Thr
                250                 255                 260

aat gac cgc gaa cac tgg ggc tac gaa tcg gag gag cgg tgg ggc acc   931
Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu Glu Arg Trp Gly Thr
            265                 270                 275

ttg gtt acc gat gaa ggc tca aag gtg att cct tca gca caa ggc gat   979
Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro Ser Ala Gln Gly Asp
        280                 285                 290

tac acc cgc ttc tac gat gcc ttt gcc ttg gct gtg gaa aac ggt ggc  1027
Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala Val Glu Asn Gly Gly
    295                 300                 305

gca ggg ccg gtg cct gca cgt gaa ggt gtt gca gtg ctc aag gtg ttg  1075
Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala Val Leu Lys Val Leu
310                 315                 320                 325

gat gct gta gcc cag agc gct gcg gaa aaa cgc acc att gag ttg agc  1123
Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg Thr Ile Glu Leu Ser
                330                 335                 340

taaggagaag tgctgctggc tgc                                       1146
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<210> 304
<211> 341
<212> PRT
<213> Corynebacterium glutamicum

<400> 304

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Met Thr Ile Arg Ile Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu
  1               5                  10                  15

Phe His Thr Pro Tyr Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly
             20                  25                  30

Val Val Ala Arg Ser Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu
         35                  40                  45

Pro Asp Val Ala Ile Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly
     50                  55                  60

Val Asp Ala Val Val Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu
 65                  70                  75                  80

Ala Leu Glu Ala Ile Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro
                 85                  90                  95

Phe Ala Pro Ser Ala Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu
            100                 105                 110

Lys Ala Gly Val Leu Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr
        115                 120                 125

His Ile Val Thr Ala Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg
    130                 135                 140

Gly Leu Asp Leu Arg Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala
145                 150                 155                 160

Gly Pro Glu Gly Gly Leu Leu Arg Asp Leu Gly Ser His Val Val Asp
                165                 170                 175

Gln Thr Leu Val Leu Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu
            180                 185                 190

Gly Ser Ile Asp Leu Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile
        195                 200                 205

Val Leu Glu His Glu Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys
    210                 215                 220

Ile Asp Arg Leu Glu Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly
225                 230                 235                 240

Ser Tyr Val Ser Asn Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln
                245                 250                 255

Gly Leu Arg Pro Thr Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu
            260                 265                 270

Glu Arg Trp Gly Thr Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro
        275                 280                 285
```

```
Ser Ala Gln Gly Asp Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala
    290                 295                 300

Val Glu Asn Gly Gly Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala
305                 310                 315                 320

Val Leu Lys Val Leu Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg
                325                 330                 335

Thr Ile Glu Leu Ser
            340


<210> 305
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1177)
<223> RXN01630

<400> 305
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ccagataaaa acctgcgggt tgcgttttag gagaattccc atg agt gat caa aaa   115
                                            Met Ser Asp Gln Lys
                                              1               5

att gtt gtt ggc ctg cta ggc atc acc cac ccg cat gcg tcg gcg cgg   163
Ile Val Val Gly Leu Leu Gly Ile Thr His Pro His Ala Ser Ala Arg
                10                  15                  20

gtg cgt gcc ctc cgt gaa att gat ggg gta gag gtc gtc gcc gcc gcg   211
Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu Val Val Ala Ala Ala
            25                  30                  35

gat act gat tcc cgc ctc cag tac ttc acc gac aaa tat gat gtt gaa   259
Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp Lys Tyr Asp Val Glu
        40                  45                  50

ccc cgc gag atc gat gac gtc ttg aac gac gat cgc atc aac gcc atc   307
Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp Arg Ile Asn Ala Ile
    55                  60                  65

atg gtt cac tcc aag agc aag gac atg gtc cct cac gcc aag cgc gcg   355
Met Val His Ser Lys Ser Lys Asp Met Val Pro His Ala Lys Arg Ala
70                  75                  80                  85

ctc gcg gcc gga aaa tcc gtc gtc gtg gag aag ccc ggc ggg gga aca   403
Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys Pro Gly Gly Gly Thr
                90                  95                  100

gtg gcg gat ctt gag gag ctc ctg gcc ctc aaa gaa gct gcc gat cct   451
Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys Glu Ala Ala Asp Pro
            105                 110                 115

cag cga atc gtg cag gtc ggg tac aac gtc cgc ctg tct gaa tcg gtt   499
Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg Leu Ser Glu Ser Val
        120                 125                 130
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cag aga tta aaa gag ctt ctc gac gcc ggc ctc atc ggc gaa gtc gtc   547
Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu Ile Gly Glu Val Val
    135                 140                 145

agc gtg caa gca cgc ggc gcc gca aaa gta ggt gag cat atc acc gag   595
Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly Glu His Ile Thr Glu
150                 155                 160                 165

cac ctc aac caa ccc gca gac atg ggc ggt gtg ttg tgg att ctt ggc   643
His Leu Asn Gln Pro Ala Asp Met Gly Gly Val Leu Trp Ile Leu Gly
                170                 175                 180

tgc cac atg ctc gat gca ttg gtg gaa gtc ttc gga gct cca gaa tcc   691
Cys His Met Leu Asp Ala Leu Val Glu Val Phe Gly Ala Pro Glu Ser
            185                 190                 195

gtg aac gcc cga gtg cat aag acc gca aaa ctc tct gac gac acc agc   739
Val Asn Ala Arg Val His Lys Thr Ala Lys Leu Ser Asp Asp Thr Ser
        200                 205                 210

cgc gaa gac tca gcc tcc gca ctg ctg tac tac cca gat ttc tcc gtc   787
Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr Pro Asp Phe Ser Val
    215                 220                 225

agc ttc agc ttc gac ggc cac gat gat ctg gaa tgg ttc gaa agc tcc   835
Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu Trp Phe Glu Ser Ser
230                 235                 240                 245

cga ctc acg gtc tat gga acc aag ggc atg atc gaa gcc gga atc ctc   883
Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile Glu Ala Gly Ile Leu
                250                 255                 260

cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag ggc tgg cca   931
Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro
            265                 270                 275

cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca ccg ttt gct   979
Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Pro Phe Ala
        280                 285                 290

cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc   1027
Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile
    295                 300                 305

agc aac ttc cgc aca gaa atg cag ggg tgg gtg aat tcc att cgc act   1075
Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr
310                 315                 320                 325

gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc   1123
Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg
                330                 335                 340

att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta   1171
Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn Gln Gly Ile Ser Val
            345                 350                 355

aac atc taagaggagc actccatgaa acc                                1200
Asn Ile
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09852900.050902

<210> 306
<211> 359
<212> PRT
<213> Corynebacterium glutamicum

<400> 306
Met Ser Asp Gln Lys Ile Val Val Gly Leu Leu Gly Ile Thr His Pro
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His Ala Ser Ala Arg Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu
20 25 30

Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp
35 40 45

Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp
50 55 60

Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro
65 70 75 80

His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys
85 90 95

Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys
100 105 110

Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg
115 120 125

Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu
130 135 140

Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly
145 150 155 160

Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val
165 170 175

Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe
180 185 190

Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu
195 200 205

Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr
210 215 220

Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu
225 230 235 240

Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile
245 250 255

Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser
260 265 270

Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe
275 280 285

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Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro
    290                 295                 300

Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val
305                 310                 315                 320

Asn Ser Ile Arg Thr Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala
                325                 330                 335

Leu Thr Val Ala Arg Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn
            340                 345                 350

Gln Gly Ile Ser Val Asn Ile
        355
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<210> 307
<211> 1212
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1189)
<223> RXN00528

<400> 307

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tcggtcgcgg ccgttatctt tttaagagga gaaattttag atg agc acg tcc acc   115
                                              Met Ser Thr Ser Thr
                                                1               5

atc agg gtt gcc att gcc gga gtc gga aac tgc gcg acc tcc ctc att   163
Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys Ala Thr Ser Leu Ile
                10                  15                  20

cag ggt gtg gaa tat tac cga aat gcg gat cct tcc gaa act gtc ccg   211
Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro Ser Glu Thr Val Pro
            25                  30                  35

ggt ttg atg cac gtc aaa ttc ggt gat tac cac gtt ggc gac att gaa   259
Gly Leu Met His Val Lys Phe Gly Asp Tyr His Val Gly Asp Ile Glu
        40                  45                  50

ttc gtg gcc gcg ttc gac gtc gac gcc gaa aaa gta ggc atc gat ctt   307
Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys Val Gly Ile Asp Leu
    55                  60                  65

gcc gac gcc acc gag gct tca caa aac tgc act atc aaa atc gcc gat   355
Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr Ile Lys Ile Ala Asp
70                  75                  80                  85

gtc cca cag acc ggc atc aac gtg ctg cgt ggc ccg act ctc gac ggc   403
Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly Pro Thr Leu Asp Gly
                90                  95                  100

ctg ggc gat cat tac cgc gcg acc atc gac gag tcc acc gcc gag cca   451
Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu Ser Thr Ala Glu Pro
            105                 110                 115
```

```
gtc gac gtt gtc cag gcg ctt atc gac gca aaa gcc gat gtt ttg gtg   499
Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys Ala Asp Val Leu Val
        120                 125                 130

tcc tac ctc cca gtg ggc tcc gaa gaa gcc gac aaa ttc tac gca caa   547
Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp Lys Phe Tyr Ala Gln
    135                 140                 145

gcc gcc atc gat gca ggc tgc gcc ttt gtc aac gct ctc cca gta ttc   595
Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn Ala Leu Pro Val Phe
150                 155                 160                 165

atc gcc tcc gac cct gag tgg gct aag aag ttc act gac gct ggc atc   643
Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe Thr Asp Ala Gly Ile
                170                 175                 180

cca att gtt ggc gat gac atc aaa tcc cag atc ggt gca acc atc acc   691
Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile Gly Ala Thr Ile Thr
            185                 190                 195

cac cgt gtc ctc gca cgc ctt ttt gaa gaa cgt ggc gtt cgc gta gat   739
His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg Gly Val Arg Val Asp
        200                 205                 210

cgc acc atg cag ctc aac gtc ggc ggc aac atg gac ttc aaa aac atg   787
Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met Asp Phe Lys Asn Met
    215                 220                 225

ctt gac cgc aat cgc ttg gaa tcc aag aag gtc tcc aaa acc caa gca   835
Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val Ser Lys Thr Gln Ala
230                 235                 240                 245

gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac   883
Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp
                250                 255                 260

cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac   931
Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp
            265                 270                 275

cgc aag tgg gct tat gtc cgc ctc gaa ggc acc gca ttc ggt gga gtt   979
Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val
        280                 285                 290

ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct  1027
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser
    295                 300                 305

gcc ggc atc atc atc gac gct gtt cgc gcc gcc aag atc gcc ctc gat  1075
Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp
310                 315                 320                 325

cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag  1123
Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys
                330                 335                 340

tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag  1171
Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu
            345                 350                 355

gca ttc atc atc gag gcg taaaattagg ctaaaaattt ggg                1212
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Ala Phe Ile Ile Glu Ala
360

<210> 308
<211> 363
<212> PRT
<213> Corynebacterium glutamicum

<400> 308
Met Ser Thr Ser Thr Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys
1 5 10 15

Ala Thr Ser Leu Ile Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro
20 25 30

Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His
35 40 45

Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys
50 55 60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr
65 70 75 80

Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly
85 90 95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu
100 105 110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys
115 120 125

Ala Asp Val Leu Val Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp
130 135 140

Lys Phe Tyr Ala Gln Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn
145 150 155 160

Ala Leu Pro Val Phe Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe
165 170 175

Thr Asp Ala Gly Ile Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile
180 185 190

Gly Ala Thr Ile Thr His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg
195 200 205

Gly Val Arg Val Asp Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met
210 215 220

Asp Phe Lys Asn Met Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val
225 230 235 240

Ser Lys Thr Gln Ala Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser
245 250 255

Gly Lys Val Glu Asp Arg Asn Val His Ile Gly Pro Ser Asp His Val
260 265 270

Sequence Listing

```
Gln Trp Leu Asp Asp Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr
        275                 280                 285

Ala Phe Gly Gly Val Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp
    290                 295                 300

Asp Ser Pro Asn Ser Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala
305                 310                 315                 320

Lys Ile Ala Leu Asp Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser
                325                 330                 335

Ser Tyr Leu Met Lys Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala
            340                 345                 350

Cys Glu Arg Leu Glu Ala Phe Ile Ile Glu Ala
        355                 360


<210> 309
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> RXN03057

<400> 309
catcaacgcc gagtacaact aaggacaact gataatgaca aatgctgcaa ttgtcggatg 60

aggagacgtc gcaaccgttc atacagaagc gctggaagct ttg gct tcc gat ctt   115
                                              Leu Ala Ser Asp Leu
                                                1               5

ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag   163
Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
                10                  15                  20

aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc   211
Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
            25                  30                  35

gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc   259
Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
        40                  45                  50

gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct   307
Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
    55                  60                  65

ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg   355
Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
70                  75                  80                  85

gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa   403
Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
                90                  95                  100

aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac   451
```

```
Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
          105                 110                 115

gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt   499
Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
        120                 125                 130

gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc   547
Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
    135                 140                 145

tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt   595
Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
150                 155                 160                 165

ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg   643
Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
                170                 175                 180

ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag   691
Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
          185                 190                 195

tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt   739
Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
        200                 205                 210

cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792
His Glu Ser Gly Val His Thr Ser Glu Val Ser
    215                 220

aca                                                               795


<210> 310
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 310
Leu Ala Ser Asp Leu Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp
  1               5                  10                  15

Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
            20                  25                  30

Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
        35                  40                  45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
    50                  55                  60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
65                  70                  75                  80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
                85                  90                  95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr
            100                 105                 110
```

```
Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp
        115                 120                 125

Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp
    130                 135                 140

Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln
145                 150                 155                 160

Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu
                165                 170                 175

Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr
            180                 185                 190

Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala
        195                 200                 205

His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser
    210                 215                 220
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09/25/2003 15:09:09

<210> 311
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> FRXA02902

<400> 311

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catcaacgcc gagtacaact aaggacaact gataatgaca aatgctgcaa ttgtcggatg 60

aggagacgtc gcaaccgttc atacagaagc gctggaagct ttg gct tcc gat ctt   115
                                              Leu Ala Ser Asp Leu
                                                1               5

ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag   163
Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
                10                  15                  20

aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc   211
Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
            25                  30                  35

gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc   259
Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
        40                  45                  50

gat gtt cta cac atc acc acc ccc cac gac caa cac att ggt ttg gct   307
Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
    55                  60                  65

ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg   355
Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
70                  75                  80                  85
```

```
gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa   403
Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
                90                  95                 100

aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac   451
Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
            105                 110                 115

gtt tcc tcc cag gaa ctg cgt cgt ctg ctc gat tca ggt gac ctc ggt   499
Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
        120                 125                 130

gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc   547
Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
    135                 140                 145

tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt   595
Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
150                 155                 160                 165

ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg   643
Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
                170                 175                 180

ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag   691
Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
            185                 190                 195

tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt   739
Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
        200                 205                 210

cac gag tcc gga gtc cac acc agt gaa gtg agt tgaaccatgc tattggtgat 792
His Glu Ser Gly Val His Thr Ser Glu Val Ser
    215                 220

aca                                                               795
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US09/900,900

<210> 312
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 312

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Leu Ala Ser Asp Leu Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp
  1               5                  10                  15

Leu Glu Thr Ala Glu Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp
             20                  25                  30

Ser Ser Glu Ser Ser Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe
         35                  40                  45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
     50                  55                  60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65                  70                  75                  80
```

```
Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
                85                  90                  95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr
            100                 105                 110

Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp
        115                 120                 125

Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp
    130                 135                 140

Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln
145                 150                 155                 160

Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu
                165                 170                 175

Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr
            180                 185                 190

Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala
        195                 200                 205

His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser
    210                 215                 220
```

US09/852,196

<210> 313
<211> 831
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(808)
<223> RXA00251

<400> 313

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aaccagcgtt ttcagcgaga tactggacat atcaactaaa atccctgaat aaaacatcta 60

acatgggttt tatacagaaa attcatacga aaggttgatc atg aag aag aag att   115
                                            Met Lys Lys Lys Ile
                                              1               5

gcg gtc gtt acc gga gcg acc gga ggc atg gga att gag atc gtc aaa   163
Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly Ile Glu Ile Val Lys
                  10                  15                  20

gac ctc tcc cgc gac cac att gtc tac gcc ttg ggc cga aat cca gag   211
Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu Gly Arg Asn Pro Glu
              25                  30                  35

cat ctg gca gct ctc gca gag atc gag gga gta gag cct atc gag tcc   259
His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val Glu Pro Ile Glu Ser
          40                  45                  50

gat atc gtg aag gaa gtg ttg gaa gag gga ggc gtc gac aag cta aaa   307
```

```
Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly Val Asp Lys Leu Lys
     55                  60                  65

aac ctc gac cac gtg gat acg ctg gtg cac gcc gcg gcg gtg gcg cgt   355
Asn Leu Asp His Val Asp Thr Leu Val His Ala Ala Ala Val Ala Arg
 70                  75                  80                  85

gac acg acc atc gaa gcc ggc agt gtg gcc gaa tgg cac gca cac ctt   403
Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu Trp His Ala His Leu
                 90                  95                 100

gat ctc aac gtc att gtc ccg gcc gag ttg agt cgc caa ctc ttg ccc   451
Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser Arg Gln Leu Leu Pro
            105                 110                 115

gcc ctc cgc gcg gca tcc ggc tgc gtc atc tac atc aac tcc ggc gcc   499
Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr Ile Asn Ser Gly Ala
        120                 125                 130

ggc aac gga cca cac ccc ggc aac acc atc tac gcc gcc agc aaa cac   547
Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr Ala Ala Ser Lys His
    135                 140                 145

gcc ctc cgc gga ctc gcc gac gcc ttc cgc aaa gaa gaa gcc aac aac   595
Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys Glu Glu Ala Asn Asn
150                 155                 160                 165

ggc atc cgc gtc agc act gtc agc ccc ggc ccc acc aac acc ccc atg   643
Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro Thr Asn Thr Pro Met
                170                 175                 180

ctg caa ggc ctc atg gac tca caa ggc acc aac ttc cgc cca gag atc   691
Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn Phe Arg Pro Glu Ile
            185                 190                 195

tac atc gaa cca aaa gaa atc gcc aac gca atc aga ttc gtg att gac   739
Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile Arg Phe Val Ile Asp
        200                 205                 210

gct ggc gaa acc acc cag atc acc aac gtg gac gta cga cca cgt atc   787
Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp Val Arg Pro Arg Ile
    215                 220                 225

gaa ctg gcg gac cgg aaa gat tagttctggg gggcttcctg ggc             831
Glu Leu Ala Asp Arg Lys Asp
230                 235
```

<210> 314
<211> 236
<212> PRT
<213> Corynebacterium glutamicum

<400> 314

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Met Lys Lys Lys Ile Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly
  1               5                  10                  15

Ile Glu Ile Val Lys Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu
             20                  25                  30

Gly Arg Asn Pro Glu His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val
```

```
         35                  40                  45

Glu Pro Ile Glu Ser Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly
     50                  55                  60

Val Asp Lys Leu Lys Asn Leu Asp His Val Asp Thr Leu Val His Ala
 65                  70                  75                  80

Ala Ala Val Ala Arg Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu
                 85                  90                  95

Trp His Ala His Leu Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser
            100                 105                 110

Arg Gln Leu Leu Pro Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr
        115                 120                 125

Ile Asn Ser Gly Ala Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr
    130                 135                 140

Ala Ala Ser Lys His Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys
145                 150                 155                 160

Glu Glu Ala Asn Asn Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro
                165                 170                 175

Thr Asn Thr Pro Met Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn
            180                 185                 190

Phe Arg Pro Glu Ile Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile
        195                 200                 205

Arg Phe Val Ile Asp Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp
    210                 215                 220

Val Arg Pro Arg Ile Glu Leu Ala Asp Arg Lys Asp
225                 230                 235


<210> 315
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXN02654

<400> 315
tattttcgga aatttataca gcaatcctcg aaatcctaat aaagatccct tatcgtggga 60

gaggtacggt agttcgttcg aggacaacgt cgagaaaggc atg att tca ttg cta   115
                                              Met Ile Ser Leu Leu
                                                1               5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc   163
Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
                10                  15                  20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att   211
```

```
Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
            25                  30                  35

ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct   259
Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala
        40                  45                  50

ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct   307
Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala
    55                  60                  65

tat gct cgc gag ggg gca gat gtt gcg atc gct tac ttg ccc gaa gaa   355
Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala Tyr Leu Pro Glu Glu
70                  75                  80                  85

caa gcc gat gct gac aga gtg ctc caa gca atc gag gaa aca ggt caa   403
Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln
                90                  95                  100

aaa gct ttt tct ttc cct ggt gat ctc cgt gat cca gaa tac tgt cgc   451
Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp Pro Glu Tyr Cys Arg
            105                 110                 115

tcg ctg gtc caa gag acg gtg aac gct tta ggt ggc cta gac atc ttg   499
Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu
        120                 125                 130

gtc aac aac gcg tca cgt cag gtg tgg gca cct ggt ttg acc gaa att   547
Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile
    135                 140                 145

acc gac gaa aac ttc gac cag act ttg cag gtt aac ctc tat ggt agt   595
Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val Asn Leu Tyr Gly Ser
150                 155                 160                 165

ttt cgg gtt acc aaa gca gct ata cct cat ctg aag ccc gga tca tcg   643
Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu Lys Pro Gly Ser Ser
                170                 175                 180

ata atc ttt aca tcg tcc att cag gcg tac caa cct tcg gaa acc ctc   691
Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln Pro Ser Glu Thr Leu
            185                 190                 195

ttg gat tac gcc atg act aag gcg gca ttg aac aat ttg tca aag ggc   739
Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn Asn Leu Ser Lys Gly
        200                 205                 210

ttg gca agt agt ctg ata ggc gat ggc att cgg gta aat tct gta gcc   787
Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg Val Asn Ser Val Ala
    215                 220                 225

cca ggt cct ttc tgg acg ccg ttg caa ccc agc cat ggt cag cca caa   835
Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser His Gly Gln Pro Gln
230                 235                 240                 245

gag aaa ata gaa gga ttt ggc cag cac gct ccg att gga aga gcg ggt   883
Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro Ile Gly Arg Ala Gly
                250                 255                 260

cac cct gtt gag ttg gca ggt gcg tac gtt ttt ctc gct tct gac gaa   931
His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe Leu Ala Ser Asp Glu
```

US 20050153394 A1

```
            265                 270                 275

gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc   979
Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro
        280                 285                 290

acc cca tagtcggtac aagcggaatc act                                 1008
Thr Pro
    295


<210> 316
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 316
Met Ile Ser Leu Leu Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp
  1               5                  10                  15

Pro Pro Lys Gln Ser Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser
             20                  25                  30

Pro Gln Ala Asp Ile Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu
         35                  40                  45

Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala
     50                  55                  60

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
 65                  70                  75                  80

Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
                 85                  90                  95

Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
            100                 105                 110

Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
        115                 120                 125

Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
    130                 135                 140

Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
145                 150                 155                 160

Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
                165                 170                 175

Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
            180                 185                 190

Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
        195                 200                 205

Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
    210                 215                 220

Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
225                 230                 235                 240
```

```
His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
               245                 250                 255

Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
           260                 265                 270

Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
       275                 280                 285

Thr Gly Gly Thr Pro Thr Pro
   290                 295
```

<210> 317
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> FRXA02654

<400> 317

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tattttcgga aatttataca gcaatcctcg aaatcctaat aaagatccct tatcgtggga 60

gaggtacggt agttcgttcg aggacaacgt cgagaaaggc atg att tca ttg cta   115
                                          Met Ile Ser Leu Leu
                                            1               5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc   163
Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
                10                  15                  20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att   211
Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
            25                  30                  35

ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct   259
Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala
        40                  45                  50

ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct   307
Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala
    55                  60                  65

tat gct cgc gag ggg gca gat gtt gcg atc gct tac ttg ccc gaa gaa   355
Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala Tyr Leu Pro Glu Glu
70                  75                  80                  85

caa gcc gat gct gac aga gtg ctc caa gca atc gag gaa aca ggt caa   403
Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln
                90                  95                  100

aaa gct ttt tct ttc cct ggt gat ctc cgt gat cca gaa tac tgt cgc   451
Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp Pro Glu Tyr Cys Arg
            105                 110                 115

tcg ctg gtc caa gag acg gtg aac gct tta ggt ggc cta gac atc ttg   499
Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu
```

```
        120                 125                 130

gtc aac aac gcg tca cgt cag gtg tgg gca cct ggt ttg acc gaa att   547
Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile
    135                 140                 145

acc gac gaa aac ttc gac cag act ttg cag gtt aac ctc tat ggt agt   595
Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val Asn Leu Tyr Gly Ser
150                 155                 160                 165

ttt cgg gtt acc aaa gca gct ata cct cat ctg aag ccc gga tca tcg   643
Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu Lys Pro Gly Ser Ser
                170                 175                 180

ata atc ttt aca tcg tcc att cag gcg tac caa cct tcg gaa acc ctc   691
Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln Pro Ser Glu Thr Leu
            185                 190                 195

ttg gat tac gcc atg act aag gcg gca ttg aac aat ttg tca aag ggc   739
Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn Asn Leu Ser Lys Gly
        200                 205                 210

ttg gca agt agt ctg ata ggc gat ggc att cgg gta aat tct gta gcc   787
Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg Val Asn Ser Val Ala
    215                 220                 225

cca ggt cct ttc tgg acg ccg ttg caa ccc agc cat ggt cag cca caa   835
Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser His Gly Gln Pro Gln
230                 235                 240                 245

gag aaa ata gaa gga ttt ggc cag cac gct ccg att gga aga gcg ggt   883
Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro Ile Gly Arg Ala Gly
                250                 255                 260

cac cct gtt gag ttg gca ggt gcg tac gtt ttt ctc gct tct gac gaa   931
His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe Leu Ala Ser Asp Glu
            265                 270                 275

gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc   979
Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro
        280                 285                 290

acc cca tagtcggtac aagcggaatc act                                1008
Thr Pro
    295


<210> 318
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<212> PRT
<213> Corynebacterium glutamicum

<400> 318
Met Ile Ser Leu Leu Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp
  1               5                  10                  15

Pro Pro Lys Gln Ser Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser
             20                  25                  30

Pro Gln Ala Asp Ile Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu
         35                  40                  45
```

```
Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala
     50                  55                  60

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
 65                  70                  75                  80

Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
                 85                  90                  95

Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
            100                 105                 110

Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
        115                 120                 125

Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
    130                 135                 140

Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
145                 150                 155                 160

Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
                165                 170                 175

Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
            180                 185                 190

Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
        195                 200                 205

Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg
    210                 215                 220

Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser
225                 230                 235                 240

His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro
                245                 250                 255

Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe
            260                 265                 270

Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val
        275                 280                 285

Thr Gly Gly Thr Pro Thr Pro
    290                 295


<210> 319
<211> 1605
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1582)
<223> RXN01049

<400> 319
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09852360.090502

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aagcacagca attgagcaat actcccatgc atgttttcgc gtgatcacgc tatatcctta 60

aagaatattc tttattagtc agacctttaa aggaaacctt atg gga tca att cca   115
                                            Met Gly Ser Ile Pro
                                              1               5

aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct   163
Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala
                 10                  15                  20

atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc   211
Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser
             25                  30                  35

ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc   259
Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr
         40                  45                  50

acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag   307
Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu
     55                  60                  65

atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac   355
Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn
 70                  75                  80                  85

atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca   403
Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser
                 90                  95                 100

tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc   451
Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr
            105                 110                 115

tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa   499
Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu
        120                 125                 130

atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc   547
Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr
    135                 140                 145

tcc tac cac cca tcg cgc ttg ctg tgg ctg aaa act gag ttc gag aaa   595
Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys Thr Glu Phe Glu Lys
150                 155                 160                 165

gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag tac gtc tac   643
Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu Tyr Val Tyr
                170                 175                 180

ttc aaa ctt gca ggc atc acc gga atg gct act tcg att gcc gcg tgg   691
Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile Ala Ala Trp
            185                 190                 195

agt ggc att ttg gac gcc cat acc ggc gaa ctt gat ctg act atc ttg   739
Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu Thr Ile Leu
        200                 205                 210

gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc aga aac cct   787
Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile Arg Asn Pro
    215                 220                 225
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US 2003/0224385 A1

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gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag tgg aag cac   835
Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys Trp Lys His
230                 235                 240                 245

ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc tgg cct tcc   883
Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly Trp Pro Ser
                250                 255                 260

aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca gtc gcc gcc   931
Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala Val Ala Ala
            265                 270                 275

gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt ccc gaa cag   979
Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val Pro Glu Gln
        280                 285                 290

atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac cag tgc atc   1027
Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp Gln Cys Ile
    295                 300                 305

gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc tgg ctg gaa   1075
Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr Trp Leu Glu
310                 315                 320                 325

cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg atc cgc gaa   1123
Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu Ile Arg Glu
                330                 335                 340

ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc ggg gaa cgc   1171
Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser Gly Glu Arg
            345                 350                 355

tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc aac att cag   1219
Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr Asn Ile Gln
        360                 365                 370

gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc gaa gcc ctc   1267
Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe Glu Ala Leu
    375                 380                 385

gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa gcc ggc gca   1315
Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys Ala Gly Ala
390                 395                 400                 405

gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc gac cac cca   1363
Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr Asp His Pro
                410                 415                 420

gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca gtc atc cct   1411
Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro Val Ile Pro
            425                 430                 435

ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt atc gtc ctt   1459
Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu Ile Val Leu
        440                 445                 450

gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca ttc ggc acg   1507
Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro Phe Gly Thr
    455                 460                 465
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US 2006/0160164 A1

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acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca aga gag ctt   1555
Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala Arg Glu Leu
470                 475                 480                 485

ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg cagtggaacg         1602
Phe Asp Ala Leu Tyr Leu Lys Leu Val
                490

cgc                                                               1605
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<210> 320
<211> 494
<212> PRT
<213> Corynebacterium glutamicum

<400> 320

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Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly
  1               5                  10                  15

Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
            20                  25                  30

Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
        35                  40                  45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
    50                  55                  60

Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
65                  70                  75                  80

Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp
                85                  90                  95

Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu
            100                 105                 110

Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu
        115                 120                 125

Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly
    130                 135                 140

Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys
145                 150                 155                 160

Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile
                165                 170                 175

Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr
            180                 185                 190

Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu
        195                 200                 205

Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly
    210                 215                 220

Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp
225                 230                 235                 240
```

Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro
245 250 255

Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr
260 265 270

Val Ala Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro
275 280 285

Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser
290 295 300

Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala
305 310 315 320

Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu
325 330 335

Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe
340 345 350

Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr
355 360 365

Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly
370 375 380

Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met
385 390 395 400

Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val
405 410 415

Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp
420 425 430

Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr
435 440 445

Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr
450 455 460

Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser
465 470 475 480

Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val
485 490

<210> 321
<211> 1134
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1111)
<223> FRXA01049

<400> 321

09/25/2003 09:52 FAX

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cacagtatgt ggagcagctg cgcgcggaaa tcgatgagaa ggcctaccac ggccgcaccg 60

gcgtctgctt gcacacctcc taccacccat cgcgcttgct gtg gtg aaa act gag   115
                                           Val Val Lys Thr Glu
                                             1               5

ttc gag aaa gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag   163
Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu
                 10                  15                  20

tac gtc tac ttc aaa ctt gca ggc atc acc gga atg gct act tcg att   211
Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile
             25                  30                  35

gcc gcg tgg agt ggc att ttg gac gcc cat acc ggc gaa ctt gat ctg   259
Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu
         40                  45                  50

act atc ttg gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc   307
Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile
     55                  60                  65

aga aac cct gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag   355
Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys
 70                  75                  80                  85

tgg aag cac ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc   403
Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly
                 90                  95                 100

tgg cct tcc aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca   451
Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala
            105                 110                 115

gtc gcc gcc gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt   499
Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val
        120                 125                 130

ccc gaa cag atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac   547
Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp
    135                 140                 145

cag tgc atc gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc   595
Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr
150                 155                 160                 165

tgg ctg gaa cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg   643
Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu
                170                 175                 180

atc cgc gaa ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc   691
Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser
            185                 190                 195

ggg gaa cgc tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc   739
Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr
        200                 205                 210

aac att cag gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc   787
Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe
    215                 220                 225
```

```
gaa gcc ctc gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa   835
Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys
230                 235                 240                 245

gcc ggc gca gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc   883
Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr
                250                 255                 260

gac cac cca gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca   931
Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro
            265                 270                 275

gtc atc cct ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt   979
Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu
        280                 285                 290

atc gtc ctt gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca   1027
Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro
    295                 300                 305

ttc ggc acg acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca   1075
Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala
310                 315                 320                 325

aga gag ctt ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg        1121
Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val
                330                 335

cagtggaacg cgc                                                   1134
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09/25/2006 15:36:26

<210> 322
<211> 337
<212> PRT
<213> Corynebacterium glutamicum

<400> 322

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Val Val Lys Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val
  1               5                  10                  15

Met Thr Ile Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly
             20                  25                  30

Met Ala Thr Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr
         35                  40                  45

Gly Glu Leu Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala
     50                  55                  60

Leu Phe Gly Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys
 65                  70                  75                  80

Val Val Asp Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His
                 85                  90                  95

Ala Ile Pro Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp
            100                 105                 110

Ser Lys Thr Val Ala Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val
        115                 120                 125
```

Ile Leu Pro Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr
130 135 140

Arg Val Ser Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val
145 150 155 160

Gly Arg Ala Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn
165 170 175

Leu Asp Glu Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val
180 185 190

Leu Pro Phe Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala
195 200 205

Gln Ala Thr Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu
210 215 220

Trp Arg Gly Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp
225 230 235 240

Glu His Met Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser
245 250 255

Gly Arg Val Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp
260 265 270

Ala Leu Asp Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu
275 280 285

Arg Gly Thr Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr
290 295 300

Arg Ala Thr Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His
305 310 315 320

His Tyr Ser Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu
325 330 335

Val

<210> 323
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> FRXA01050

<400> 323
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aagaatattc tttattagtc agacctttaa aggaaacctt atg gga tca att cca 115
Met Gly Ser Ile Pro
1 5

```
aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct   163
Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala
                10                  15                  20

atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc   211
Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser
            25                  30                  35

ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc   259
Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr
        40                  45                  50

acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag   307
Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu
    55                  60                  65

atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac   355
Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn
70                  75                  80                  85

atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca   403
Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser
                90                  95                  100

tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc   451
Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr
            105                 110                 115

tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa   499
Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu
        120                 125                 130

atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc   547
Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr
    135                 140                 145

tcc tac cac cca tcg cgc ttg ctg tgg tgaaaactga gttcgagaaa         594
Ser Tyr His Pro Ser Arg Leu Leu Trp
150                 155

gag                                                              597
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<210> 324
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 324

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Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly
  1               5                  10                  15

Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
            20                  25                  30

Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
        35                  40                  45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
    50                  55                  60
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Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65                  70                  75                  80

Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp
                 85                  90                  95

Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu
            100                 105                 110

Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu
        115                 120                 125

Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly
    130                 135                 140

Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp
145                 150                 155


<210> 325
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1042)
<223> RXA00202

<400> 325
ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60

aaacaaaacc tctaagtaat tcctgaaagg aaattttcac atg tac gct cgt aaa   115
                                            Met Tyr Ala Arg Lys
                                              1               5

ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct   163
Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala
                  10                  15                  20

tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat   211
Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp
              25                  30                  35

ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg   259
Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val
          40                  45                  50

cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc   307
Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr
      55                  60                  65

ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag   355
Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln
  70                  75                  80                  85

ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca   403
Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro
                  90                  95                 100

act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct   451
```

```
Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala
            105                 110                 115

gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg   499
Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val
        120                 125                 130

gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct   547
Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala
    135                 140                 145

gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg   595
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu
150                 155                 160                 165

caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt   643
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe
                170                 175                 180

gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag   691
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln
            185                 190                 195

acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg   739
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu
        200                 205                 210

ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag   787
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu
    215                 220                 225

atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat   835
Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp
230                 235                 240                 245

gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt   883
Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val
                250                 255                 260

gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg   931
Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu
            265                 270                 275

gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac   979
Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp
        280                 285                 290

gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac   1027
Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn
    295                 300                 305

gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt                    1065
Val Ala Asp Phe Lys
310
```

<210> 326
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 326

```
Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala
  1               5                  10                  15

Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
             20                  25                  30

Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
         35                  40                  45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
     50                  55                  60

Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65                  70                  75                  80

Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
                 85                  90                  95

Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
            100                 105                 110

Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
        115                 120                 125

Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
    130                 135                 140

Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
145                 150                 155                 160

Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
                165                 170                 175

Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
            180                 185                 190

Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
        195                 200                 205

Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
    210                 215                 220

Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
225                 230                 235                 240

Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
                245                 250                 255

Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
            260                 265                 270

Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
        275                 280                 285

Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr
    290                 295                 300

Val Lys Leu Asp Asn Val Ala Asp Phe Lys
305                 310
```

<210> 327
<211> 1077
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1054)
<223> RXN00872

<400> 327
gaaatgtatt gctttgtcag gacaatgtgt tattgtcatg acatgcgatc gtgagggtcg 60

ccacattcca tcaaaaatga gtgaagggtt gcatcgccac atg act aac ttg acg 115
Met Thr Asn Leu Thr
1 5

agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163
Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr
10 15 20

cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag 211
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys
25 30 35

tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat 259
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His
40 45 50

gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc 307
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly
55 60 65

gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac 355
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr
70 75 80 85

gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att 403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile
90 95 100

ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct 451
Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala
105 110 115

ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc 499
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg
120 125 130

gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca 547
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro
135 140 145

agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc 595
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg
150 155 160 165

cac acc atc ttt gat ctg gac tac cga cca atg ttc tgg gaa tcc cca 643
His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met Phe Trp Glu Ser Pro
170 175 180

```
gaa gag gcc acc aag cag gcg gaa tgg gcg ttg cag cat tcc acg gtg   691
Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu Gln His Ser Thr Val
            185                 190                 195

gcg gtt ggc aac aag gaa gaa tgc gaa atc gca gtg ggc gag acc gag   739
Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala Val Gly Glu Thr Glu
        200                 205                 210

cca gag cgc gcg ggc cga gca ctg ttg gaa cgc ggt gtg gag ttg gcc   787
Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg Gly Val Glu Leu Ala
    215                 220                 225

atc gtc aag cag gga cct aag ggt gtc atg gcg atg acc aag gac gaa   835
Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala Met Thr Lys Asp Glu
230                 235                 240                 245

acc gta gaa gtt cct ccg ttc ttc gtc gat gtc atc aac ggt ctt ggt   883
Thr Val Glu Val Pro Pro Phe Phe Val Asp Val Ile Asn Gly Leu Gly
                250                 255                 260

gcc ggc gat gca ttc ggc ggc gcg ctg tgc cac ggt ctg ctc tct gaa   931
Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His Gly Leu Leu Ser Glu
            265                 270                 275

tgg ccg ttg gaa aag gtt ctc cgt ttt gcc aac acc gcg ggt gcg ctt   979
Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn Thr Ala Gly Ala Leu
        280                 285                 290

gtg gcg tcc cgt ctt gaa tgc tcc acc gca atg cct act acc gat gag   1027
Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met Pro Thr Thr Asp Glu
    295                 300                 305

gtg gaa gcc tcc ctc aac cag aaa gtc tgatatgact cctccgatta         1074
Val Glu Ala Ser Leu Asn Gln Lys Val
310                 315

tct                                                              1077
```

<210> 328
<211> 318
<212> PRT
<213> Corynebacterium glutamicum

<400> 328

```
Met Thr Asn Leu Thr Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu
  1               5                  10                  15

Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val
             20                  25                  30

Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val
         35                  40                  45

Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly
     50                  55                  60

Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly
 65                  70                  75                  80
```

```
Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val
                85                  90                  95

Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr
            100                 105                 110

Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser
        115                 120                 125

Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly
    130                 135                 140

Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr
145                 150                 155                 160

Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met
                165                 170                 175

Phe Trp Glu Ser Pro Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu
            180                 185                 190

Gln His Ser Thr Val Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala
        195                 200                 205

Val Gly Glu Thr Glu Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg
    210                 215                 220

Gly Val Glu Leu Ala Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala
225                 230                 235                 240

Met Thr Lys Asp Glu Thr Val Glu Val Pro Pro Phe Phe Val Asp Val
                245                 250                 255

Ile Asn Gly Leu Gly Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His
            260                 265                 270

Gly Leu Leu Ser Glu Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn
        275                 280                 285

Thr Ala Gly Ala Leu Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met
    290                 295                 300

Pro Thr Thr Asp Glu Val Glu Ala Ser Leu Asn Gln Lys Val
305                 310                 315


<210> 329
<211> 622
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(622)
<223> FRXA00872

<400> 329
gaaatgtatt gctttgtcag gacaatgtgt tattgtcatg acatgcgatc gtgagggtcg 60

ccacattcca tcaaaaatga gtgaagggtt gcatcgccac atg act aac ttg acg   115
                                                Met Thr Asn Leu Thr
```

```
                                                    1               5

agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac   163
Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr
                 10                  15                  20

cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag   211
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys
             25                  30                  35

tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat   259
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His
         40                  45                  50

gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc   307
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly
     55                  60                  65

gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac   355
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr
 70                  75                  80                  85

gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att   403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile
                 90                  95                 100

ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct   451
Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala
            105                 110                 115

ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc   499
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg
        120                 125                 130

gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca   547
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro
    135                 140                 145

agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc   595
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg
150                 155                 160                 165

cac acc atc ttt gat ctg gac tac cga                              622
His Thr Ile Phe Asp Leu Asp Tyr Arg
                170
```

<210> 330
<211> 174
<212> PRT
<213> Corynebacterium glutamicum

<400> 330

```
Met Thr Asn Leu Thr Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu
  1               5                  10                  15

Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val
             20                  25                  30

Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val
         35                  40                  45
```

```
Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly
     50                  55                  60

Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly
 65                  70                  75                  80

Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val
                 85                  90                  95

Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr
            100                 105                 110

Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser
        115                 120                 125

Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly
    130                 135                 140

Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr
145                 150                 155                 160

Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg
                165                 170
```

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<210> 331
<211> 1767
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1744)
<223> RXN00799

<400> 331

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ttgtctaacc ccgtataggt gagaaatgtt ggacaagtgt ctgtttttttg tgggggaaat 60

ctgactacga tggtaagaaa taaggaaaga gattaccatt atg tct caa gag cgg   115
                                            Met Ser Gln Glu Arg
                                              1               5

cct caa atc ggc tcc cgc ctc tct cgt gtc att gaa caa gac ggc cta   163
Pro Gln Ile Gly Ser Arg Leu Ser Arg Val Ile Glu Gln Asp Gly Leu
                 10                  15                  20

caa ttc cgc gat ctc gac ggc gac ggc gta ctt gca cct tat gaa gat   211
Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu Asp
             25                  30                  35

tgg cgt cta acc cca gca gag cgt gcc gct gac ctg gtg aaa cgt atg   259
Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg Met
         40                  45                  50

aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac ccc   307
Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr Pro
     55                  60                  65

gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa aag   355
Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu Lys
```

```
 70                  75                  80                  85

tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac ccg   403
Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn Pro
                90                  95                 100

atc acg ggt gtt cct ttc acc gag cct gtg ctg gca act tct tcc act   451
Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser Thr
            105                 110                 115

gaa aat gcc att aac ctg cgc aat cag cgt tac tta att gtt cgt gac   499
Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg Asp
        120                 125                 130

aac ctg cca gct cgt ggg ctt gct act tgg acc aat gct gtt cag gaa   547
Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln Glu
    135                 140                 145

gtc gcg gag cga tcc cgt ttg ggt att cct gtt gcg ttt gcg tcg aat   595
Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser Asn
150                 155                 160                 165

cct cgt aac cac gtc gcg ctc gtt gcg cag ttc ggt gtg aac gag tcc   643
Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu Ser
                170                 175                 180

gcg ggt gtg ttc tct gag tgg cct ggc gag ctg ggt ctt gct gcg ctt   691
Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala Leu
            185                 190                 195

cgc gat gct gaa ctg atg gag act ttc ggt acc gag gct gct aaa gaa   739
Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys Glu
        200                 205                 210

tgg cgt gcc ggt ggt gtg cac aag ctg tac ggt tac atg gct gac ctc   787
Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp Leu
    215                 220                 225

gct tct gag cct cgt tgg tcc cgc ttc aac ggt act ttt ggt gag gat   835
Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu Asp
230                 235                 240                 245

ccg gag ttg atc tct gat tac atc gct gct gtt gtg cgt ggt ttg cag   883
Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu Gln
                250                 255                 260

ggc cct gag ctg tcc aag aat tcc gtg tcg acc acc att aag cac ttc   931
Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His Phe
            265                 270                 275

cca ggt ggc ggc gtg cgc ctc gac ggc cac gat cct cac ttc cac tgg   979
Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp Pro His Phe His Trp
        280                 285                 290

ggt cag acc aat gag tac cca acc gaa gat gcg ctg ggc aag tac cat  1027
Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala Leu Gly Lys Tyr His
    295                 300                 305

ctg cct cct ttc cag gca gct atc gac gct ggc tgc gcc tcg atc atg  1075
Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly Cys Ala Ser Ile Met
310                 315                 320                 325
```

```
cct tac tac gca cgg cca atg aac aac tcc gcc aac cag ctc gat cag   1123
Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala Asn Gln Leu Asp Gln
                330                 335                 340

cag ctg tgg caa aac ccg acc acg cag ttc gaa gag gtt gcg ttt gcc   1171
Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu Glu Val Ala Phe Ala
            345                 350                 355

tac aac cgc acc ttc att cag gat ttg ctt cgc gac gcc atg ggc cac   1219
Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly His
        360                 365                 370

cgt ggg tac gtc aac tcc gac tcc ggc gtc atc gac gcc atg atg tgg   1267
Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met Trp
    375                 380                 385

ggc gtg gag gaa ctc agc gag cca gaa cgc ttc gcc gca gca gtg cgt   1315
Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe Ala Ala Ala Val Arg
390                 395                 400                 405

gca ggc acc gac att ttc tcc gac atg gct aac cca cgt cga ctg ctc   1363
Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn Pro Arg Arg Leu Leu
                410                 415                 420

gaa gca gtt gct gag gga cac ctt gat gag tca gag ctg aat cag cca   1411
Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser Glu Leu Asn Gln Pro
            425                 430                 435

gtc cag cga ctc ctg gag gaa atc ttc cag ctt ggt ctg ttt gag aac   1459
Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu Gly Leu Phe Glu Asn
        440                 445                 450

cca tat gtc tct gaa gat gaa gca gaa aag atc att ggt gcg cca gag   1507
Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro Glu
    455                 460                 465

gtt tct gca ttg ggc aac aaa gca cag ctt gat tcc gtc acc ttg ctg   1555
Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Leu Leu
470                 475                 480                 485

cgt aac aac ccc atc cgt gct gcc act gga tcc tgc agc aag cct gaa   1603
Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro Glu
                490                 495                 500

gat cta ccc att ggt tac tgg ccg tac caa gat cga cga ggt tca act   1651
Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser Thr
            505                 510                 515

aca gct gga agc agc cat tcg cgc aga act ccc agg ggt aac ctt ggt   1699
Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro Arg Gly Asn Leu Gly
        520                 525                 530

gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc       1744
Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg Val Gly Ser Pro
    535                 540                 545

tgaaattgca ctgtttgaag atg                                        1767
```

<210> 332

<211> 548
<212> PRT
<213> Corynebacterium glutamicum

<400> 332

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Met Ser Gln Glu Arg Pro Gln Ile Gly Ser Arg Leu Ser Arg Val Ile
  1               5                  10                  15

Glu Gln Asp Gly Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu
            20                  25                  30

Ala Pro Tyr Glu Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp
        35                  40                  45

Leu Val Lys Arg Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile
    50                  55                  60

Gly Ser His Tyr Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly
65                  70                  75                  80

Lys Asp Ala Glu Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp
                85                  90                  95

Arg Glu Asp Asn Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu
            100                 105                 110

Ala Thr Ser Ser Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr
        115                 120                 125

Leu Ile Val Arg Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr
    130                 135                 140

Asn Ala Val Gln Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val
145                 150                 155                 160

Ala Phe Ala Ser Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe
                165                 170                 175

Gly Val Asn Glu Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu
            180                 185                 190

Gly Leu Ala Ala Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr
        195                 200                 205

Glu Ala Ala Lys Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly
    210                 215                 220

Tyr Met Ala Asp Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly
225                 230                 235                 240

Thr Phe Gly Glu Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val
                245                 250                 255

Val Arg Gly Leu Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr
            260                 265                 270

Thr Ile Lys His Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp
        275                 280                 285

Pro His Phe His Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala
    290                 295                 300
```

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```
Leu Gly Lys Tyr His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly
305                 310                 315                 320

Cys Ala Ser Ile Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala
                325                 330                 335

Asn Gln Leu Asp Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu
            340                 345                 350

Glu Val Ala Phe Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg
        355                 360                 365

Asp Ala Met Gly His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile
    370                 375                 380

Asp Ala Met Met Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe
385                 390                 395                 400

Ala Ala Ala Val Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn
                405                 410                 415

Pro Arg Arg Leu Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser
            420                 425                 430

Glu Leu Asn Gln Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu
        435                 440                 445

Gly Leu Phe Glu Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile
    450                 455                 460

Ile Gly Ala Pro Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp
465                 470                 475                 480

Ser Val Thr Leu Leu Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser
                485                 490                 495

Cys Ser Lys Pro Glu Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp
            500                 505                 510

Arg Arg Gly Ser Thr Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro
        515                 520                 525

Arg Gly Asn Leu Gly Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg
    530                 535                 540

Val Gly Ser Pro
545
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<210> 333
<211> 1607
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1584)
<223> FRXA00799

<400> 333

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cta caa ttc cgc gat ctc gac ggc gac ggc gta ctt gca cct tat gaa   48
Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu
  1               5                  10                  15

gat tgg cgt cta acc cca gca gag cgt gcc gct gac ctg gtg aaa cgt   96
Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg
            20                  25                  30

atg aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac   144
Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr
        35                  40                  45

ccc gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa   192
Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu
    50                  55                  60

aag tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac   240
Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn
65                  70                  75                  80

ccg atc acg ggt gtt cct ttc acc gag cct gtg ctg gca act tct tcc   288
Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser
                85                  90                  95

act gaa aat gcc att aac ctg cgc aat cag cgt tac tta att gtt cgt   336
Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg
            100                 105                 110

gac aac ctg cca gct cgt ggg ctt gct act tgg acc aat gct gtt cag   384
Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln
        115                 120                 125

gaa gtc gcg gag cga tcc cgt ttg ggt att cct gtt gcg ttt gcg tcg   432
Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser
    130                 135                 140

aat cct cgt aac cac gtc gcg ctc gtt gcg cag ttc ggt gtg aac gag   480
Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu
145                 150                 155                 160

tcc gcg ggt gtg ttc tct gag tgg cct ggc gag ctg ggt ctt gct gcg   528
Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala
                165                 170                 175

ctt cgc gat gct gaa ctg atg gag act ttc ggt acc gag gct gct aaa   576
Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys
            180                 185                 190

gaa tgg cgt gcc ggt ggt gtg cac aag ctg tac ggt tac atg gct gac   624
Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp
        195                 200                 205

ctc gct tct gag cct cgt tgg tcc cgc ttc aac ggt act ttt ggt gag   672
Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu
    210                 215                 220

gat ccg gag ttg atc tct gat tac atc gct gct gtt gtg cgt ggt ttg   720
Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu
225                 230                 235                 240

cag ggc cct gag ctg tcc aag aat tcc gtg tcg acc acc att aag cac   768
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Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His
                245                 250                 255

ttc cca ggt ggc ggc gtg cgc ctc gac ggc cac gat cct cac ttc cac   816
Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp Pro His Phe His
            260                 265                 270

tgg ggt cag acc aat gag tac cca acc gaa gat gcg ctg ggc aag tac   864
Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala Leu Gly Lys Tyr
        275                 280                 285

cat ctg cct cct ttc cag gca gct atc gac gct ggc tgc gcc tcg atc   912
His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly Cys Ala Ser Ile
    290                 295                 300

atg cct tac tac gca cgg cca atg aac aac tcc gcc aac cag ctc gat   960
Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala Asn Gln Leu Asp
305                 310                 315                 320

cag cag ctg tgg caa aac ccg acc acg cag ttc gaa gag gtt gcg ttt   1008
Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu Glu Val Ala Phe
                325                 330                 335

gcc tac aac cgc acc ttc att cag gat ttg ctt cgc gac gcc atg ggc   1056
Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly
            340                 345                 350

cac cgt ggg tac gtc aac tcc gac tcc ggc gtc atc gac gcc atg atg   1104
His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met
        355                 360                 365

tgg ggc gtg gag gaa ctc agc gag cca gaa cgc ttc gcc gca gca gtg   1152
Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe Ala Ala Ala Val
    370                 375                 380

cgt gca ggc acc gac att ttc tcc gac atg gct aac cca cgt cga ctg   1200
Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn Pro Arg Arg Leu
385                 390                 395                 400

ctc gaa gca gtt gct gag gga cac ctt gat gag tca gag ctg aat cag   1248
Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser Glu Leu Asn Gln
                405                 410                 415

cca gtc cag cga ctc ctg gag gaa atc ttc cag ctt ggt ctg ttt gag   1296
Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu Gly Leu Phe Glu
            420                 425                 430

aac cca tat gtc tct gaa gat gaa gca gaa aag atc att ggt gcg cca   1344
Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro
        435                 440                 445

gag gtt tct gca ttg ggc aac aaa gca cag ctt gat tcc gtc acc ttg   1392
Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Leu
    450                 455                 460

ctg cgt aac aac ccc atc cgt gct gcc act gga tcc tgc agc aag cct   1440
Leu Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro
465                 470                 475                 480

gaa gat cta ccc att ggt tac tgg ccg tac caa gat cga cga ggt tca   1488
Glu Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser
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                485                 490                 495

act aca gct gga agc agc cat tcg cgc aga act ccc agg ggt aac ctt   1536
Thr Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro Arg Gly Asn Leu
            500                 505                 510

ggt gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc   1584
Gly Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg Val Gly Ser Pro
        515                 520                 525

tgaaattgca ctgtttgaag atg                                        1607


<210> 334
<211> 528
<212> PRT
<213> Corynebacterium glutamicum

<400> 334
Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu
  1               5                  10                  15

Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg
             20                  25                  30

Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr
         35                  40                  45

Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu
     50                  55                  60

Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn
 65                  70                  75                  80

Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser
                 85                  90                  95

Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg
            100                 105                 110

Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln
        115                 120                 125

Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser
    130                 135                 140

Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu
145                 150                 155                 160

Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala
                165                 170                 175

Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys
            180                 185                 190

Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp
        195                 200                 205

Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu
    210                 215                 220
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Document: 2005/0196848

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Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu
225                 230                 235                 240

Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His
                245                 250                 255

Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp Pro His Phe His
            260                 265                 270

Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala Leu Gly Lys Tyr
        275                 280                 285

His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly Cys Ala Ser Ile
    290                 295                 300

Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala Asn Gln Leu Asp
305                 310                 315                 320

Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu Glu Val Ala Phe
                325                 330                 335

Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly
            340                 345                 350

His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met
        355                 360                 365

Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe Ala Ala Ala Val
    370                 375                 380

Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn Pro Arg Arg Leu
385                 390                 395                 400

Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser Glu Leu Asn Gln
                405                 410                 415

Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu Gly Leu Phe Glu
            420                 425                 430

Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro
        435                 440                 445

Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Leu
    450                 455                 460

Leu Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro
465                 470                 475                 480

Glu Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser
                485                 490                 495

Thr Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro Arg Gly Asn Leu
            500                 505                 510

Gly Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg Val Gly Ser Pro
        515                 520                 525
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Date Recue/Date Received 2020-12-15

<210> 335
<211> 1632
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1609)
<223> RXA00032

<400> 335
cacttgctga agacgcccac atcgaagacc ttgcagatgt aaacgcaaac gcctaactgt 60

ttttcgagct aaacccatcc ttgaaaggat cttttccacc atg aac acc cca ctc 115
Met Asn Thr Pro Leu
1 5

cag ctc aac act gaa aac ctg cag gaa atc gct tcg act tcc gga gtg 163
Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala Ser Thr Ser Gly Val
10 15 20

cag atc cca gcg ttc aac cgc gct gac gtc gcc ccg ggc att gtc cac 211
Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala Pro Gly Ile Val His
25 30 35

ttc ggt gtt ggc gga ttc cat cgc gct cac caa gcg atg tac ctc aat 259
Phe Gly Val Gly Gly Phe His Arg Ala His Gln Ala Met Tyr Leu Asn
40 45 50

gaa ttg atg aat gag ggc aag gcc ttg gat tgg ggc atc atc ggc atg 307
Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp Gly Ile Ile Gly Met
55 60 65

ggt gtc atg cct tcc gat gtg cgc atg cgc gat gcc ctg gcc agc caa 355
Gly Val Met Pro Ser Asp Val Arg Met Arg Asp Ala Leu Ala Ser Gln
70 75 80 85

gat cac ctt tat acc ctg acc act aaa gct cct gat gga act ctt gat 403
Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro Asp Gly Thr Leu Asp
90 95 100

caa aaa atc atc gga tcc atc att gac tac gtg ttc gct ccc gag gac 451
Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val Phe Ala Pro Glu Asp
105 110 115

cca gca cgg gcc gtt gca acc ctc gcg cag gac tcc atc cgc att gtt 499
Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp Ser Ile Arg Ile Val
120 125 130

tcc ctc acg gtg act gaa ggc gga tac aac atc gat ccg gcg aca gaa 547
Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile Asp Pro Ala Thr Glu
135 140 145

gat ttc gac cac acc aac cct cga atc gtt gct gac cgc gaa gcc ctg 595
Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala Asp Arg Glu Ala Leu
150 155 160 165

cag gcg ggc gat act tcc act ttg cag acc ttc ttt ggg ttg atc act 643
Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe Phe Gly Leu Ile Thr
170 175 180

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gcc gca ttg att tcc cga aaa gaa tca gga tct acg cca ttt acc atc   691
Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser Thr Pro Phe Thr Ile
            185                 190                 195

atg agc tgc gat aac atc caa ggc aac ggc gat ctg gct aag cgt ttc   739
Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp Leu Ala Lys Arg Phe
        200                 205                 210

ttc ctc gcc ttc gca cat tcc gtg tct tct gag ctc ggc gaa tgg gtg   787
Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu Leu Gly Glu Trp Val
    215                 220                 225

gaa aac aac gtg gcc ttc ccc aac tcc atg gtg gac cgc atc acc cct   835
Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val Asp Arg Ile Thr Pro
230                 235                 240                 245

gaa acc acc gac ggc gac cgc gat gac atc aag gaa atc ggc tac atc   883
Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys Glu Ile Gly Tyr Ile
                250                 255                 260

gat gcg tgg cca gtg gtt tct gaa gat ttc acc caa tgg gtc ctc gag   931
Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr Gln Trp Val Leu Glu
            265                 270                 275

gat gcc ttc acc cag ggc cgc ccc gcg tac gag gag gtt ggc gtg cag   979
Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu Glu Val Gly Val Gln
        280                 285                 290

gtc gtc tcc gac gtg gag cct tat gaa tta atg aag ctg cgc ctg ctc   1027
Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met Lys Leu Arg Leu Leu
    295                 300                 305

aac gcc tcc cac cag gga ctt tgc tac ttc ggc cac ttg gct ggc cac   1075
Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly His Leu Ala Gly His
310                 315                 320                 325

cac atg gtc cac gac gtc atg gcg gat acc cgc ttc cag gat ttc ctc   1123
His Met Val His Asp Val Met Ala Asp Thr Arg Phe Gln Asp Phe Leu
                330                 335                 340

ctg gct tac atg gag cgc gaa gcc acc cct acc ctc aag gaa ctt cca   1171
Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr Leu Lys Glu Leu Pro
            345                 350                 355

ggt gtc gat cta gat gct tat cga cgc caa ctc atc gcg cga ttc ggc   1219
Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu Ile Ala Arg Phe Gly
        360                 365                 370

aac gcc gca gtc aaa gac acc gta ccg cgc ctg tgt gcg gaa tcc tcc   1267
Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu Cys Ala Glu Ser Ser
    375                 380                 385

gac cgc att cca aag tgg ctg ttg cca gtc gta cgc gaa aac ctc gca   1315
Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val Arg Glu Asn Leu Ala
390                 395                 400                 405

gca ggc cgc gac gtc aca ctt tct gca gcc atc gtc gca tcc tgg gcg   1363
Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile Val Ala Ser Trp Ala
                410                 415                 420

cgc tac gca gaa ggc acc gac gag cag ggc aac cca ata aag att gtt   1411
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Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn Pro Ile Lys Ile Val
            425                 430                 435

gac cgt ttg agt gag cgc gtc caa gaa aac gca tca gga aat cgc acc   1459
Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala Ser Gly Asn Arg Thr
        440                 445                 450

gat att ttg tca ttc atc cgc gac cgt gga atc ttc gga gac ttg gtc   1507
Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile Phe Gly Asp Leu Val
    455                 460                 465

gat gct gaa cca ttc acc aag gca tac tcc gag aca ctg tcc tcc ctt   1555
Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu Thr Leu Ser Ser Leu
470                 475                 480                 485

cat gac cgt ggc gcg gaa gca acc atc gat gca ctt ctt acg cag gta   1603
His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala Leu Leu Thr Gln Val
                490                 495                 500

act gtc taaatccgtt gcgcgctagg gtt                                1632
Thr Val
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US 2005/0287630 A1

<210> 336
<211> 503
<212> PRT
<213> Corynebacterium glutamicum

<400> 336

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Met Asn Thr Pro Leu Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala
  1               5                  10                  15

Ser Thr Ser Gly Val Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala
             20                  25                  30

Pro Gly Ile Val His Phe Gly Val Gly Gly Phe His Arg Ala His Gln
         35                  40                  45

Ala Met Tyr Leu Asn Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp
     50                  55                  60

Gly Ile Ile Gly Met Gly Val Met Pro Ser Asp Val Arg Met Arg Asp
 65                  70                  75                  80

Ala Leu Ala Ser Gln Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro
                 85                  90                  95

Asp Gly Thr Leu Asp Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val
            100                 105                 110

Phe Ala Pro Glu Asp Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp
        115                 120                 125

Ser Ile Arg Ile Val Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile
    130                 135                 140

Asp Pro Ala Thr Glu Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala
145                 150                 155                 160

Asp Arg Glu Ala Leu Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe
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                165                 170                 175

Phe Gly Leu Ile Thr Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser
            180                 185                 190

Thr Pro Phe Thr Ile Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp
        195                 200                 205

Leu Ala Lys Arg Phe Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu
    210                 215                 220

Leu Gly Glu Trp Val Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val
225                 230                 235                 240

Asp Arg Ile Thr Pro Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys
                245                 250                 255

Glu Ile Gly Tyr Ile Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr
            260                 265                 270

Gln Trp Val Leu Glu Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu
        275                 280                 285

Glu Val Gly Val Gln Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met
    290                 295                 300

Lys Leu Arg Leu Leu Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly
305                 310                 315                 320

His Leu Ala Gly His His Met Val His Asp Val Met Ala Asp Thr Arg
                325                 330                 335

Phe Gln Asp Phe Leu Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr
            340                 345                 350

Leu Lys Glu Leu Pro Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu
        355                 360                 365

Ile Ala Arg Phe Gly Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu
    370                 375                 380

Cys Ala Glu Ser Ser Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val
385                 390                 395                 400

Arg Glu Asn Leu Ala Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile
                405                 410                 415

Val Ala Ser Trp Ala Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn
            420                 425                 430

Pro Ile Lys Ile Val Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala
        435                 440                 445

Ser Gly Asn Arg Thr Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile
    450                 455                 460

Phe Gly Asp Leu Val Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu
465                 470                 475                 480

Thr Leu Ser Ser Leu His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala
                485                 490                 495
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Document: 3602.txt

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Leu Leu Thr Gln Val Thr Val
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<210> 337
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1075)
<223> RXA02528

<400> 337
ctggcgcggt atcgattaca atctggttgg ttatcggtgg tttgtggatg aatgtcatcg 60

gactctggta atcgaaaatt aaaggtaagg gggtgtggag atg tca gca aaa tcg   115
                                              Met Ser Ala Lys Ser
                                                1               5

agc ctc aag gaa gtt gct gag tta gct gga gtc ggt tat gcc aca gcc   163
Ser Leu Lys Glu Val Ala Glu Leu Ala Gly Val Gly Tyr Ala Thr Ala
                10                  15                  20

tcg agg gca cta tct ggc aag ggg tat gtg tcc ccg cag acg cgg gag   211
Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser Pro Gln Thr Arg Glu
            25                  30                  35

aaa gtt cag gcg gcg gct aaa gag ctg aac tat gta cca aat cag ctg   259
Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr Val Pro Asn Gln Leu
        40                  45                  50

gcc aag gcg ttg cgg gaa cat cgc agt gcc ttg gtg ggg gtc att gtt   307
Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu Val Gly Val Ile Val
    55                  60                  65

ccg gat ttg tcc aat gag tat tat tcg gaa tcg ctg cag act att cag   355
Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser Leu Gln Thr Ile Gln
70                  75                  80                  85

cag gat ctg aaa gct gct ggc tat caa atg ctg gtt gcg gag gcc aac   403
Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu Val Ala Glu Ala Asn
                90                  95                 100

agt gtg cag gcg cag gac gtg gtg atg gaa tcg ttg atc tcg att caa   451
Ser Val Gln Ala Gln Asp Val Val Met Glu Ser Leu Ile Ser Ile Gln
            105                 110                 115

gct gca gga att atc cac gtt cca gtg gtc ggc tca att gct cct gaa   499
Ala Ala Gly Ile Ile His Val Pro Val Val Gly Ser Ile Ala Pro Glu
        120                 125                 130

gga atc ccc atg gtg cag ttg act cgt ggt gaa ttg ggt cct ggt ttc   547
Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu Leu Gly Pro Gly Phe
    135                 140                 145

cct cgg gtg ttg tgt gat gat gag gct ggg ttt ttt cag ctg acc gag   595
Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe Phe Gln Leu Thr Glu
150                 155                 160                 165
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tcg gtg ctg ggc ggc agc gga atg aac att gct gct ttg gtt ggt gaa   643
Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala Ala Leu Val Gly Glu
                170                 175                 180

gaa tca ctt tcc acc acg cag gaa cga atg cgc ggt att agt cat gcg   691
Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg Gly Ile Ser His Ala
            185                 190                 195

gcg tcg ata tat ggg gct gag gtg acg ttc cat ttt ggc cac tat tct   739
Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His Phe Gly His Tyr Ser
        200                 205                 210

gtc gaa tct ggc gaa gag atg gct cag gtg gtg ttt aac aac ggc ctt   787
Val Glu Ser Gly Glu Glu Met Ala Gln Val Val Phe Asn Asn Gly Leu
    215                 220                 225

ccc gat gca ttg att gtg gcg tct cct cgg ctg atg gct ggg gtg atg   835
Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu Met Ala Gly Val Met
230                 235                 240                 245

cgt gct ttt act cgc ctg aat gtc cgc gtt ccc cac gat gtg gtg att   883
Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro His Asp Val Val Ile
                250                 255                 260

ggt ggt tat gac gat cct gag tgg tac agc ttt gtc ggc gcg ggg att   931
Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe Val Gly Ala Gly Ile
            265                 270                 275

acc acg ttt gtt cca ccg cat gag gag atg ggg aaa gag gcc gtg cgc   979
Thr Thr Phe Val Pro Pro His Glu Glu Met Gly Lys Glu Ala Val Arg
        280                 285                 290

ttg ttg gta gat ctg att gaa aat ccc gaa ctt ccc acc ggc gat gtg   1027
Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu Pro Thr Gly Asp Val
    295                 300                 305

gtt ttg cag ggg cag gtg atc ctt cgg ggg tcg agc aca cat tcc ggg   1075
Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser Ser Thr His Ser Gly
310                 315                 320                 325

tagaattgcc caaatgtcat caa                                        1098
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<210> 338
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 338

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Met Ser Ala Lys Ser Ser Leu Lys Glu Val Ala Glu Leu Ala Gly Val
  1               5                  10                  15

Gly Tyr Ala Thr Ala Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser
             20                  25                  30

Pro Gln Thr Arg Glu Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr
         35                  40                  45

Val Pro Asn Gln Leu Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu
     50                  55                  60
```

```
Val Gly Val Ile Val Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser
 65                  70                  75                  80

Leu Gln Thr Ile Gln Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu
                 85                  90                  95

Val Ala Glu Ala Asn Ser Val Gln Ala Gln Asp Val Val Met Glu Ser
            100                 105                 110

Leu Ile Ser Ile Gln Ala Ala Gly Ile Ile His Val Pro Val Val Gly
        115                 120                 125

Ser Ile Ala Pro Glu Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu
    130                 135                 140

Leu Gly Pro Gly Phe Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe
145                 150                 155                 160

Phe Gln Leu Thr Glu Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala
                165                 170                 175

Ala Leu Val Gly Glu Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg
            180                 185                 190

Gly Ile Ser His Ala Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His
        195                 200                 205

Phe Gly His Tyr Ser Val Glu Ser Gly Glu Glu Met Ala Gln Val Val
    210                 215                 220

Phe Asn Asn Gly Leu Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu
225                 230                 235                 240

Met Ala Gly Val Met Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro
                245                 250                 255

His Asp Val Val Ile Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe
            260                 265                 270

Val Gly Ala Gly Ile Thr Thr Phe Val Pro Pro His Glu Glu Met Gly
        275                 280                 285

Lys Glu Ala Val Arg Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu
    290                 295                 300

Pro Thr Gly Asp Val Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser
305                 310                 315                 320

Ser Thr His Ser Gly
                325
```

<210> 339
<211> 1246
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1246)

<223> RXN00316

<400> 339

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agcgcatgat cgatgcctgc gagtccgcag gggtccaact tggcgtgctc ttccagcgcc 60

gcttctggcc cgcggctcaa aaaatgaaaa aggagccgtc atg ggc caa tgc acg   115
                                            Met Gly Gln Cys Thr
                                              1               5

gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga   163
Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg
                  10                  15                  20

gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc   211
Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile
              25                  30                  35

cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt   259
His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val
          40                  45                  50

ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa   307
Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu
      55                  60                  65

gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca   355
Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr
  70                  75                  80                  85

att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag   403
Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln
                  90                  95                 100

gtg atg gga aca aag ggt gcc acc atg acg atc ctg gaa ttc cct gaa   451
Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile Leu Glu Phe Pro Glu
              105                 110                 115

ggt acc gac ggc agg ctc att gtt cgc agt gaa aac gac acc cgt cga   499
Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu Asn Asp Thr Arg Arg
          120                 125                 130

aac cac ccc att cca ccc cgc gga tct tta tcc caa tgc cga tct ttc   547
Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser Gln Cys Arg Ser Phe
      135                 140                 145

cat cat caa cgg tgc ttt gat ccc gta tca cac cgc cca gat cgc aga   595
His His Gln Arg Cys Phe Asp Pro Val Ser His Arg Pro Asp Arg Arg
  150                 155                 160                 165

ctt tat cga tgc gct caa cga agg ccg ccc acc act gat cac cgg ccg   643
Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr Thr Asp His Arg Pro
                  170                 175                 180

cga tgc cac cag agc tct gaa agt tct cct tgg tgt cta cga atc agc   691
Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp Cys Leu Arg Ile Ser
              185                 190                 195

agc cac cca cca gcc ggt ctc ttt gat cta acg gaa gct ttt aaa acg   739
Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr Glu Ala Phe Lys Thr
          200                 205                 210
```

```
tca cgc caa atc ggt ctt gca cct tta tcc tcc ctg tcc aca cca cct   787
Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser Leu Ser Thr Pro Pro
    215                 220                 225

gat caa cta gtg cgc ctc gca gct gcc act ggt ttc tcc ttt gtc ggt   835
Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly Phe Ser Phe Val Gly
230                 235                 240                 245

ctg cgc gtc atc gca gta acc ccc aac gaa cgt gta tat gac ctt tcc   883
Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg Val Tyr Asp Leu Ser
                250                 255                 260

cca gga tcc cca ctg ctg gct gca acc caa caa gcg ttg aaa gaa acc   931
Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln Ala Leu Lys Glu Thr
            265                 270                 275

gcc ctg tat gtg ctc gac act gaa ttc cta cag gta aac gca gac acc   979
Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln Val Asn Ala Asp Thr
        280                 285                 290

acc cgc gag gcc tgg ctt ccc gca cta gaa gcc gcc gga gca ctg gga   1027
Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala Ala Gly Ala Leu Gly
    295                 300                 305

gct aaa acc ttc acc atc gcc gcc ggt gat gac aac att gcg ccc ctg   1075
Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp Asn Ile Ala Pro Leu
310                 315                 320                 325

acc gac acg atc ggt gcc atg gtt gac gat gcc cgt gat ttc gga gtc   1123
Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala Arg Asp Phe Gly Val
                330                 335                 340

acc cca gcc cta gag cca atc tct tac cgc agc gtg cat tcc att ccg   1171
Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser Val His Ser Ile Pro
            345                 350                 355

cag gca gca gca atc gcc aga gac tcc ggc gga aaa gtc gtg gcg gac   1219
Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly Lys Val Val Ala Asp
        360                 365                 370

acc ttg cac atg gcc agg ttc gga gcc                              1246
Thr Leu His Met Ala Arg Phe Gly Ala
    375                 380
```

<210> 340
<211> 382
<212> PRT
<213> Corynebacterium glutamicum

<400> 340

```
Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr
  1               5                  10                  15

Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
            20                  25                  30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly
        35                  40                  45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
```

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```
     50                  55                  60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
 65                  70                  75                  80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
                 85                  90                  95

Gly Ala Gln Val Gln Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile
            100                 105                 110

Leu Glu Phe Pro Glu Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu
        115                 120                 125

Asn Asp Thr Arg Arg Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser
    130                 135                 140

Gln Cys Arg Ser Phe His His Gln Arg Cys Phe Asp Pro Val Ser His
145                 150                 155                 160

Arg Pro Asp Arg Arg Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr
                165                 170                 175

Thr Asp His Arg Pro Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp
            180                 185                 190

Cys Leu Arg Ile Ser Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr
        195                 200                 205

Glu Ala Phe Lys Thr Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser
    210                 215                 220

Leu Ser Thr Pro Pro Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly
225                 230                 235                 240

Phe Ser Phe Val Gly Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg
                245                 250                 255

Val Tyr Asp Leu Ser Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln
            260                 265                 270

Ala Leu Lys Glu Thr Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln
        275                 280                 285

Val Asn Ala Asp Thr Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala
    290                 295                 300

Ala Gly Ala Leu Gly Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp
305                 310                 315                 320

Asn Ile Ala Pro Leu Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala
                325                 330                 335

Arg Asp Phe Gly Val Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser
            340                 345                 350

Val His Ser Ile Pro Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly
        355                 360                 365

Lys Val Val Ala Asp Thr Leu His Met Ala Arg Phe Gly Ala
    370                 375                 380
```

<210> 341
<211> 412
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(412)
<223> FRXA00309

<400> 341
agcgcatgat cgatgcctgc gagtccgcag gggtccaact tggcgtgctc ttccagcgcc 60

gcttctggcc cgcggctcaa aaaatgaaaa aggagccgtc atg ggc caa tgc acg 115
Met Gly Gln Cys Thr
1 5

gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga 163
Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg
10 15 20

gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc 211
Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile
25 30 35

cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt 259
His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val
40 45 50

ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa 307
Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu
55 60 65

gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca 355
Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr
70 75 80 85

att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag 403
Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln
90 95 100

gtg atg gga 412
Val Met Gly

<210> 342
<211> 104
<212> PRT
<213> Corynebacterium glutamicum

<400> 342
Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr
1 5 10 15

Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
20 25 30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly

```
         35                  40                  45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
     50                  55                  60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
 65                  70                  75                  80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
                 85                  90                  95

Gly Ala Gln Val Gln Val Met Gly
            100
```

<210> 343
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> RXN00310

<400> 343

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ttgcgggatt catcatcggc gcaatcgcac tgtctgccgc agttatttttg accaccaagg 60

aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc   115
                                          Met Ser Asp Lys Ile
                                            1               5

tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc   163
Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
                 10                  15                  20

gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat   211
Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
            25                  30                  35

gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct   259
Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
        40                  45                  50

ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att   307
Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
    55                  60                  65

gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc   355
Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
70                  75                  80                  85

gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc   403
Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
                90                  95                  100

gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg   451
Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
            105                 110                 115

gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa   499
```

Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
120 125 130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545
Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
135 140 145

ccgagagcat tcc 558

<210> 344
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 344
Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
1 5 10 15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
20 25 30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
35 40 45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
50 55 60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
65 70 75 80

Thr Val Val Leu Ala Ala Ala Ala Ala Gly Val His Val Leu Cys Glu
85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala
100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe
115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala
130 135 140

Arg
145

<210> 345
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> FRXA00310

<400> 345
ttgcgggatt catcatcggc gcaatcgcac tgtctgccgc agttattttg accaccaagg 60

aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115

```
                                                    Met Ser Asp Lys Ile
                                                      1               5

tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc   163
Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
                 10                  15                  20

gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat   211
Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
             25                  30                  35

gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct   259
Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
         40                  45                  50

ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att   307
Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
     55                  60                  65

gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc   355
Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
 70                  75                  80                  85

gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc   403
Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
                 90                  95                 100

gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg   451
Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
             105                 110                 115

gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa   499
Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
         120                 125                 130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta        545
Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
     135                 140                 145

ccgagagcat tcc                                                   558
```

<210> 346
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 346

```
Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
  1               5                  10                  15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
             20                  25                  30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
         35                  40                  45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
     50                  55                  60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
```

65 70 75 80

Thr Val Val Leu Ala Ala Ala Ala Ala Gly Val His Val Leu Cys Glu
85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala
100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe
115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala
130 135 140

Arg
145

<210> 347
<211> 1342
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1342)
<223> RXA00041

<400> 347
atgaagcagc agcatccaag ctggaaaacg ctgatcacta ccgtctcatg gagcaattaa 60

agctgcgcta gaaacaaaaa ggaaagtagt gtgtggggct atg cac aca gaa ctt 115
Met His Thr Glu Leu
1 5

tcc agt ttg cgc cct gcg tac cat gtg act cct ccg cag ggc agg ctc 163
Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro Pro Gln Gly Arg Leu
10 15 20

aat gat ccc aac gga atg tac gtc gat ggc gat acc ctc cac gtc tac 211
Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp Thr Leu His Val Tyr
25 30 35

tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggc tgg 259
Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly Trp
40 45 50

gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg acg 307
Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp Thr
55 60 65

cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat gga 355
His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp Gly
70 75 80 85

tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt ttc 403
Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu Phe
90 95 100

tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa aac 451
Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln Asn

```
            105                 110                 115

ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat cgc   499
Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His Arg
        120                 125                 130

cgt tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttc aca   547
Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe Thr
    135                 140                 145

ccc cat tac cgc gat ccc atg atc agc cct gat ggt gat ggt tgg aaa   595
Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp Lys
150                 155                 160                 165

atg gtt ctt ggg gcc caa cgc gaa aac ctc acc ggt gca gcg gtt cta   643
Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val Leu
                170                 175                 180

tac cgc tcg aca gat ctt gaa aac tgg gaa ttc tcc ggt gaa atc acc   691
Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile Thr
            185                 190                 195

ttt gac ctc agt gat gca caa cct ggt tct gct cct gat ctc gtt ccc   739
Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala Pro Asp Leu Val Pro
        200                 205                 210

ggt ggc tac atg tgg gaa tgc ccc aac ctt ttt acg ctt cgc gat gaa   787
Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe Thr Leu Arg Asp Glu
    215                 220                 225

gaa act ggc gaa gat ctc gac gtg ctg att ttc tgt cca caa gga ttg   835
Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe Cys Pro Gln Gly Leu
230                 235                 240                 245

gac cga atc cac gat gag gtt act cac tac gca agc tct gac cag tgc   883
Asp Arg Ile His Asp Glu Val Thr His Tyr Ala Ser Ser Asp Gln Cys
                250                 255                 260

gga tat gtc gtc ggc aag ctt gaa gga acg acc ttc cgc gtc ttg cga   931
Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr Phe Arg Val Leu Arg
            265                 270                 275

gga ttc agc gag ctg gat ttc ggc cat gaa ttc tac gca ccg cag gtt   979
Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe Tyr Ala Pro Gln Val
        280                 285                 290

gca gta aac ggt tct gat gcc tgg ctc gtg ggc tgg atg ggg ctg ccc  1027
Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly Trp Met Gly Leu Pro
    295                 300                 305

gcg cag gat gat cac cca aca gtt gca cgg gaa gga tgg gtg cac tgc  1075
Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu Gly Trp Val His Cys
310                 315                 320                 325

ctg act gtg ccc cgc aag ctt cat ttg cgc aac cac gcg atc tat caa  1123
Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn His Ala Ile Tyr Gln
                330                 335                 340

gag ctt ctt ctc cca gag ggg gag tca ggg gta atc aga tct gta tta  1171
Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val Ile Arg Ser Val Leu
            345                 350                 355
```

```
ggt tct gaa cct gtc cga gta gac atc cga ggc aat att tcc ctc gag   1219
Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly Asn Ile Ser Leu Glu
        360                 365                 370

tgg gat ggt gtc cgt ttg tct gtg gat cgt ggt ggt gat cgt cgc gta   1267
Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly Gly Asp Arg Arg Val
    375                 380                 385

gct gag gta aaa cct ggc gaa tta gtg atc gcg gac gat aat aca gcc   1315
Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala Asp Asp Asn Thr Ala
390                 395                 400                 405

att gag ata act gca ggt gat gga cag                              1342
Ile Glu Ile Thr Ala Gly Asp Gly Gln
                410
```

<210> 348
<211> 414
<212> PRT
<213> Corynebacterium glutamicum

<400> 348

```
Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro
  1               5                  10                  15

Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp
            20                  25                  30

Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro
        35                  40                  45

Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln
    50                  55                  60

Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser
65                  70                  75                  80

Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly
                85                  90                  95

Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg
            100                 105                 110

Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met
        115                 120                 125

Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro
    130                 135                 140

Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp
145                 150                 155                 160

Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr
                165                 170                 175

Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe
            180                 185                 190

Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala
```

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```
        195                 200                 205

Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe
    210                 215                 220

Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe
225                 230                 235                 240

Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val Thr His Tyr Ala
                245                 250                 255

Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr
            260                 265                 270

Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe
        275                 280                 285

Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly
    290                 295                 300

Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu
305                 310                 315                 320

Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn
                325                 330                 335

His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val
            340                 345                 350

Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly
        355                 360                 365

Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly
    370                 375                 380

Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala
385                 390                 395                 400

Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp Gly Gln
                405                 410
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<210> 349
<211> 720
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(720)
<223> RXA02026

<400> 349

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cca ttt cat ata caa cca gaa aca ggt tta tta aat gat ccc aac gga   48
Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
  1               5                  10                  15

ctt att ttt tat aaa ggg aag tat tat gtt tca cat caa tgg ttc cca   96
Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
             20                  25                  30
```

```
tta ggc gca gta cat ggc tta aag tat tgg tat aac tac acg agt gat   144
Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp
         35                  40                  45

gac tta ata aac ttt aaa cct gaa ggg cca ata tta aat cca gat act   192
Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr
     50                  55                  60

aaa tat gac agc cat ggt gtt tat agc ggt agc gct ttt gaa tat aac   240
Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn
 65                  70                  75                  80

ggg cat tta tat tat atg tac aca gga aat cat cga gat aat cat tgg   288
Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp
                 85                  90                  95

caa cga cat gcg agt cag atg atc gca cga ttg aaa gaa gac ggt tca   336
Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser
            100                 105                 110

gtt gaa aag ttt cca aag cca gta att agc cag caa cca gaa gga tat   384
Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr
        115                 120                 125

aca agt cat ttt aga gat cct aaa gtt ttt aaa tat ggt gag aaa tat   432
Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr
    130                 135                 140

tat gca atc att ggc gca caa aat aat gat cag caa ggt cga tta tta   480
Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu
145                 150                 155                 160

ctt tat aat act gaa gat ata att aat tgg cat tat tta ggt gaa ata   528
Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile
                165                 170                 175

aat aca gag tta gat gat ttt gga tat atg tgg gaa tgc cca gat tac   576
Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr
            180                 185                 190

ttt aat tta gat aat caa gat gtc ata ctt att tgt cca caa ggt att   624
Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile
        195                 200                 205

gaa cca aaa ggc aat cag ttc aaa aat att tat caa agt ggt tat ata   672
Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile
    210                 215                 220

ctt gga aag ttt gat att gaa aag tta aca tat gaa cat gaa aat ttt   720
Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe
225                 230                 235                 240
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<210> 350
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

<400> 350

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Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
  1               5                  10                  15
```

```
Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
            20                  25                  30

Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp
        35                  40                  45

Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr
    50                  55                  60

Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn
65                  70                  75                  80

Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp
                85                  90                  95

Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser
            100                 105                 110

Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr
        115                 120                 125

Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr
    130                 135                 140

Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu
145                 150                 155                 160

Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile
                165                 170                 175

Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr
            180                 185                 190

Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile
        195                 200                 205

Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile
    210                 215                 220

Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe
225                 230                 235                 240
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<210> 351
<211> 1617
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1594)
<223> RXA02061

<400> 351
taacctgcct tcacctggga ttatccaccc atgtgtgatg aaatcgctac cctgaatcaa 60

agacactggc gtaattgagt gaaggcagga caataaagag atg acg aac gtt tcc 115

```
                                                    Met Thr Asn Val Ser
                                                      1               5

ggg tat cac cga cca gag ctg cac atc acc gct gaa agt ggt gtt ttg   163
Gly Tyr His Arg Pro Glu Leu His Ile Thr Ala Glu Ser Gly Val Leu
                 10                  15                  20

ttt gca cct gca ggc gtt ctg ttg gat gac gac acg tgg cat ttc ttc   211
Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Asp Thr Trp His Phe Phe
             25                  30                  35

cac cag tac cgt ccc tca cca gat cac ggc ccc agg tgg gcg cac caa   259
His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro Arg Trp Ala His Gln
         40                  45                  50

ttc gca gag cgc act cca ttt gtg tgg gat atc tgc gat gac gtg cta   307
Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile Cys Asp Asp Val Leu
     55                  60                  65

gcc cct gaa ggc gat gaa acc cag gtt cgc gct ggc tca gtg gtg tcc   355
Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala Gly Ser Val Val Ser
 70                  75                  80                  85

aac aac ggt ggc gtt gat ctg tac ttc acc tcg gtt gtt ggc ccc act   403
Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser Val Val Gly Pro Thr
                 90                  95                 100

tcc act atc cag ttg gca cac atc aac aac atc cgt ggc acc acc gaa   451
Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile Arg Gly Thr Thr Glu
            105                 110                 115

ctg atc aat gag gac gag ctg ggg ctc gat cca gat gtc tcc cga atc   499
Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro Asp Val Ser Arg Ile
        120                 125                 130

ggc gaa gtg gtt ggc aac act gat ggt tat gta aag ttc cgc tca ccg   547
Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val Lys Phe Arg Ser Pro
    135                 140                 145

tgc gtt atc cca ggt tgg gaa gac caa gga aac cgc gat gaa ggc cac   595
Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn Arg Asp Glu Gly His
150                 155                 160                 165

tca gga tgg ttg atg ctc gca gtt act ggc cca gtt gaa gcc cca aca   643
Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro Val Glu Ala Pro Thr
                170                 175                 180

gta gtg gtc ctc gac tcg cca gat gga aga gaa tgg tcc att aca ggt   691
Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu Trp Ser Ile Thr Gly
            185                 190                 195

ccc ctg tct ctc aac ggc ctc tct gga tta gag tca gac gaa gtt cta   739
Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu Ser Asp Glu Val Leu
        200                 205                 210

gtt gct cct cgc atg att cgt ctg cgc gat gaa gtg gat cat gaa atc   787
Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu Val Asp His Glu Ile
    215                 220                 225

tac gat gtc ctc att gtc acc att gaa caa gac ggg att gac att tcg   835
Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp Gly Ile Asp Ile Ser
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230                 235                 240                 245

gga tac ctg gta ggc cag ctc aac ggc tca gaa ttc gat gtg aag act   883
Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu Phe Asp Val Lys Thr
                250                 255                 260

cca ttt acc cgc atc gat ttt ggc cat gat ttc tct cgc ccc cgc aac   931
Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe Ser Arg Pro Arg Asn
            265                 270                 275

acc aac tac gcc gaa acc acc atc ggc tac gac ttc gcc cac atc ttt   979
Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp Phe Ala His Ile Phe
        280                 285                 290

ggt ctc atg aat ggc gta ggt cgt ttg gac tcc ccc act gag cat ctc   1027
Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser Pro Thr Glu His Leu
    295                 300                 305

agt tgg aag gaa gaa ggc tgg gca aac gct att tct ttc cca cgt att   1075
Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile Ser Phe Pro Arg Ile
310                 315                 320                 325

gtc acg ctc cag gac ggt acg gtc ttc cag acc cct cca gaa gga ttg   1123
Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr Pro Pro Glu Gly Leu
                330                 335                 340

ctt gat gcc att cat gaa tcc gag gca gcg gca ggt tgg acc gga ctg   1171
Leu Asp Ala Ile His Glu Ser Glu Ala Ala Ala Gly Trp Thr Gly Leu
            345                 350                 355

tgc gaa atc cca tca aac agc gca gtt gaa gtg gcg ttg aag gac caa   1219
Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val Ala Leu Lys Asp Gln
        360                 365                 370

gaa ggt gaa atc gct gca aca atc act cac cgc cac aat cag cta gtc   1267
Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg His Asn Gln Leu Val
    375                 380                 385

gtt gat cgg tcc atg aac ccc aac cac gcg ggt gat cca cac gcg att   1315
Val Asp Arg Ser Met Asn Pro Asn His Ala Gly Asp Pro His Ala Ile
390                 395                 400                 405

gca cca ttg act gat gat gaa aca gat tca ctg ttc att gtc gtt gac   1363
Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu Phe Ile Val Val Asp
                410                 415                 420

ggc tct aca gta gaa gtt ttt gct gat ggc ggt tat gta tca atg gca   1411
Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly Tyr Val Ser Met Ala
            425                 430                 435

agc cgt gtg tat ttc aac aac gga cca ttc agc gaa ttt gag gtc acc   1459
Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser Glu Phe Glu Val Thr
        440                 445                 450

acc acc ggt gac gca agc att att cgc cag gaa agt cac ttc cct gtt   1507
Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu Ser His Phe Pro Val
    455                 460                 465

gat ttc agt tcg gtg tcc cta gat ata gat gat ctc act gcg ctc atg   1555
Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp Leu Thr Ala Leu Met
470                 475                 480                 485
```

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```
cag ttc gat gaa aac gaa ccg cat gaa ggc cca gtg aga taagagttag    1604
Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro Val Arg
                490                 495

atgcgttcca gcc                                                   1617
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<210> 352
<211> 498
<212> PRT
<213> Corynebacterium glutamicum

<400> 352

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Met Thr Asn Val Ser Gly Tyr His Arg Pro Glu Leu His Ile Thr Ala
  1               5                  10                  15

Glu Ser Gly Val Leu Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Asp
            20                  25                  30

Thr Trp His Phe Phe His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro
        35                  40                  45

Arg Trp Ala His Gln Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile
    50                  55                  60

Cys Asp Asp Val Leu Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala
65                  70                  75                  80

Gly Ser Val Val Ser Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser
                85                  90                  95

Val Val Gly Pro Thr Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile
            100                 105                 110

Arg Gly Thr Thr Glu Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro
        115                 120                 125

Asp Val Ser Arg Ile Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val
    130                 135                 140

Lys Phe Arg Ser Pro Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn
145                 150                 155                 160

Arg Asp Glu Gly His Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro
                165                 170                 175

Val Glu Ala Pro Thr Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu
            180                 185                 190

Trp Ser Ile Thr Gly Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu
        195                 200                 205

Ser Asp Glu Val Leu Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu
    210                 215                 220

Val Asp His Glu Ile Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp
225                 230                 235                 240

Gly Ile Asp Ile Ser Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu
                245                 250                 255
```

Phe Asp Val Lys Thr Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe
260 265 270

Ser Arg Pro Arg Asn Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp
275 280 285

Phe Ala His Ile Phe Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser
290 295 300

Pro Thr Glu His Leu Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile
305 310 315 320

Ser Phe Pro Arg Ile Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr
325 330 335

Pro Pro Glu Gly Leu Leu Asp Ala Ile His Glu Ser Glu Ala Ala Ala
340 345 350

Gly Trp Thr Gly Leu Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val
355 360 365

Ala Leu Lys Asp Gln Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg
370 375 380

His Asn Gln Leu Val Val Asp Arg Ser Met Asn Pro Asn His Ala Gly
385 390 395 400

Asp Pro His Ala Ile Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu
405 410 415

Phe Ile Val Val Asp Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly
420 425 430

Tyr Val Ser Met Ala Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser
435 440 445

Glu Phe Glu Val Thr Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu
450 455 460

Ser His Phe Pro Val Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp
465 470 475 480

Leu Thr Ala Leu Met Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro
485 490 495

Val Arg

<210> 353
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXN01369

<400> 353

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ctgcgacgga cctagcaaag gggcgctgac acaagcactg cgtttgctgg tgcgcggaca 60

gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa   115
                                          Met Glu Leu Leu Glu
                                            1               5

ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat   163
Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp
                10                  15                  20

ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg   211
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp
            25                  30                  35

ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc   259
Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu
        40                  45                  50

aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt   307
Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val
    55                  60                  65

gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca   355
Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala
70                  75                  80                  85

gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc   403
Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala
                90                  95                  100

cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca   451
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala
            105                 110                 115

ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt   499
Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val
        120                 125                 130

gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac   547
Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn
    135                 140                 145

acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac   595
Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr
150                 155                 160                 165

cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg   643
Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu
                170                 175                 180

ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc   691
Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile
            185                 190                 195

gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt   739
Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg
        200                 205                 210

gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa   787
Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu
    215                 220                 225
```

```
cag tac ccc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg aac ttc   835
Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu Asn Phe
230                 235                 240                 245

tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca aac ctt   883
Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala Asn Leu
                250                 255                 260

cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac tcc gac   931
His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn Ser Asp
            265                 270                 275

aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc ccg gag   979
Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val Pro Glu
        280                 285                 290

ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc gtg gac   1027
Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg Val Asp
    295                 300                 305

gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc aac gaa   1075
Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile Asn Glu
310                 315                 320                 325

ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc aac cac   1123
Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala Asn His
                330                 335                 340

gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc ttg gaa   1171
Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser Leu Glu
            345                 350                 355

gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca tgg gtt   1219
Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala Trp Val
        360                 365                 370

cca gca aac gac cca acc att gcg atg cgt tct gag gac gca gaa gta   1267
Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala Glu Val
    375                 380                 385

ttc ctc gct agg gtt tagatctttt tagattaaaa tca                    1305
Phe Leu Ala Arg Val
390
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<210> 354
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 354

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Met Glu Leu Leu Glu Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg
  1               5                  10                  15

Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro
             20                  25                  30

Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile
         35                  40                  45
```

```
Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala
     50                  55                  60

Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu
 65                  70                  75                  80

Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro
                 85                  90                  95

Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly
            100                 105                 110

Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys
        115                 120                 125

Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe
    130                 135                 140

Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu
145                 150                 155                 160

Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu
                165                 170                 175

Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys
            180                 185                 190

Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu
        195                 200                 205

Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile
    210                 215                 220

Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala
225                 230                 235                 240

Leu Leu Leu Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu
                245                 250                 255

Asp Ala Ala Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile
            260                 265                 270

Met Ala Asn Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr
        275                 280                 285

Val Asp Val Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu
    290                 295                 300

Asn Ala Arg Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro
305                 310                 315                 320

Val Pro Ile Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu
                325                 330                 335

Ala Glu Ala Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly
            340                 345                 350

Thr Val Ser Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly
        355                 360                 365

His Ala Ala Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser
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    370                 375                 380

Glu Asp Ala Glu Val Phe Leu Ala Arg Val
385                 390


<210> 355
<211> 524
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(501)
<223> FRXA01369

<400> 355
aac gaa cag tgc ctc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg   48
Asn Glu Gln Cys Leu Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu
  1               5                  10                  15

aac ttc tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca   96
Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
            20                  25                  30

aac ctt cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac   144
Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
         35                  40                  45

tcc gac aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc   192
Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
     50                  55                  60

ccg gag ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc   240
Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
 65                  70                  75                  80

gtg gac gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc   288
Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
                85                  90                  95

aac gaa ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc   336
Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
            100                 105                 110

aac cac gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc   384
Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
        115                 120                 125

ttg gaa gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca   432
Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
    130                 135                 140

tgg gtt cca gca aac gac cca acc att gcg atg cgt tct gag gac gca   480
Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
145                 150                 155                 160

gaa gta ttc ctc gct agg gtt tagatctttt tagattaaaa tca             524
Glu Val Phe Leu Ala Arg Val
                165
```

<210> 356
<211> 167
<212> PRT
<213> Corynebacterium glutamicum

<400> 356
Asn Glu Gln Cys Leu Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu
1 5 10 15

Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
20 25 30

Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
35 40 45

Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
50 55 60

Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
65 70 75 80

Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
85 90 95

Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
100 105 110

Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
115 120 125

Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
130 135 140

Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
145 150 155 160

Glu Val Phe Leu Ala Arg Val
165

<210> 357
<211> 808
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(808)
<223> FRXA01373

<400> 357
ctgcgacgga cctagcaaag gggcgctgac acaagcactg cgtttgctgg tgcgcggaca 60

gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa 115
Met Glu Leu Leu Glu
1 5

ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat 163
Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp
10 15 20

```
ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg   211
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp
            25                  30                  35

ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc   259
Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu
        40                  45                  50

aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt   307
Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val
    55                  60                  65

gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca   355
Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala
70                  75                  80                  85

gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc   403
Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala
                90                  95                  100

cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca   451
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala
            105                 110                 115

ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt   499
Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val
        120                 125                 130

gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac   547
Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn
    135                 140                 145

acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac   595
Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr
150                 155                 160                 165

cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg   643
Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu
                170                 175                 180

ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc   691
Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile
            185                 190                 195

gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt   739
Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg
        200                 205                 210

gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa   787
Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu
    215                 220                 225

cag tac ccc ggc gat gtc ggc                                      808
Gln Tyr Pro Gly Asp Val Gly
230                 235
```

<210> 358
<211> 236
<212> PRT

<213> Corynebacterium glutamicum

<400> 358

```
Met Glu Leu Leu Glu Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg
  1               5                  10                  15

Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro
             20                  25                  30

Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile
         35                  40                  45

Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala
     50                  55                  60

Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu
 65                  70                  75                  80

Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro
                 85                  90                  95

Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly
            100                 105                 110

Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys
        115                 120                 125

Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe
    130                 135                 140

Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu
145                 150                 155                 160

Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu
                165                 170                 175

Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys
            180                 185                 190

Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu
        195                 200                 205

Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile
    210                 215                 220

Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly
225                 230                 235
```

<210> 359
<211> 1775
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1752)
<223> RXA02611

<400> 359

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gat gcg tgg tcg gat cct atg gct acg tgg cgt cat gcg att acc act   48
```

```
Asp Ala Trp Ser Asp Pro Met Ala Thr Trp Arg His Ala Ile Thr Thr
  1               5                  10                  15

aag att gag gcc ggc cag ggt tcg gat gag ttg tat aac gac ttt gag   96
Lys Ile Glu Ala Gly Gln Gly Ser Asp Glu Leu Tyr Asn Asp Phe Glu
            20                  25                  30

cac ggg gct cag ctg ttt gag cgt gct gcg gag aat ttg tct aaa gag   144
His Gly Ala Gln Leu Phe Glu Arg Ala Ala Glu Asn Leu Ser Lys Glu
        35                  40                  45

gat agg act gcg ctt ttc gac gtc gcc tcc tct ctg cgg cgc ggc ggc   192
Asp Arg Thr Ala Leu Phe Asp Val Ala Ser Ser Leu Arg Arg Gly Gly
    50                  55                  60

gat gta cgc gca cgt ctc gcc cca gcg ctc acc gcg agt gtc act cat   240
Asp Val Arg Ala Arg Leu Ala Pro Ala Leu Thr Ala Ser Val Thr His
65                  70                  75                  80

ctt tta gaa ctt aac ccg ttg cgt gag ttg gtc acg atg ggt gaa aac   288
Leu Leu Glu Leu Asn Pro Leu Arg Glu Leu Val Thr Met Gly Glu Asn
                85                  90                  95

ctg cag gtt cgt gtc gag cgt cgt gcc gct ttg gtc aac tct tgg tat   336
Leu Gln Val Arg Val Glu Arg Arg Ala Ala Leu Val Asn Ser Trp Tyr
            100                 105                 110

gag ctt ttc cct cgt tcc aca ggt ggt tgg gat gag tcc ggc acc ccc   384
Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro
        115                 120                 125

gtt cat ggc act ttc gct acc act gct cag gcg ttg gag cgt gtc gcg   432
Val His Gly Thr Phe Ala Thr Thr Ala Gln Ala Leu Glu Arg Val Ala
    130                 135                 140

aag atg ggc ttc gat act gtt tac ttc ccg ccg atc cat ccg att ggc   480
Lys Met Gly Phe Asp Thr Val Tyr Phe Pro Pro Ile His Pro Ile Gly
145                 150                 155                 160

gag gtc aac cgc aag ggc cgc aat aat acg ctg acc ccg gaa cct cat   528
Glu Val Asn Arg Lys Gly Arg Asn Asn Thr Leu Thr Pro Glu Pro His
                165                 170                 175

gat gtg ggt tcg ccg tgg gct att ggt tct aaa gat ggt ggg cat gat   576
Asp Val Gly Ser Pro Trp Ala Ile Gly Ser Lys Asp Gly Gly His Asp
            180                 185                 190

gca acg cat ccg cgg ttg ggc acc att gaa gat ttc cag gcg ttg ttg   624
Ala Thr His Pro Arg Leu Gly Thr Ile Glu Asp Phe Gln Ala Leu Leu
        195                 200                 205

gct cgc gca cgg gaa ctc aat ttg gaa gtt gca ctc gat cta gct ctg   672
Ala Arg Ala Arg Glu Leu Asn Leu Glu Val Ala Leu Asp Leu Ala Leu
    210                 215                 220

cag gct gcc cct gat cat cca tgg gcg cag gaa cac cgc gag ttt ttc   720
Gln Ala Ala Pro Asp His Pro Trp Ala Gln Glu His Arg Glu Phe Phe
225                 230                 235                 240

acg gtg ttg gct gat ggc acc att gcg tat gca gaa aac cca ccg aag   768
Thr Val Leu Ala Asp Gly Thr Ile Ala Tyr Ala Glu Asn Pro Pro Lys
```

Doc ID: 9609264.1

```
                245                 250                 255

aag tac cag gat att tat ccc atc aac ttt gat aat gat gct ccg aag   816
Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Asn Asp Ala Pro Lys
            260                 265                 270

atc tac gaa gag gtc tat cgt gtg gtg aag ttc tgg gtg gat ttg ggt   864
Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly
        275                 280                 285

gtg acc aca ttc cgc gtg gat aac ccg cac act aag ccc gct aat ttc   912
Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe
    290                 295                 300

tgg cag tgg ctt att tct gcc atc cat aaa tca aac cct gag gtc att   960
Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile
305                 310                 315                 320

ttc cta gcg gag gcg tct act cgc ccg gca cgt ctg tat ttc ttg tcc   1008
Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser
                325                 330                 335

aag att ggt ttc tcc cag tct tac acc tac ttc acc tgg aag gtc acc   1056
Lys Ile Gly Phe Ser Gln Ser Tyr Thr Tyr Phe Thr Trp Lys Val Thr
            340                 345                 350

aac gag gag ctc acc gag ttc gct act gag atc gcc ccc atg gcg gat   1104
Asn Glu Glu Leu Thr Glu Phe Ala Thr Glu Ile Ala Pro Met Ala Asp
        355                 360                 365

att tct cgt ccg aac ctg ttt gtg aac act ccc gac att ttg cat gcg   1152
Ile Ser Arg Pro Asn Leu Phe Val Asn Thr Pro Asp Ile Leu His Ala
    370                 375                 380

tct ctg cag cat ggt gga cgc gcc atg ttc gct atc cgc gcc gca ttg   1200
Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu
385                 390                 395                 400

gcc gcc acg atg tct cct gtg tgg ggc gta tat tcc gga tat gag ctc   1248
Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu
                405                 410                 415

ttt gag cac gag gcc gtc aag cct ggt tcg gaa gag tac ttg gat tct   1296
Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser
            420                 425                 430

gag aag tac gag ctg cgt ccc cgc gat ttc gag ggt gct ctg gaa cgt   1344
Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg
        435                 440                 445

ggc gat tct ctc gag gat tac atc gct ctg ctc aac cag atc cgt cgc   1392
Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg
    450                 455                 460

gcg aac cct gcc ttg cag caa cta cgc aac atc cac ttc cac gaa gcg   1440
Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala
465                 470                 475                 480

gac aat gat cag atc atc gcc tac tcc aag gtt gat gct ttg acc gga   1488
Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly
                485                 490                 495
```

```
aat acc gtg ttg att gtg gtc aac ttg gat cca cgt agt gct cgt gag   1536
Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu
            500                 505                 510

gct act gtt cgc ctt gat ctt gga gcg ctt ggc tta gaa gcg ggt gca   1584
Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala
        515                 520                 525

cag ttt gag gtg cgc gat gcg atc acc ggc tcc cgt tac ctg tgg tca   1632
Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser
    530                 535                 540

gag acg aac ttt gtc cgc ctc gag ccc cta cgc gat gtc gcc cac atc   1680
Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile
545                 550                 555                 560

ttt gtt ctt cct gaa ctt cca gcg tct cgc cgt gag cgt ctc gcg tgg   1728
Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp
                565                 570                 575

cgc gaa atc aag acc tac cgc gcg taatttccca tctctgtacc ttc         1775
Arg Glu Ile Lys Thr Tyr Arg Ala
            580
```

<210> 360
<211> 584
<212> PRT
<213> Corynebacterium glutamicum

<400> 360

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Asp Ala Trp Ser Asp Pro Met Ala Thr Trp Arg His Ala Ile Thr Thr
  1               5                  10                  15

Lys Ile Glu Ala Gly Gln Gly Ser Asp Glu Leu Tyr Asn Asp Phe Glu
             20                  25                  30

His Gly Ala Gln Leu Phe Glu Arg Ala Ala Glu Asn Leu Ser Lys Glu
         35                  40                  45

Asp Arg Thr Ala Leu Phe Asp Val Ala Ser Ser Leu Arg Arg Gly Gly
     50                  55                  60

Asp Val Arg Ala Arg Leu Ala Pro Ala Leu Thr Ala Ser Val Thr His
 65                  70                  75                  80

Leu Leu Glu Leu Asn Pro Leu Arg Glu Leu Val Thr Met Gly Glu Asn
                 85                  90                  95

Leu Gln Val Arg Val Glu Arg Arg Ala Ala Leu Val Asn Ser Trp Tyr
            100                 105                 110

Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro
        115                 120                 125

Val His Gly Thr Phe Ala Thr Thr Ala Gln Ala Leu Glu Arg Val Ala
    130                 135                 140

Lys Met Gly Phe Asp Thr Val Tyr Phe Pro Pro Ile His Pro Ile Gly
145                 150                 155                 160
```

```
Glu Val Asn Arg Lys Gly Arg Asn Asn Thr Leu Thr Pro Glu Pro His
                165                 170                 175

Asp Val Gly Ser Pro Trp Ala Ile Gly Ser Lys Asp Gly Gly His Asp
            180                 185                 190

Ala Thr His Pro Arg Leu Gly Thr Ile Glu Asp Phe Gln Ala Leu Leu
        195                 200                 205

Ala Arg Ala Arg Glu Leu Asn Leu Glu Val Ala Leu Asp Leu Ala Leu
    210                 215                 220

Gln Ala Ala Pro Asp His Pro Trp Ala Gln Glu His Arg Glu Phe Phe
225                 230                 235                 240

Thr Val Leu Ala Asp Gly Thr Ile Ala Tyr Ala Glu Asn Pro Pro Lys
                245                 250                 255

Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Asn Asp Ala Pro Lys
            260                 265                 270

Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly
        275                 280                 285

Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe
    290                 295                 300

Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile
305                 310                 315                 320

Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser
                325                 330                 335

Lys Ile Gly Phe Ser Gln Ser Tyr Thr Tyr Phe Thr Trp Lys Val Thr
            340                 345                 350

Asn Glu Glu Leu Thr Glu Phe Ala Thr Glu Ile Ala Pro Met Ala Asp
        355                 360                 365

Ile Ser Arg Pro Asn Leu Phe Val Asn Thr Pro Asp Ile Leu His Ala
    370                 375                 380

Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu
385                 390                 395                 400

Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu
                405                 410                 415

Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser
            420                 425                 430

Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg
        435                 440                 445

Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg
    450                 455                 460

Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala
465                 470                 475                 480
```

```
Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly
                485                 490                 495

Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu
            500                 505                 510

Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala
        515                 520                 525

Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser
    530                 535                 540

Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile
545                 550                 555                 560

Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp
                565                 570                 575

Arg Glu Ile Lys Thr Tyr Arg Ala
            580
```

<210> 361
<211> 2316
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2293)
<223> RXA02612

<400> 361
gaacttccag cgtctcgccg tgagcgtctc gcgtggcgcg aaatcaagac ctaccgcgcg 60

```
taatttccca tctctgtacc ttctatcaag gattatcatc atg acc gtt gac ccc   115
                                          Met Thr Val Asp Pro
                                            1               5

gcg agc cac atc acc atc cct gaa gca gat ctg gcc cgc ctg cgc cac   163
Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu Ala Arg Leu Arg His
                10                  15                  20

tgc aac cat cac gat cct cat gga ttt tat ggt tgg cat gag acc gaa   211
Cys Asn His His Asp Pro His Gly Phe Tyr Gly Trp His Glu Thr Glu
            25                  30                  35

gct ggt tcg gtt atc cgc acg cgc cag gtc ggc gcg acg cag gtt aat   259
Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly Ala Thr Gln Val Asn
        40                  45                  50

ttg ctt atc gac gac acc tcc cac gtc atg acc cct atc ggc gac gac   307
Leu Leu Ile Asp Asp Thr Ser His Val Met Thr Pro Ile Gly Asp Asp
    55                  60                  65

att ttc gca att gac tta ggt cac cgc gag cgc gct gac tat cgc ttg   355
Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg Ala Asp Tyr Arg Leu
70                  75                  80                  85

gaa gtc acc tgg cct gat caa gaa ccg cag gtc aag gct gat cca tac   403
Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val Lys Ala Asp Pro Tyr
```

```
                    90                  95                  100

tac ttc ctc ccc acc gta ggc gag atg gat att tac ctc ttc tct gag   451
Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile Tyr Leu Phe Ser Glu
            105                 110                 115

gga cgc cat gag cgt ttg tgg gag att ctc ggt gcc aac atc aag acc   499
Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly Ala Asn Ile Lys Thr
        120                 125                 130

tac caa act gcg ctc gga aca gtt cgt ggc acc gca ttt act gtg tgg   547
Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr Ala Phe Thr Val Trp
    135                 140                 145

gct cca aac gca att ggc tgc gca gtg gtc ggt ggc ttc aac ggt tgg   595
Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly Gly Phe Asn Gly Trp
150                 155                 160                 165

aat gca tcc cag cat ccg atg cgt tct atg ggt ggt tcg ggt ctg tgg   643
Asn Ala Ser Gln His Pro Met Arg Ser Met Gly Gly Ser Gly Leu Trp
                170                 175                 180

gag ctg ttc atc cca ggc ata gag gaa ggc gaa gtg tac aaa ttc gcc   691
Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu Val Tyr Lys Phe Ala
            185                 190                 195

gtc caa acc agg gaa ggc caa cgt cgt gat aag gcc gat ccg atg gct   739
Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys Ala Asp Pro Met Ala
        200                 205                 210

cgt cgc gca gaa ctg gcg ccg gca acc gga tct att gtc gct tcc tct   787
Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser Ile Val Ala Ser Ser
    215                 220                 225

gag tac cag tgg cag gat tcc gag tgg ctg cgc gag cgt tcc caa act   835
Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg Glu Arg Ser Gln Thr
230                 235                 240                 245

gat ctc gca tcc aag cca atg agt gtc tac gag gtc cac ctc ggt tct   883
Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu Val His Leu Gly Ser
                250                 255                 260

tgg cgc tgg ggt aag aac tat gag gat ttg gct act gag ctg gtt gat   931
Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala Thr Glu Leu Val Asp
            265                 270                 275

tac gtc gca gat ctt ggc tac acc cac gtg gaa ttc ctc cct gtc gca   979
Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu Phe Leu Pro Val Ala
        280                 285                 290

gag cac ccc ttc ggt ggt tcc tgg ggt tac cag gtc acc ggc tac tac   1027
Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln Val Thr Gly Tyr Tyr
    295                 300                 305

gca ccg acc tct cgt tgg ggt act cca gat cag ttc cgt gcg cta gtc   1075
Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln Phe Arg Ala Leu Val
310                 315                 320                 325

gac gct ttc cac gcc cgc ggt att ggc gtg atc atg gac tgg gtt cct   1123
Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile Met Asp Trp Val Pro
                330                 335                 340
```

EDITED - DO NOT ENTER

```
gcc cac ttc cct aag gat gat tgg gct ctt gcc cgc ttt gat ggc gaa   1171
Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala Arg Phe Asp Gly Glu
            345                 350                 355

gcc ctc tat gaa cac cct gac tgg agg cgc ggc gaa caa aag gat tgg   1219
Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly Glu Gln Lys Asp Trp
        360                 365                 370

ggc acc ctg gtc ttt gac ttc ggt cgc aac gaa gtc cgc aac ttc ctc   1267
Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu Val Arg Asn Phe Leu
    375                 380                 385

gtc gct aat gcg ttg tac tgg att gaa gaa ttc cac atc gat ggt ctg   1315
Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe His Ile Asp Gly Leu
390                 395                 400                 405

cgc gtc gac gcc gtg gcc tcc atg ctg tac ctc gat tac tcc cgt gag   1363
Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu Asp Tyr Ser Arg Glu
                410                 415                 420

cac ggc gaa tgg gaa cca aac atc tac ggt ggt cgc gag aac ctc gag   1411
His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly Arg Glu Asn Leu Glu
            425                 430                 435

gca gtg cag ttc ctg cag gaa atg aac gcc acg gtg ctg cga ctg cac   1459
Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr Val Leu Arg Leu His
        440                 445                 450

cct ggt gcg ctc acc atc gct gag gaa tca act tca tgg cct ggc gtg   1507
Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr Ser Trp Pro Gly Val
    455                 460                 465

acc gca cca acg tgg gac ggc ggc ttg gga ttc tcc ctc aag tgg aac   1555
Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe Ser Leu Lys Trp Asn
470                 475                 480                 485

atg ggc tgg atg cac gac acc tta gag tac ttc tcc aaa aac cct gtg   1603
Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe Ser Lys Asn Pro Val
                490                 495                 500

cac cgc gca ttc cac cac agt gag ctc act ttc tcc ttg gtg tac gca   1651
His Arg Ala Phe His His Ser Glu Leu Thr Phe Ser Leu Val Tyr Ala
            505                 510                 515

ttc tct gag cgt ttt gta ctt ccg atc tct cac gat gaa gtc gtc cac   1699
Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His Asp Glu Val Val His
        520                 525                 530

ggc aag ggt tcc ctg tgg gac cgt atg cct ggc gat acg tgg aac aag   1747
Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly Asp Thr Trp Asn Lys
    535                 540                 545

gcc gct ggt ctt cgc acc ttc ctt gcg tac atg tgg tca cac cca ggc   1795
Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met Trp Ser His Pro Gly
550                 555                 560                 565

aag aag ctg ctt ttc atg ggt cag gag ttt ggt cag cgt gaa gag tgg   1843
Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly Gln Arg Glu Glu Trp
                570                 575                 580
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gct gaa ggc cag gga ctg cca tgg gat att gtc gac ggc tgg caa ggc   1891
Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val Asp Gly Trp Gln Gly
            585                 590                 595

gag tac cac gaa gcc atc cgc act ctg acc cgc tcc ctc aac ggt gtc   1939
Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg Ser Leu Asn Gly Val
        600                 605                 610

tac tca gac tcc cct gcg ctg cac act cag gat ttc acc gga gaa ggc   1987
Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp Phe Thr Gly Glu Gly
    615                 620                 625

ttc aca tgg aat aag ggc gac gac gcc acc aac aac att ttg gcg ttc   2035
Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn Asn Ile Leu Ala Phe
630                 635                 640                 645

act cgt ttc ggc agc gac ggc tcc cag atg ctg tgt gta ttc aac ctg   2083
Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu Cys Val Phe Asn Leu
                650                 655                 660

tct gga acc tcc cag cct gag tac cag ctc ggt gtt gca gcg ggt ggc   2131
Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly Val Ala Ala Gly Gly
            665                 670                 675

gaa tgg aag ctc gtt ctc aac act gat gat gct gaa ttc ctc ggt gca   2179
Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala Glu Phe Leu Gly Ala
        680                 685                 690

gaa aac gat atc gct act tcc gtt caa gca gca gcg aca cca cgc gat   2227
Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala Ala Thr Pro Arg Asp
    695                 700                 705

aat ttc gcc tac tca ctc tca ctg cat gtc cca gcg atg agt gct cag   2275
Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro Ala Met Ser Ala Gln
710                 715                 720                 725

ttc tac tca ctg cag aag taggacacag gaaaatgcat cct                2316
Phe Tyr Ser Leu Gln Lys
                730
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<210> 362
<211> 731
<212> PRT
<213> Corynebacterium glutamicum

<400> 362

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Met Thr Val Asp Pro Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu
  1               5                  10                  15

Ala Arg Leu Arg His Cys Asn His His Asp Pro His Gly Phe Tyr Gly
             20                  25                  30

Trp His Glu Thr Glu Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly
         35                  40                  45

Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr
     50                  55                  60

Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg
 65                  70                  75                  80
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Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val
85 90 95

Lys Ala Asp Pro Tyr Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile
100 105 110

Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly
115 120 125

Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr
130 135 140

Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly
145 150 155 160

Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly
165 170 175

Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu
180 185 190

Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys
195 200 205

Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser
210 215 220

Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg
225 230 235 240

Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu
245 250 255

Val His Leu Gly Ser Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala
260 265 270

Thr Glu Leu Val Asp Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu
275 280 285

Phe Leu Pro Val Ala Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln
290 295 300

Val Thr Gly Tyr Tyr Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln
305 310 315 320

Phe Arg Ala Leu Val Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile
325 330 335

Met Asp Trp Val Pro Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala
340 345 350

Arg Phe Asp Gly Glu Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly
355 360 365

Glu Gln Lys Asp Trp Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu
370 375 380

Val Arg Asn Phe Leu Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe
385 390 395 400

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His Ile Asp Gly Leu Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu
405 410 415

Asp Tyr Ser Arg Glu His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly
420 425 430

Arg Glu Asn Leu Glu Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr
435 440 445

Val Leu Arg Leu His Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr
450 455 460

Ser Trp Pro Gly Val Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe
465 470 475 480

Ser Leu Lys Trp Asn Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe
485 490 495

Ser Lys Asn Pro Val His Arg Ala Phe His His Ser Glu Leu Thr Phe
500 505 510

Ser Leu Val Tyr Ala Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His
515 520 525

Asp Glu Val Val His Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly
530 535 540

Asp Thr Trp Asn Lys Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met
545 550 555 560

Trp Ser His Pro Gly Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly
565 570 575

Gln Arg Glu Glu Trp Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val
580 585 590

Asp Gly Trp Gln Gly Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg
595 600 605

Ser Leu Asn Gly Val Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp
610 615 620

Phe Thr Gly Glu Gly Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn
625 630 635 640

Asn Ile Leu Ala Phe Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu
645 650 655

Cys Val Phe Asn Leu Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly
660 665 670

Val Ala Ala Gly Gly Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala
675 680 685

Glu Phe Leu Gly Ala Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala
690 695 700

Ala Thr Pro Arg Asp Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro
705 710 715 720

Ala Met Ser Ala Gln Phe Tyr Ser Leu Gln Lys

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725 730

<210> 363
<211> 1913
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1890)
<223> RXN01884

<400> 363

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gtg act gcc att gaa ttg atg ccg gtc cac cag ttc ctg cag gat gat   48
Val Thr Ala Ile Glu Leu Met Pro Val His Gln Phe Leu Gln Asp Asp
  1               5                  10                  15

cgt ctc cgc gac cta gga atg cgc aac tac tgg ggc tac aac tct ttc   96
Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe
            20                  25                  30

ggc ttc ttt gcg ccc tac aac gat tac gct gcc aac aag aac ccc ggt   144
Gly Phe Phe Ala Pro Tyr Asn Asp Tyr Ala Ala Asn Lys Asn Pro Gly
        35                  40                  45

ggc gcc gtg gcc gag ttc aaa ggc ttg gtg cgc agc tac cac gaa gcg   192
Gly Ala Val Ala Glu Phe Lys Gly Leu Val Arg Ser Tyr His Glu Ala
    50                  55                  60

ggc ctc gaa gta att ttg gat gtg gtc tac aac cac acc gcc gag ggc   240
Gly Leu Glu Val Ile Leu Asp Val Val Tyr Asn His Thr Ala Glu Gly
65                  70                  75                  80

aac cac atg ggc ccc acc atc gcg ttc cga ggc att gac aac gag gcg   288
Asn His Met Gly Pro Thr Ile Ala Phe Arg Gly Ile Asp Asn Glu Ala
                85                  90                  95

tac tac cga ctg gtt gag ggc gat cgc cgt cat tac atg gac tac acc   336
Tyr Tyr Arg Leu Val Glu Gly Asp Arg Arg His Tyr Met Asp Tyr Thr
            100                 105                 110

ggt act ggt aac tcc ctc aat gtc cgc gac ccg cac tca ctg cag ctg   384
Gly Thr Gly Asn Ser Leu Asn Val Arg Asp Pro His Ser Leu Gln Leu
        115                 120                 125

att atg gat tcg ctg cgc tac tgg gtc acc gag atg cat gtc gac ggc   432
Ile Met Asp Ser Leu Arg Tyr Trp Val Thr Glu Met His Val Asp Gly
    130                 135                 140

ttc cgc ttc gac ctt gcc tct acc ctt gct cgt gaa ttt gat gat gtt   480
Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg Glu Phe Asp Asp Val
145                 150                 155                 160

gac cgc ctg gca acc ttc ttc gac ctg gtc caa caa gac ccg gtg gtc   528
Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln Gln Asp Pro Val Val
                165                 170                 175

tcc cag gtc aag ctc att gct gag ccg tgg gat gtt ggc gaa ggc gga   576
Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp Val Gly Glu Gly Gly
            180                 185                 190
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tac caa gtg ggt aac ttc cca cca ctg tgg act gag tgg aac ggt aaa   624
Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr Glu Trp Asn Gly Lys
        195                 200                 205

tac cgc gac act gtc cgt gat ttc tgg cgt ggt gag cca gca acc ttg   672
Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly Glu Pro Ala Thr Leu
    210                 215                 220

ggt gaa ttc gct tcc cga cta act ggt tcc tct gat ttg tat gca aac   720
Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser Asp Leu Tyr Ala Asn
225                 230                 235                 240

aac ggc cgt cgc ccc act gca tcg atc aac ttt gtg act gct cac gac   768
Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe Val Thr Ala His Asp
                245                 250                 255

ggc ttc acc ctc aat gac ttg gtc agt tac aac gag aag cac aac atg   816
Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn Glu Lys His Asn Met
            260                 265                 270

gcc aac ggt gaa gac ggt cgg gac ggt gaa tca cac aac cgt tcc tgg   864
Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser His Asn Arg Ser Trp
        275                 280                 285

aac tgt ggc gtc gaa gga cca act gac gat cct gag att atg cag ctg   912
Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro Glu Ile Met Gln Leu
    290                 295                 300

cgt gct cag caa cga cgc aac ttc ctc acc acc ttg ttg ctg tcc cag   960
Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr Leu Leu Leu Ser Gln
305                 310                 315                 320

ggc acc cct atg ttg tcc cac ggt gat gaa atg gcc cgt acc caa aac  1008
Gly Thr Pro Met Leu Ser His Gly Asp Glu Met Ala Arg Thr Gln Asn
                325                 330                 335

ggc aac aac aac gtc tac tgc caa gac aat gaa ctg gcg tgg gtg aat  1056
Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu Leu Ala Trp Val Asn
            340                 345                 350

tgg gat cag gct gaa gaa aac gct gac ttg gtg agc ttc acc agg cgt  1104
Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val Ser Phe Thr Arg Arg
        355                 360                 365

ttg ctg cgt atc cga gca aac cac cca gta ttt agg cgc agg cag ttc  1152
Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Arg Gln Phe
    370                 375                 380

ctt gcc ggt ggc cct ttg ggc gcc gat gtt cgt gac cgc gat atc gca  1200
Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala
385                 390                 395                 400

tgg ctg gta cca aat gga acc ttg atg act caa gat gac tgg gac ttc  1248
Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe
                405                 410                 415

gct ttc ggt aaa tca ctg cag gtg ttc ttc aac ggc gat gcc atc gaa  1296
Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu
            420                 425                 430
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gag cct gat tat cga gga cag aaa atc cac gat gac tcc ttc atc ttg   1344
Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu
        435                 440                 445

atg ttc aac gct cac ttc gaa cct atc gat ttc aat ctc cct cct gag   1392
Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu
    450                 455                 460

cat ttc ggt atg aag tgg aag ctt ttg gtc gat acc acc gaa gcg gtg   1440
His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val
465                 470                 475                 480

ggc cac ccg ctg gag gat ctc acc atc gaa gct ggc gga acc atc act   1488
Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr
                485                 490                 495

gtt cct gcc cgt tcc acg atg ctg ctg cgc cag gtg gag gct ccg gac   1536
Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp
            500                 505                 510

tac acc aag ctt gag gaa aag atc gct gct gaa aag cgt gag caa gaa   1584
Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu
        515                 520                 525

ctt gcg gca gag aag gaa gct gct gag aag cgc gaa ttg gaa ctg gcg   1632
Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala
    530                 535                 540

gca gca aag gaa gct gaa gat gct gct gag gct ctc cac ctt gcg gca   1680
Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala
545                 550                 555                 560

gaa cgt gct tcg act cag gaa gct gaa ttg gcc cat caa cac ggt gct   1728
Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala
                565                 570                 575

gat gcg att gcc gat gag gta gcg gaa gaa cca caa gag ctg cca caa   1776
Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln
            580                 585                 590

gat gaa gta gcg gca gag gtc gag act gag ccc gac acc gag cct gac   1824
Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp
        595                 600                 605

act gaa tct gac tcc gag cag gct gag gta gct tca gag gag cct gaa   1872
Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu
    610                 615                 620

gcg gac gaa gaa gag aag tagtacaccg aaagtggcgt cgc                 1913
Ala Asp Glu Glu Glu Lys
625                 630
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<210> 364
<211> 630
<212> PRT
<213> Corynebacterium glutamicum

<400> 364

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Val Thr Ala Ile Glu Leu Met Pro Val His Gln Phe Leu Gln Asp Asp
  1               5                  10                  15
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Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe
20 25 30

Gly Phe Phe Ala Pro Tyr Asn Asp Tyr Ala Ala Asn Lys Asn Pro Gly
35 40 45

Gly Ala Val Ala Glu Phe Lys Gly Leu Val Arg Ser Tyr His Glu Ala
50 55 60

Gly Leu Glu Val Ile Leu Asp Val Val Tyr Asn His Thr Ala Glu Gly
65 70 75 80

Asn His Met Gly Pro Thr Ile Ala Phe Arg Gly Ile Asp Asn Glu Ala
85 90 95

Tyr Tyr Arg Leu Val Glu Gly Asp Arg Arg His Tyr Met Asp Tyr Thr
100 105 110

Gly Thr Gly Asn Ser Leu Asn Val Arg Asp Pro His Ser Leu Gln Leu
115 120 125

Ile Met Asp Ser Leu Arg Tyr Trp Val Thr Glu Met His Val Asp Gly
130 135 140

Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg Glu Phe Asp Asp Val
145 150 155 160

Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln Gln Asp Pro Val Val
165 170 175

Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp Val Gly Glu Gly Gly
180 185 190

Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr Glu Trp Asn Gly Lys
195 200 205

Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly Glu Pro Ala Thr Leu
210 215 220

Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser Asp Leu Tyr Ala Asn
225 230 235 240

Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe Val Thr Ala His Asp
245 250 255

Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn Glu Lys His Asn Met
260 265 270

Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser His Asn Arg Ser Trp
275 280 285

Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro Glu Ile Met Gln Leu
290 295 300

Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr Leu Leu Leu Ser Gln
305 310 315 320

Gly Thr Pro Met Leu Ser His Gly Asp Glu Met Ala Arg Thr Gln Asn
325 330 335

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Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu Leu Ala Trp Val Asn
            340                 345                 350

Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val Ser Phe Thr Arg Arg
        355                 360                 365

Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Arg Gln Phe
    370                 375                 380

Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala
385                 390                 395                 400

Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe
                405                 410                 415

Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu
            420                 425                 430

Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu
        435                 440                 445

Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu
    450                 455                 460

His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val
465                 470                 475                 480

Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr
                485                 490                 495

Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp
            500                 505                 510

Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu
        515                 520                 525

Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala
    530                 535                 540

Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala
545                 550                 555                 560

Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala
                565                 570                 575

Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln
            580                 585                 590

Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp
        595                 600                 605

Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu
    610                 615                 620

Ala Asp Glu Glu Glu Lys
625                 630
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<210> 365
<211> 1496
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1473)
<223> FRXA01884

<400> 365

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atg cat gtc gac ggc ttc cgc ttc gac ctt gcc tct acc ctt gct cgt   48
Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg
  1               5                  10                  15

gaa ttt gat gat gtt gac cgc ctg gca acc ttc ttc gac ctg gtc caa   96
Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln
             20                  25                  30

caa gac ccg gtg gtc tcc cag gtc aag ctc att gct gag ccg tgg gat   144
Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp
         35                  40                  45

gtt ggc gaa ggc gga tac caa gtg ggt aac ttc cca cca ctg tgg act   192
Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr
     50                  55                  60

gag tgg aac ggt aaa tac cgc gac act gtc cgt gat ttc tgg cgt ggt   240
Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly
 65                  70                  75                  80

gag cca gca acc ttg ggt gaa ttc gct tcc cga cta act ggt tcc tct   288
Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser
                 85                  90                  95

gat ttg tat gca aac aac ggc cgt cgc ccc act gca tcg atc aac ttt   336
Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe
            100                 105                 110

gtg act gct cac gac ggc ttc acc ctc aat gac ttg gtc agt tac aac   384
Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn
        115                 120                 125

gag aag cac aac atg gcc aac ggt gaa gac ggt cgg gac ggt gaa tca   432
Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser
    130                 135                 140

cac aac cgt tcc tgg aac tgt ggc gtc gaa gga cca act gac gat cct   480
His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro
145                 150                 155                 160

gag att atg cag ctg cgt gct cag caa cga cgc aac ttc ctc acc acc   528
Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr
                165                 170                 175

ttg ttg ctg tcc cag ggc acc cct atg ttg tcc cac ggt gat gaa atg   576
Leu Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met
            180                 185                 190

gcc cgt acc caa aac ggc aac aac aac gtc tac tgc caa gac aat gaa   624
Ala Arg Thr Gln Asn Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu
        195                 200                 205

ctg gcg tgg gtg aat tgg gat cag gct gaa gaa aac gct gac ttg gtg   672
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09623410.090502

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Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val
    210                 215                 220

agc ttc acc agg cgt ttg ctg cgt atc cga gca aac cac cca gta ttt   720
Ser Phe Thr Arg Arg Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe
225                 230                 235                 240

agg cgc agg cag ttc ctt gcc ggt ggc cct ttg ggc gcc gat gtt cgt   768
Arg Arg Arg Gln Phe Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg
                245                 250                 255

gac cgc gat atc gca tgg ctg gta cca aat gga acc ttg atg act caa   816
Asp Arg Asp Ile Ala Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln
            260                 265                 270

gat gac tgg gac ttc gct ttc ggt aaa tca ctg cag gtg ttc ttc aac   864
Asp Asp Trp Asp Phe Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn
        275                 280                 285

ggc gat gcc atc gaa gag cct gat tat cga gga cag aaa atc cac gat   912
Gly Asp Ala Ile Glu Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp
    290                 295                 300

gac tcc ttc atc ttg atg ttc aac gct cac ttc gaa cct atc gat ttc   960
Asp Ser Phe Ile Leu Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe
305                 310                 315                 320

aat ctc cct cct gag cat ttc ggt atg aag tgg aag ctt ttg gtc gat   1008
Asn Leu Pro Pro Glu His Phe Gly Met Lys Trp Lys Leu Leu Val Asp
                325                 330                 335

acc acc gaa gcg gtg ggc cac ccg ctg gag gat ctc acc atc gaa gct   1056
Thr Thr Glu Ala Val Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala
            340                 345                 350

ggc gga acc atc act gtt cct gcc cgt tcc acg atg ctg ctg cgc cag   1104
Gly Gly Thr Ile Thr Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln
        355                 360                 365

gtg gag gct ccg gac tac acc aag ctt gag gaa aag atc gct gct gaa   1152
Val Glu Ala Pro Asp Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu
    370                 375                 380

aag cgt gag caa gaa ctt gcg gca gag aag gaa gct gct gag aag cgc   1200
Lys Arg Glu Gln Glu Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg
385                 390                 395                 400

gaa ttg gaa ctg gcg gca gca aag gaa gct gaa gat gct gct gag gct   1248
Glu Leu Glu Leu Ala Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala
                405                 410                 415

ctc cac ctt gcg gca gaa cgt gct tcg act cag gaa gct gaa ttg gcc   1296
Leu His Leu Ala Ala Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala
            420                 425                 430

cat caa cac ggt gct gat gcg att gcc gat gag gta gcg gaa gaa cca   1344
His Gln His Gly Ala Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro
        435                 440                 445

caa gag ctg cca caa gat gaa gta gcg gca gag gtc gag act gag ccc   1392
Gln Glu Leu Pro Gln Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro
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    450                 455                 460

gac acc gag cct gac act gaa tct gac tcc gag cag gct gag gta gct   1440
Asp Thr Glu Pro Asp Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala
465                 470                 475                 480

tca gag gag cct gaa gcg gac gaa gaa gag aag tagtacaccg aaagtggcgt 1493
Ser Glu Glu Pro Glu Ala Asp Glu Glu Glu Lys
                485                 490

cgc                                                               1496
```

<210> 366
<211> 491
<212> PRT
<213> Corynebacterium glutamicum

<400> 366

```
Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg
  1               5                  10                  15

Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln
            20                  25                  30

Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp
        35                  40                  45

Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr
    50                  55                  60

Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly
65                  70                  75                  80

Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser
                85                  90                  95

Asp Leu Tyr Ala Asn Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe
            100                 105                 110

Val Thr Ala His Asp Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn
        115                 120                 125

Glu Lys His Asn Met Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser
    130                 135                 140

His Asn Arg Ser Trp Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro
145                 150                 155                 160

Glu Ile Met Gln Leu Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr
                165                 170                 175

Leu Leu Leu Ser Gln Gly Thr Pro Met Leu Ser His Gly Asp Glu Met
            180                 185                 190

Ala Arg Thr Gln Asn Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu
        195                 200                 205

Leu Ala Trp Val Asn Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val
    210                 215                 220
```

```
Ser Phe Thr Arg Arg Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe
225                 230                 235                 240

Arg Arg Arg Gln Phe Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg
                245                 250                 255

Asp Arg Asp Ile Ala Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln
            260                 265                 270

Asp Asp Trp Asp Phe Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn
        275                 280                 285

Gly Asp Ala Ile Glu Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp
    290                 295                 300

Asp Ser Phe Ile Leu Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe
305                 310                 315                 320

Asn Leu Pro Pro Glu His Phe Gly Met Lys Trp Lys Leu Leu Val Asp
                325                 330                 335

Thr Thr Glu Ala Val Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala
            340                 345                 350

Gly Gly Thr Ile Thr Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln
        355                 360                 365

Val Glu Ala Pro Asp Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu
    370                 375                 380

Lys Arg Glu Gln Glu Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg
385                 390                 395                 400

Glu Leu Glu Leu Ala Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala
                405                 410                 415

Leu His Leu Ala Ala Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala
            420                 425                 430

His Gln His Gly Ala Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro
        435                 440                 445

Gln Glu Leu Pro Gln Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro
    450                 455                 460

Asp Thr Glu Pro Asp Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala
465                 470                 475                 480

Ser Glu Glu Pro Glu Ala Asp Glu Glu Glu Lys
                485                 490
```

<210> 367
<211> 547
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(547)
<223> RXA01111

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<400> 367
agaaaaccct gccgatgcaa actttgagga gagattcaat caaggaatag aaatcattct 60

ggtgggtcta gacgcgcttg ggcatataag atgacgttcc atg aca tca acg att 115
Met Thr Ser Thr Ile
1 5

gag cac tcg tac caa gtt tgg cct gga cat gct tat cct ctg ggt tca 163
Glu His Ser Tyr Gln Val Trp Pro Gly His Ala Tyr Pro Leu Gly Ser
10 15 20

acc tat gac ggt gct gga acg aac ttc gca ctc ttc tcc gac gtt gca 211
Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu Phe Ser Asp Val Ala
25 30 35

gag cgt gtt gag ctg tgt cta tta gat gca gat aac aac gag act cga 259
Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp Asn Asn Glu Thr Arg
40 45 50

att cca ctc gaa gag cgc gat gcc cac att tgg cat tgc tac ctt cct 307
Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp His Cys Tyr Leu Pro
55 60 65

ggc gtt caa cct gga cag cgc tac gga ttc cga gtt cat ggc ccg tgg 355
Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg Val His Gly Pro Trp
70 75 80 85

aac cca gat gag ggt aag cgg tgc gac gcg aac aaa ctt cta gtt gat 403
Asn Pro Asp Glu Gly Lys Arg Cys Asp Ala Asn Lys Leu Leu Val Asp
90 95 100

ccc tat gct cgt gct ttc gat gga gat ttt gat gga cat ccg tca cta 451
Pro Tyr Ala Arg Ala Phe Asp Gly Asp Phe Asp Gly His Pro Ser Leu
105 110 115

ttt tct tac gac atc acc aat cca aat gac ccc aac ggt cgc aat acc 499
Phe Ser Tyr Asp Ile Thr Asn Pro Asn Asp Pro Asn Gly Arg Asn Thr
120 125 130

gaa gac agc att gat cac aca atg aag tct gtc gtg gtg aac cca ttc 547
Glu Asp Ser Ile Asp His Thr Met Lys Ser Val Val Val Asn Pro Phe
135 140 145

<210> 368
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 368
Met Thr Ser Thr Ile Glu His Ser Tyr Gln Val Trp Pro Gly His Ala
1 5 10 15

Tyr Pro Leu Gly Ser Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu
20 25 30

Phe Ser Asp Val Ala Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp
35 40 45

Asn Asn Glu Thr Arg Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp

```
     50                  55                  60

His Cys Tyr Leu Pro Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg
 65                  70                  75                  80

Val His Gly Pro Trp Asn Pro Asp Glu Gly Lys Arg Cys Asp Ala Asn
                 85                  90                  95

Lys Leu Leu Val Asp Pro Tyr Ala Arg Ala Phe Asp Gly Asp Phe Asp
            100                 105                 110

Gly His Pro Ser Leu Phe Ser Tyr Asp Ile Thr Asn Pro Asn Asp Pro
        115                 120                 125

Asn Gly Arg Asn Thr Glu Asp Ser Ile Asp His Thr Met Lys Ser Val
    130                 135                 140

Val Val Asn Pro Phe
145
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<210> 369
<211> 1635
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1612)
<223> RXN01550

<400> 369

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ttcgccagca gtacttcttc acctctgctt ccctgcaggc catgattcag ggccacctgg 60

cgcaccacaa ggacctcagc aactttgccg agttcactcc gtg cag ctc aat gac   115
                                            Val Gln Leu Asn Asp
                                              1               5

act cac cca gtg ttg gct atc cct gag ctt atg cgt ctg ctc atg gac   163
Thr His Pro Val Leu Ala Ile Pro Glu Leu Met Arg Leu Leu Met Asp
                 10                  15                  20

gag cat gac atg ggc tgg gaa gaa tcc tgg gca atc gtg ttc aag acc   211
Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala Ile Val Phe Lys Thr
             25                  30                  35

ttc gca tac acc aac cac acc gtg ctc acc gaa gct ctt gag cag tgg   259
Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu Ala Leu Glu Gln Trp
         40                  45                  50

gat cag cag atc ttc caa cag ctg ttc tgg cgc gtg tgg gaa atc atc   307
Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile
     55                  60                  65

aca gag atc gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg   355
Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu
 70                  75                  80                  85

gat gaa gag acc atc gac cgc atg gct cca atc cag cac ggc act gtt   403
Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile Gln His Gly Thr Val
                 90                  95                 100
```

```
cat atg gca tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg   451
His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val
            105                 110                 115

gca gcg ctg cac acc gag atc atc aag gcc gag acc ttg gct gac tgg   499
Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp
        120                 125                 130

tac gca ctg tgg cca gag aag ttc aac aac aag act aac ggt gtt acc   547
Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr
    135                 140                 145

cca cgc cgt tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc   595
Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu
150                 155                 160                 165

act cga ctt tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg   643
Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu
                170                 175                 180

aag aag ctg cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc   691
Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu
            185                 190                 195

cgc gct atc aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc   739
Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu
        200                 205                 210

gag cgc cag ggc att gag att gat cca gaa tcc atc ttt gac gtg cag   787
Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln
    215                 220                 225

att aag cgc ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac   835
Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr
230                 235                 240                 245

gta cta gac ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc   883
Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile
                250                 255                 260

cca gca cgc act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc   931
Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val
            265                 270                 275

cgc gcc aag gcg att atc aag ctc atc aac tct att gct gac ttg gta   979
Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val
        280                 285                 290

aac aac gat cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag   1027
Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu
    295                 300                 305

aac tac aac gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc   1075
Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val
310                 315                 320                 325

tcc gaa cag att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac   1123
Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn
                330                 335                 340
```

```
atg aag ttc atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc   1171
Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly
            345                 350                 355

gcc aac gta gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc   1219
Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile
        360                 365                 370

ttc ggt gct cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag   1267
Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu
    375                 380                 385

cca tat gag ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac   1315
Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp
390                 395                 400                 405

gcc ctg gat aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac   1363
Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr
                410                 415                 420

gac ctc aag cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac   1411
Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp
            425                 430                 435

acc tac tac gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac   1459
Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp
        440                 445                 450

cgt atg gcc gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg   1507
Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met
    455                 460                 465

gcc tgg atc aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc   1555
Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr
470                 475                 480                 485

atc cgc gat tat gcc acc gag atc tgg aag ctc gag cca act cct gct   1603
Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala
                490                 495                 500

gtt aag aag taggttttaa cctccgcttc taa                             1635
Val Lys Lys
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<210> 370
<211> 504
<212> PRT
<213> Corynebacterium glutamicum

<400> 370

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Val Gln Leu Asn Asp Thr His Pro Val Leu Ala Ile Pro Glu Leu Met
  1               5                  10                  15

Arg Leu Leu Met Asp Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala
            20                  25                  30

Ile Val Phe Lys Thr Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu
        35                  40                  45

Ala Leu Glu Gln Trp Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg
```

```
     50                  55                  60

Val Trp Glu Ile Ile Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg
 65                  70                  75                  80

Ala Ala Asp Gly Leu Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile
                 85                  90                  95

Gln His Gly Thr Val His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr
            100                 105                 110

Ser Ile Asn Gly Val Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu
        115                 120                 125

Thr Leu Ala Asp Trp Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys
    130                 135                 140

Thr Asn Gly Val Thr Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly
145                 150                 155                 160

Leu Ser Asp Leu Leu Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr
                165                 170                 175

Asp Leu Asp Glu Leu Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser
            180                 185                 190

Val Leu Glu Glu Leu Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe
        195                 200                 205

Ala Glu Trp Ile Leu Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser
    210                 215                 220

Ile Phe Asp Val Gln Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu
225                 230                 235                 240

Met Asn Ala Leu Tyr Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp
                245                 250                 255

Gly Leu Thr Asp Ile Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala
            260                 265                 270

Ala Pro Gly Tyr Val Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser
        275                 280                 285

Ile Ala Asp Leu Val Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys
    290                 295                 300

Val Val Phe Val Glu Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu
305                 310                 315                 320

Pro Ala Ser Asp Val Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala
                325                 330                 335

Ser Gly Thr Ser Asn Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu
            340                 345                 350

Gly Thr Met Asp Gly Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu
        355                 360                 365

Glu Asn Ala Tyr Ile Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu
    370                 375                 380
```

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```
Arg Glu Ser Tyr Glu Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu
385                 390                 395                 400

Lys Arg Ala Leu Asp Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn
                405                 410                 415

Ser Gly Leu Phe Tyr Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly
            420                 425                 430

Lys Asp Ala Ser Asp Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr
        435                 440                 445

Arg Glu Thr Arg Asp Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu
    450                 455                 460

Gly Trp Ala Arg Met Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe
465                 470                 475                 480

Ser Ser Asp Arg Thr Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu
                485                 490                 495

Glu Pro Thr Pro Ala Val Lys Lys
            500
```

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<210> 371
<211> 1367
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1344)
<223> FRXA01550

<400> 371

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atc ttc caa cag ctg ttc tgg cgc gtg tgg gaa atc atc aca gag atc   48
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu Ile
  1               5                  10                  15

gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg gat gaa gag   96
Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu
             20                  25                  30

acc atc gac cgc atg gct cca atc cag cgc ggc act gtt cat atg gca  144
Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala
         35                  40                  45

tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg gca gcg ctg  192
Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu
     50                  55                  60

cac acc gag atc atc aag gcc gag acc ttg gct gac tgg tac gca ctg  240
His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu
 65                  70                  75                  80

tgg cca gag aag ttc aac aac aag act aac ggt gtt acc cca cgc cgt  288
Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg
                 85                  90                  95
```

```
tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc act cga ctt   336
Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu
            100                 105                 110

tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg aag aag ctg   384
Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu
        115                 120                 125

cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc cgc gct atc   432
Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile
    130                 135                 140

aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc gag cgc cag   480
Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln
145                 150                 155                 160

ggc att gag att gat cca gaa tcc atc ttt gac gtg cag att aag cgc   528
Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg
                165                 170                 175

ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac gta cta gac   576
Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp
            180                 185                 190

ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc cca gca cgc   624
Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg
        195                 200                 205

act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc cgc gcc aag   672
Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys
    210                 215                 220

gcg att atc aag ctc atc aac tct att gct gac ttg gta aac aac gat   720
Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp
225                 230                 235                 240

cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag aac tac aac   768
Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn
                245                 250                 255

gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc tcc gaa cag   816
Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln
            260                 265                 270

att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac atg aag ttc   864
Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe
        275                 280                 285

atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc gcc aac gta   912
Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val
    290                 295                 300

gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc ttc ggt gct   960
Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala
305                 310                 315                 320

cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag cca tat gag   1008
Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu
                325                 330                 335

ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac gcc ctg gat   1056
```

0602740 - 0602940

```
Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp
            340                 345                 350

aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac gac ctc aag   1104
Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys
        355                 360                 365

cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac acc tac tac   1152
His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr
    370                 375                 380

gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac cgt atg gcc   1200
Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala
385                 390                 395                 400

gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg gcc tgg atc   1248
Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile
                405                 410                 415

aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc atc cgc gat   1296
Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp
            420                 425                 430

tat gcc acc gag atc tgg aag ctc gag cca act cct gct gtt aag aag   1344
Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys
        435                 440                 445

taggttttaa cctccgcttc taa                                        1367


<210> 372
<211> 448
<212> PRT
<213> Corynebacterium glutamicum

<400> 372
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu Ile
  1               5                  10                  15

Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu
             20                  25                  30

Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala
         35                  40                  45

Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu
     50                  55                  60

His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu
 65                  70                  75                  80

Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg
                 85                  90                  95

Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu
            100                 105                 110

Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu
        115                 120                 125

Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile
```

```
    130                 135                 140

Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln
145                 150                 155                 160

Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg
                165                 170                 175

Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp
            180                 185                 190

Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg
        195                 200                 205

Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys
    210                 215                 220

Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp
225                 230                 235                 240

Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn
                245                 250                 255

Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln
            260                 265                 270

Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe
        275                 280                 285

Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val
    290                 295                 300

Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala
305                 310                 315                 320

Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu
                325                 330                 335

Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp
            340                 345                 350

Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys
        355                 360                 365

His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr
    370                 375                 380

Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala
385                 390                 395                 400

Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile
                405                 410                 415

Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp
            420                 425                 430

Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys
        435                 440                 445
```

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<210> 373
<211> 2348
<212> DNA
<213> Corynebacterium glutamicum

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<222> (1)..(2325)
<223> RXN02100

<400> 373

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Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser
  1               5                  10                  15

gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga   96
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
            20                  25                  30

gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc   144
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
        35                  40                  45

ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg   192
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
    50                  55                  60

aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc   240
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
65                  70                  75                  80

tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag   288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
                85                  90                  95

cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca   336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
            100                 105                 110

gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca   384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
        115                 120                 125

ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc   432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
    130                 135                 140

atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag   480
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
145                 150                 155                 160

ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc   528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
                165                 170                 175

atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac   576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
            180                 185                 190
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gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc   624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
        195                 200                 205

aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc   672
Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
    210                 215                 220

atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg   720
Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
225                 230                 235                 240

tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc   768
Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
                245                 250                 255

ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa   816
Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
            260                 265                 270

gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt   864
Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
        275                 280                 285

ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt   912
Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
    290                 295                 300

cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta   960
Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
305                 310                 315                 320

agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa  1008
Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
                325                 330                 335

gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc  1056
Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
            340                 345                 350

aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat  1104
Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
        355                 360                 365

ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag  1152
Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
    370                 375                 380

aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt  1200
Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
385                 390                 395                 400

gct cgc gct gca act gca aag tcc tgg tct cac cgt gga cac acc gaa  1248
Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu
                405                 410                 415

gca gaa ctt gcg tgg acc tcc cgc gtt ctg gat cca aac gtg ctg acc  1296
Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr
            420                 425                 430

att ggt ttc gca cgt cgc gta tcc acc tac aag cgc ttg acc ttg atg  1344
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Sequence Listing

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Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met
        435                 440                 445

ctg cgc aac cct gaa cgc ctg cgt tcc atc ttg ctt aat gag gaa cgc   1392
Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg
    450                 455                 460

cca gtt cag ttc gtt att gct ggt aag gca cac cca cat gac atg ggt   1440
Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly
465                 470                 475                 480

ggc aag aag ctc atg cag gaa atc gtc cac ttc gct gat caa gct ggt   1488
Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly
                485                 490                 495

gtc cgt gac cgt ttc ctc ttc ctg cct gat tac gac atc aac ctg gcc   1536
Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala
            500                 505                 510

agc tac ctg atc tct ggt gct gac gtg tgg ctg aac aac cca gtg cgc   1584
Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg
        515                 520                 525

cct cag gaa gca tcg gga acc tcc ggt atg aag gcc gtc atg aat ggt   1632
Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly
    530                 535                 540

ggc ctg acc ctg tcc atc tct gat ggt tgg tgg gat gaa atg cct aag   1680
Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys
545                 550                 555                 560

gag acc acc ggc tgg acc atc cca acc gtt gag tcc cag gac ttg gaa   1728
Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu
                565                 570                 575

tgc cgc gac cac ctg gaa tcc cag gcg ctg tac gac ctg ctg gaa aac   1776
Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn
            580                 585                 590

gaa gtt gca ccg ctg ttt tac aag cgc gac aag aac ggc atc cca cag   1824
Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln
        595                 600                 605

gac tgg ctg gac ctg gtt cgc gaa tcc tgg acc acc ctg tca cca atg   1872
Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met
    610                 615                 620

gtc acc tcc acc cgc atg gtg cgc gac tac acc acc cag tac tac cgc   1920
Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg
625                 630                 635                 640

cca acc aaa cac cag gca gag ctc att gcg cag cct gca gaa gca gcg   1968
Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala
                645                 650                 655

gat tac gcg gca tgg ctt gag cac atc aaa gca gag tgg gct ggc gtc   2016
Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val
            660                 665                 670

aag gtc tca gac ctg aag atc agc gag agc gcc atc acg gcg cag gag   2064
Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu
```

```
        675                 680                 685

ctt gaa gtc agc gtt cgc gtt gat tcc ggt tcg ctt aac gac gac gag   2112
Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu
    690                 695                 700

ttc caa gct cag gca ctc ttt ggt gcg ctc gga cac aac ggt gac atc   2160
Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile
705                 710                 715                 720

gaa gat cca gaa atc acc gtt ttg acc cca cgc ggc gat ggc gcc tac   2208
Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr
                725                 730                 735

gcg gca aag gtc agc act gac ctg cca ggc aac tac ggc atc act gcc   2256
Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala
            740                 745                 750

cgc gtt gtt cca aac aac agg atg ctg gtc agc cca gcg gaa acc cgc   2304
Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg
        755                 760                 765

ctg atc acc tac ttg gag aac tagggcgaaa ctagctttac caa             2348
Leu Ile Thr Tyr Leu Glu Asn
    770                 775
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<210> 374
<211> 775
<212> PRT
<213> Corynebacterium glutamicum

<400> 374

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Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser
  1               5                  10                  15

Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
             20                  25                  30

Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
         35                  40                  45

Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
     50                  55                  60

Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
 65                  70                  75                  80

Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
                 85                  90                  95

Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
            100                 105                 110

Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
        115                 120                 125

Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
    130                 135                 140

Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
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US 2005/0196848 A1

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145                 150                 155                 160

Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
                165                 170                 175

Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
            180                 185                 190

Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
        195                 200                 205

Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
    210                 215                 220

Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
225                 230                 235                 240

Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
                245                 250                 255

Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
            260                 265                 270

Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
        275                 280                 285

Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
    290                 295                 300

Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
305                 310                 315                 320

Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
                325                 330                 335

Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
            340                 345                 350

Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
        355                 360                 365

Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
    370                 375                 380

Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
385                 390                 395                 400

Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu
                405                 410                 415

Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr
            420                 425                 430

Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met
        435                 440                 445

Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg
    450                 455                 460

Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly
465                 470                 475                 480
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US 2005/0260186 A1

Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly
485 490 495

Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala
500 505 510

Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg
515 520 525

Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly
530 535 540

Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys
545 550 555 560

Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu
565 570 575

Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn
580 585 590

Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln
595 600 605

Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met
610 615 620

Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg
625 630 635 640

Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala
645 650 655

Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val
660 665 670

Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu
675 680 685

Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu
690 695 700

Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile
705 710 715 720

Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr
725 730 735

Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala
740 745 750

Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg
755 760 765

Leu Ile Thr Tyr Leu Glu Asn
770 775

<210> 375
<211> 941

EP 2 395 076 A1

<212> DNA
<213> Corynebacterium glutamicum

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<222> (1)..(918)
<223> FRXA02100

<400> 375

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att gct ggt aag gca cac cca cat gac atg ggt ggc aag aag ctc atg   48
Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met
  1               5                  10                  15

cag gaa atc gtc cac ttc gct gat caa gct ggt gtc cgt gac cgt ttc   96
Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe
            20                  25                  30

ctc ttc ctg cct gat tac gac atc aac ctg gcc agc tac ctg atc tct  144
Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser
        35                  40                  45

ggt gct gac gtg tgg ctg aac aac cca gtg cgc cct cag gaa gca tcg  192
Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser
    50                  55                  60

gga acc tcc ggt atg aag gcc gtc atg aat ggt ggc ctg acc ctg tcc  240
Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser
65                  70                  75                  80

atc tct gat ggt tgg tgg gat gaa atg cct aag gag acc acc ggc tgg  288
Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp
                85                  90                  95

acc atc cca acc gtt gag tcc cag gac ttg gaa tgc cgc gac cac ctg  336
Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu
            100                 105                 110

gaa tcc cag gcg ctg tac gac ctg ctg gaa aac gaa gtt gca ccg ctg  384
Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu
        115                 120                 125

ttt tac aag cgc gac aag aac ggc atc cca cag gac tgg ctg gac ctg  432
Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu
    130                 135                 140

gtt cgc gaa tcc tgg acc acc ctg tca cca atg gtc acc tcc acc cgc  480
Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg
145                 150                 155                 160

atg gtg cgc gac tac acc acc cag tac tac cgc cca acc aaa cac cag  528
Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln
                165                 170                 175

gca gag ctc att gcg cag cct gca gaa gca gcg gat tac gcg gca tgg  576
Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp
            180                 185                 190

ctt gag cac atc aaa gca gag tgg gct ggc gtc aag gtc tca gac ctg  624
Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu
        195                 200                 205
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20050148.0

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aag atc agc gag agc gcc atc acg gcg cag gag ctt gaa gtc agc gtt   672
Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val
    210                 215                 220

cgc gtt gat tcc ggt tcg ctt aac gac gac gag ttc caa gct cag gca   720
Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
225                 230                 235                 240

ctc ttt ggt gcg ctc gga cac aac ggt gac atc gaa gat cca gaa atc   768
Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
                245                 250                 255

acc gtt ttg acc cca cgc ggc gat ggc gcc tac gcg gca aag gtc agc   816
Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
            260                 265                 270

act gac ctg cca ggc aac tac ggc atc act gcc cgc gtt gtt cca aac   864
Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
        275                 280                 285

aac agg atg ctg gtc agc cca gcg gaa acc cgc ctg atc acc tac ttg   912
Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
    290                 295                 300

gag aac tagggcgaaa ctagctttac caa                                941
Glu Asn
305
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US 2006/0160180 A1

<210> 376
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 376

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Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe
            20                  25                  30

Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser
        35                  40                  45

Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser
    50                  55                  60

Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser
65                  70                  75                  80

Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp
                85                  90                  95

Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu
            100                 105                 110

Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu
        115                 120                 125

Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu
    130                 135                 140
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```
Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg
145                 150                 155                 160

Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln
                165                 170                 175

Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp
            180                 185                 190

Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu
        195                 200                 205

Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val
    210                 215                 220

Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
225                 230                 235                 240

Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
                245                 250                 255

Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
            260                 265                 270

Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
        275                 280                 285

Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
    290                 295                 300

Glu Asn
305
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09822360 - 060205

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<211> 1206
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1206)
<223> FRXA02113

<400> 377

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  1               5                  10                  15

gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga   96
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
             20                  25                  30

gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc   144
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
         35                  40                  45

ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg   192
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
     50                  55                  60
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aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc   240
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
 65                  70                  75                  80

tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag   288
Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
                85                  90                  95

cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca   336
Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
            100                 105                 110

gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca   384
Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
        115                 120                 125

ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc   432
Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
    130                 135                 140

atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag   480
Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
145                 150                 155                 160

ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc   528
Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
                165                 170                 175

atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac   576
Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
            180                 185                 190

gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc   624
Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
        195                 200                 205

aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc   672
Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
    210                 215                 220

atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg   720
Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
225                 230                 235                 240

tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc   768
Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
                245                 250                 255

ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa   816
Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
            260                 265                 270

gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt   864
Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
        275                 280                 285

ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt   912
Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
    290                 295                 300
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Doc. No. 5,605,793

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cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta   960
Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
305                 310                 315                 320

agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa   1008
Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
                325                 330                 335

gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc   1056
Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
            340                 345                 350

aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat   1104
Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
        355                 360                 365

ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag   1152
Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
    370                 375                 380

aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt   1200
Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
385                 390                 395                 400

gct cgc                                                          1206
Ala Arg
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09605248.090905

<210> 378
<211> 402
<212> PRT
<213> Corynebacterium glutamicum

<400> 378

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Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser
  1               5                  10                  15

Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
             20                  25                  30

Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
         35                  40                  45

Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
     50                  55                  60

Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
 65                  70                  75                  80

Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
                 85                  90                  95

Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
            100                 105                 110

Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
        115                 120                 125

Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
    130                 135                 140
```

Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
145 150 155 160

Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
165 170 175

Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
180 185 190

Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
195 200 205

Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
210 215 220

Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
225 230 235 240

Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
245 250 255

Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
260 265 270

Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
275 280 285

Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
290 295 300

Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
305 310 315 320

Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
325 330 335

Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
340 345 350

Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
355 360 365

Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
370 375 380

Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
385 390 395 400

Ala Arg

<210> 379
<211> 1140
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1117)

<223> RXA02147

<400> 379

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aaaagttgag agcggcttgc ttcttttcct tggctaggct tttgtaatcg ggttagagta 60

gtggagttgc ttgaatgagg ttgatagggg atttttgaag atg ttt ggt cgc cgt  115
                                            Met Phe Gly Arg Arg
                                              1               5

tgg gtg agc gtt gtg gcg tca tgt gtt atc gca agc acg ctg att ctg  163
Trp Val Ser Val Val Ala Ser Cys Val Ile Ala Ser Thr Leu Ile Leu
                 10                  15                  20

gtg cct tcg cat tcc ggt gcg gag gaa gtc gat caa ctg att gct gat  211
Val Pro Ser His Ser Gly Ala Glu Glu Val Asp Gln Leu Ile Ala Asp
             25                  30                  35

atc gag cat gtc tct cag gaa acg tct gcc cag aat gag gaa gtc aaa  259
Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln Asn Glu Glu Val Lys
         40                  45                  50

cag ctt gag att gat att gag gct cgt gag gtc acg atc aag gaa gtt  307
Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val Thr Ile Lys Glu Val
     55                  60                  65

cag gag cag tcg gta agc tac cgt gag gcg gct gat caa gca tcg gag  355
Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala Asp Gln Ala Ser Glu
 70                  75                  80                  85

aat gtc gaa gct tat cgt tcg gag atc aat cgg atc gct cag gcg aag  403
Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg Ile Ala Gln Ala Lys
                 90                  95                 100

tat cgt ggc aca gtc acg gat cct ttg agc att gcg gtg tct gca gaa  451
Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile Ala Val Ser Ala Glu
            105                 110                 115

gat cca caa aac gtg att gat cgg atg agc tac ctt tca acg ttg act  499
Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr Leu Ser Thr Leu Thr
        120                 125                 130

aag tcc act agt gat gtg gtt gaa tcc ctc aac gcg gag act gag aag  547
Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn Ala Glu Thr Glu Lys
    135                 140                 145

tcc gca gaa gct gtg tat caa gca aac cgt act aag gcg gaa gcg gag  595
Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr Lys Ala Glu Ala Glu
150                 155                 160                 165

ttc cag ttg ggg cag ctg aag gta cgc cag gcg gag ctt gaa tct gaa  643
Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala Glu Leu Glu Ser Glu
                170                 175                 180

aag gaa gca ttg gat ggt cga aaa tcg gag atc cga gac cgg gtg gat  691
Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile Arg Asp Arg Val Asp
            185                 190                 195

gcc ctg acg cca cag gag cgg gaa atg tgg gtt gct aag aat ggt cca  739
Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val Ala Lys Asn Gly Pro
        200                 205                 210
```

```
ttg gac att gat ctg act gat ttg ctt ggt ctt tcc gct gcg act tcg   787
Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu Ser Ala Ala Thr Ser
    215                 220                 225

ggt gcg gtg gat gct gcc ttg tct aag ttg gga agc cct tat ggt tgg   835
Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly Ser Pro Tyr Gly Trp
230                 235                 240                 245

ggt ggc att ggc cca aat gag ttt gat tgc tca ggt ttg atc tat tgg   883
Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser Gly Leu Ile Tyr Trp
                250                 255                 260

gcg tat cag cag atg ggt aag act ttg cca cgt acg tct caa gct cag   931
Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg Thr Ser Gln Ala Gln
            265                 270                 275

atg gct ggc gga acg ccg gtg agc aga gat gag ctg cag cct ggc gat   979
Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu Leu Gln Pro Gly Asp
        280                 285                 290

gtc att gga tat tac cca ggt gct act cac gtg gga ctg tat att ggg   1027
Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val Gly Leu Tyr Ile Gly
    295                 300                 305

gac gga aag att gtg cac gcc tca gac tac gga atc cct gtg cag gtg   1075
Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly Ile Pro Val Gln Val
310                 315                 320                 325

gta tct gtt gat tca gca ccg ttt tat ggt gcg cgt cgc tac           1117
Val Ser Val Asp Ser Ala Pro Phe Tyr Gly Ala Arg Arg Tyr
                330                 335

taagaaatag ttcgtcagga gaa                                        1140


<210> 380
<211> 339
<212> PRT
<213> Corynebacterium glutamicum

<400> 380
Met Phe Gly Arg Arg Trp Val Ser Val Val Ala Ser Cys Val Ile Ala
  1               5                  10                  15

Ser Thr Leu Ile Leu Val Pro Ser His Ser Gly Ala Glu Glu Val Asp
             20                  25                  30

Gln Leu Ile Ala Asp Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln
         35                  40                  45

Asn Glu Glu Val Lys Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val
     50                  55                  60

Thr Ile Lys Glu Val Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala
 65                  70                  75                  80

Asp Gln Ala Ser Glu Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg
                 85                  90                  95

Ile Ala Gln Ala Lys Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile
            100                 105                 110
```

Ala Val Ser Ala Glu Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr
115 120 125

Leu Ser Thr Leu Thr Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn
130 135 140

Ala Glu Thr Glu Lys Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr
145 150 155 160

Lys Ala Glu Ala Glu Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala
165 170 175

Glu Leu Glu Ser Glu Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile
180 185 190

Arg Asp Arg Val Asp Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val
195 200 205

Ala Lys Asn Gly Pro Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu
210 215 220

Ser Ala Ala Thr Ser Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly
225 230 235 240

Ser Pro Tyr Gly Trp Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser
245 250 255

Gly Leu Ile Tyr Trp Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg
260 265 270

Thr Ser Gln Ala Gln Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu
275 280 285

Leu Gln Pro Gly Asp Val Ile Gly Tyr Tyr Pro Gly Ala Thr His Val
290 295 300

Gly Leu Tyr Ile Gly Asp Gly Lys Ile Val His Ala Ser Asp Tyr Gly
305 310 315 320

Ile Pro Val Gln Val Val Ser Val Asp Ser Ala Pro Phe Tyr Gly Ala
325 330 335

Arg Arg Tyr

<210> 381
<211> 1959
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1936)
<223> RXA01478

<400> 381
gcgggttttg ttgtggaggg gcgcgtcgaa aagcaatttt ttttccaaga tagctcactt 60

tattggagtc acctggcctg aaatcctcta ctctgggcgc atg acc att cca gga 115

```
                                                  Met Thr Ile Pro Gly
                                                    1               5

gct tcc aca cag act gat atc cct ctg gac aca ctt ctt gag gat tac   163
Ala Ser Thr Gln Thr Asp Ile Pro Leu Asp Thr Leu Leu Glu Asp Tyr
                10                  15                  20

gcg cta ctg tca gac act cac acc ggc gct ctg ctg tcc aac atg ggc   211
Ala Leu Leu Ser Asp Thr His Thr Gly Ala Leu Leu Ser Asn Met Gly
            25                  30                  35

agt ttg gac tgg ttg tgc ctg cct cgt ttt gat tcc caa gcc atg ttc   259
Ser Leu Asp Trp Leu Cys Leu Pro Arg Phe Asp Ser Gln Ala Met Phe
        40                  45                  50

acc agg ctg ctt ggt gat cgc gag cac gga cac tgg agt ttg cgt gtc   307
Thr Arg Leu Leu Gly Asp Arg Glu His Gly His Trp Ser Leu Arg Val
    55                  60                  65

cca ggt ggt gag gtg atc agc caa aac tac ctc ggc gat tcc ttc gtg   355
Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu Gly Asp Ser Phe Val
70                  75                  80                  85

gtg cag acc gtg tgg cgt tca gag acc ggt act gcc cgg gtt gtt gat   403
Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr Ala Arg Val Val Asp
                90                  95                  100

ttc atg cca att cac ggt caa gaa caa ccc gat atc acc gac ctg gtg   451
Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp Ile Thr Asp Leu Val
            105                 110                 115

cgc tct gtg cac tgc gtg gaa ggc gaa gtg gat gtg gaa tcg atc ctg   499
Arg Ser Val His Cys Val Glu Gly Glu Val Asp Val Glu Ser Ile Leu
        120                 125                 130

cgc ctg cgt ttt gat tat ggc gag tcc act ccg tat ttc cgc acc agc   547
Arg Leu Arg Phe Asp Tyr Gly Glu Ser Thr Pro Tyr Phe Arg Thr Ser
    135                 140                 145

act gtc gac ggc atc agc atc gtg cag gct gtc gcc ggc ccc aat gcg   595
Thr Val Asp Gly Ile Ser Ile Val Gln Ala Val Ala Gly Pro Asn Ala
150                 155                 160                 165

gta tat gtt cgt gga cct gag atg cca cac cgc cct gca aag gat tgt   643
Val Tyr Val Arg Gly Pro Glu Met Pro His Arg Pro Ala Lys Asp Cys
                170                 175                 180

cac agt ggc acc ttc cac ctg acg gcc ggc gaa tcc gtg gaa tgg gtt   691
His Ser Gly Thr Phe His Leu Thr Ala Gly Glu Ser Val Glu Trp Val
            185                 190                 195

ctc acc tgg gca ccg tcg ttc gaa ccg cat ccc ccc atg ccg gat tac   739
Leu Thr Trp Ala Pro Ser Phe Glu Pro His Pro Pro Met Pro Asp Tyr
        200                 205                 210

acc cgc tct ttg gag agc acc ttg agc ttc tgg gca tca tgg gtt gaa   787
Thr Arg Ser Leu Glu Ser Thr Leu Ser Phe Trp Ala Ser Trp Val Glu
    215                 220                 225

gag ctc ccc cac cag cgc ctc tac gac gct gaa gtc cgc cgc tcc atg   835
Glu Leu Pro His Gln Arg Leu Tyr Asp Ala Glu Val Arg Arg Ser Met
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230                 235                 240                 245

ctc gta ctg cgc gcc ttg acc gat cta caa acc ggt ggc atc gtg gcc   883
Leu Val Leu Arg Ala Leu Thr Asp Leu Gln Thr Gly Gly Ile Val Ala
                250                 255                 260

gca ccg acc acc tca cta cca gag gat ttc gga ggc atc cgt aac tgg   931
Ala Pro Thr Thr Ser Leu Pro Glu Asp Phe Gly Gly Ile Arg Asn Trp
            265                 270                 275

gac tac cgc tac gtg tgg ctg cgc gac tcc gca ctc acc att gaa gcc   979
Asp Tyr Arg Tyr Val Trp Leu Arg Asp Ser Ala Leu Thr Ile Glu Ala
        280                 285                 290

ctc gtg gaa tac gga ttc tcc caa gca gcc ctc caa tgg cgc acc tgg   1027
Leu Val Glu Tyr Gly Phe Ser Gln Ala Ala Leu Gln Trp Arg Thr Trp
    295                 300                 305

ctg ctg cgc gcc atc gca ggc gac ccg gaa aac ctc cgc atc atg tat   1075
Leu Leu Arg Ala Ile Ala Gly Asp Pro Glu Asn Leu Arg Ile Met Tyr
310                 315                 320                 325

ggc ctc ggc ggc gaa cga cac ctc cct gaa cgc gaa ctc caa cac ctg   1123
Gly Leu Gly Gly Glu Arg His Leu Pro Glu Arg Glu Leu Gln His Leu
                330                 335                 340

cgc gga tac gaa aac tcc gtg cct gtt cgc gtt ggc aat gga gcc gcc   1171
Arg Gly Tyr Glu Asn Ser Val Pro Val Arg Val Gly Asn Gly Ala Ala
            345                 350                 355

gaa caa tac caa gca gat gtc gtc ggc gaa gta atg gtc gcg ctt gaa   1219
Glu Gln Tyr Gln Ala Asp Val Val Gly Glu Val Met Val Ala Leu Glu
        360                 365                 370

acc atc cgc cgc gcc ggg tgc ctc gag gac gaa ttc tcc tgg ggc atg   1267
Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu Phe Ser Trp Gly Met
    375                 380                 385

caa aaa gcc atc ctc gat ttc caa gaa gcc aac ttc gac cgc aag gat   1315
Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn Phe Asp Arg Lys Asp
390                 395                 400                 405

caa ggc atc tgg gaa atg cgc tcc gaa ccg caa tat ttc acc cac ggc   1363
Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln Tyr Phe Thr His Gly
                410                 415                 420

cgc gcc atg atg tgg gcc ggc ttc gac cgc ggc atc aaa gcc atc gaa   1411
Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly Ile Lys Ala Ile Glu
            425                 430                 435

gaa ttc aac ctc gac ggc ccc atc gag cgc tgg cgt gaa ctc cgc gcc   1459
Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp Arg Glu Leu Arg Ala
        440                 445                 450

aaa ctc cgc gaa gaa atc atg acc aac ggc ttc aac gaa gag atc caa   1507
Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe Asn Glu Glu Ile Gln
    455                 460                 465

tcc ttc acc cag tgc tac gac aac acc caa gtc gac gcc tcg ctg ctt   1555
Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val Asp Ala Ser Leu Leu
470                 475                 480                 485
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cag ctc gcc caa ata ggc ttc atc ggc ttc gac gat cca aaa atg ctc   1603
Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp Asp Pro Lys Met Leu
                490                 495                 500

agc acc gta gcg cgc att gag caa gag ctt ctc gac gcc cac ggc ttt   1651
Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu Asp Ala His Gly Phe
            505                 510                 515

ctt cac agg tac cac acc gac ggg tct gac ggc ctt gcc ggc gac gaa   1699
Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly Leu Ala Gly Asp Glu
        520                 525                 530

tac ccc ttc ctc atc tgt tca ttc tgg ctg gta gaa caa tac gca agc   1747
Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val Glu Gln Tyr Ala Ser
    535                 540                 545

tcc aac cgc ctc gac gag gcc aaa gaa aag atg aac cgc atc ctt gcc   1795
Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met Asn Arg Ile Leu Ala
550                 555                 560                 565

gtc caa agc cca ctt ggc cta ctg gct gag gaa tac tcc acc cac cat   1843
Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu Tyr Ser Thr His His
                570                 575                 580

ggc agg ctc gct gga aac tac cct cag gcc ttt tcc cac att ggt ctg   1891
Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe Ser His Ile Gly Leu
            585                 590                 595

atc agc gct gcc cgt gcc ata aat ttc gaa gaa gcg cga aac agg       1936
Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu Ala Arg Asn Arg
        600                 605                 610

tagagtctaa ggtgtcattc ttg                                        1959
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<210> 382
<211> 612
<212> PRT
<213> Corynebacterium glutamicum

<400> 382

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Met Thr Ile Pro Gly Ala Ser Thr Gln Thr Asp Ile Pro Leu Asp Thr
  1               5                  10                  15

Leu Leu Glu Asp Tyr Ala Leu Leu Ser Asp Thr His Thr Gly Ala Leu
             20                  25                  30

Leu Ser Asn Met Gly Ser Leu Asp Trp Leu Cys Leu Pro Arg Phe Asp
         35                  40                  45

Ser Gln Ala Met Phe Thr Arg Leu Leu Gly Asp Arg Glu His Gly His
     50                  55                  60

Trp Ser Leu Arg Val Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu
 65                  70                  75                  80

Gly Asp Ser Phe Val Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr
                 85                  90                  95

Ala Arg Val Val Asp Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp
```

```
            100                 105                 110

Ile Thr Asp Leu Val Arg Ser Val His Cys Val Glu Gly Glu Val Asp
        115                 120                 125

Val Glu Ser Ile Leu Arg Leu Arg Phe Asp Tyr Gly Glu Ser Thr Pro
    130                 135                 140

Tyr Phe Arg Thr Ser Thr Val Asp Gly Ile Ser Ile Val Gln Ala Val
145                 150                 155                 160

Ala Gly Pro Asn Ala Val Tyr Val Arg Gly Pro Glu Met Pro His Arg
                165                 170                 175

Pro Ala Lys Asp Cys His Ser Gly Thr Phe His Leu Thr Ala Gly Glu
            180                 185                 190

Ser Val Glu Trp Val Leu Thr Trp Ala Pro Ser Phe Glu Pro His Pro
        195                 200                 205

Pro Met Pro Asp Tyr Thr Arg Ser Leu Glu Ser Thr Leu Ser Phe Trp
    210                 215                 220

Ala Ser Trp Val Glu Glu Leu Pro His Gln Arg Leu Tyr Asp Ala Glu
225                 230                 235                 240

Val Arg Arg Ser Met Leu Val Leu Arg Ala Leu Thr Asp Leu Gln Thr
                245                 250                 255

Gly Gly Ile Val Ala Ala Pro Thr Thr Ser Leu Pro Glu Asp Phe Gly
            260                 265                 270

Gly Ile Arg Asn Trp Asp Tyr Arg Tyr Val Trp Leu Arg Asp Ser Ala
        275                 280                 285

Leu Thr Ile Glu Ala Leu Val Glu Tyr Gly Phe Ser Gln Ala Ala Leu
    290                 295                 300

Gln Trp Arg Thr Trp Leu Leu Arg Ala Ile Ala Gly Asp Pro Glu Asn
305                 310                 315                 320

Leu Arg Ile Met Tyr Gly Leu Gly Gly Glu Arg His Leu Pro Glu Arg
                325                 330                 335

Glu Leu Gln His Leu Arg Gly Tyr Glu Asn Ser Val Pro Val Arg Val
            340                 345                 350

Gly Asn Gly Ala Ala Glu Gln Tyr Gln Ala Asp Val Val Gly Glu Val
        355                 360                 365

Met Val Ala Leu Glu Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu
    370                 375                 380

Phe Ser Trp Gly Met Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn
385                 390                 395                 400

Phe Asp Arg Lys Asp Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln
                405                 410                 415

Tyr Phe Thr His Gly Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly
            420                 425                 430
```

```
Ile Lys Ala Ile Glu Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp
        435                 440                 445

Arg Glu Leu Arg Ala Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe
    450                 455                 460

Asn Glu Glu Ile Gln Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val
465                 470                 475                 480

Asp Ala Ser Leu Leu Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp
                485                 490                 495

Asp Pro Lys Met Leu Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu
            500                 505                 510

Asp Ala His Gly Phe Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly
        515                 520                 525

Leu Ala Gly Asp Glu Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val
    530                 535                 540

Glu Gln Tyr Ala Ser Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met
545                 550                 555                 560

Asn Arg Ile Leu Ala Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu
                565                 570                 575

Tyr Ser Thr His His Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe
            580                 585                 590

Ser His Ile Gly Leu Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu
        595                 600                 605

Ala Arg Asn Arg
    610
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09550148 - 082505

<210> 383
<211> 658
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(658)
<223> RXA01888

<400> 383
agtagatact agataccacc cattgatgcc gtcaaggggt ttcctgtaaa gatgtaagag 60

attaagaaaa gaggtagata tggcgtcaaa gcgaccgaca atg gct gat gtg gca 115
                                              Met Ala Asp Val Ala
                                                1   5

aaa gct gct gga gta tcc act gcg ctg gtc tcc atc gtg ttt cgc gat 163
Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser Ile Val Phe Arg Asp
                10   15   20

gcc ccc gga gca agt gaa tcc acc cgc aac cat gtg aaa gaa aaa gcc 211
Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His Val Lys Glu Lys Ala

```
            25                  30                  35

gcc gaa ctc gga tac att cct gat cga cga gcc caa aaa ctt cgc caa   259
Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala Gln Lys Leu Arg Gln
        40                  45                  50

aac cgc tcc gga ctc atc ggt gtg gca ttc gaa atg cac caa gca ttc   307
Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu Met His Gln Ala Phe
    55                  60                  65

cac ggc gat atc gtc gaa cac ctc tat ccc acc gcc cga aaa cat ggc   355
His Gly Asp Ile Val Glu His Leu Tyr Pro Thr Ala Arg Lys His Gly
70                  75                  80                  85

ttc gac ctg tac ctt agc gcg atc aca ccg act cgc act gaa aaa gat   403
Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr Arg Thr Glu Lys Asp
                90                  95                  100

gcc gtc aac gcc ctg atc agg gaa cga tgc gaa gca gta att ctt cta   451
Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu Ala Val Ile Leu Leu
            105                 110                 115

gga tct cgc atg tca cct agt gat ttg gaa aca atc gca cag caa ctt   499
Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr Ile Ala Gln Gln Leu
        120                 125                 130

ccc gtc caa gta att gcc cgc ggt tcc gga acc ccc aaa gtc agt tcc   547
Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr Pro Lys Val Ser Ser
    135                 140                 145

gtc cat gtc gac gac gca gtt ggc gcc caa tta gcc ctc aac cac ctc   595
Val His Val Asp Asp Ala Val Gly Ala Gln Leu Ala Leu Asn His Leu
150                 155                 160                 165

atc gaa tta ggc cac gaa cac atc atc tac atc gat ggt ggc gac gcc   643
Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile Asp Gly Gly Asp Ala
                170                 175                 180

cct ggc acc cag gaa                                              658
Pro Gly Thr Gln Glu
            185
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<210> 384
<211> 186
<212> PRT
<213> Corynebacterium glutamicum

<400> 384

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Met Ala Asp Val Ala Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser
  1               5                  10                  15

Ile Val Phe Arg Asp Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His
             20                  25                  30

Val Lys Glu Lys Ala Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala
         35                  40                  45

Gln Lys Leu Arg Gln Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu
     50                  55                  60
```

Met His Gln Ala Phe His Gly Asp Ile Val Glu His Leu Tyr Pro Thr
65 70 75 80

Ala Arg Lys His Gly Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr
85 90 95

Arg Thr Glu Lys Asp Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu
100 105 110

Ala Val Ile Leu Leu Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr
115 120 125

Ile Ala Gln Gln Leu Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr
130 135 140

Pro Lys Val Ser Ser Val His Val Asp Asp Ala Val Gly Ala Gln Leu
145 150 155 160

Ala Leu Asn His Leu Ile Glu Leu Gly His Glu His Ile Ile Tyr Ile
165 170 175

Asp Gly Gly Asp Ala Pro Gly Thr Gln Glu
180 185

<210> 385
<211> 1503
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1480)
<223> RXN01927

<400> 385
gagcagcggg atcttttgcg taattcgcgc gcgcagatcc atgtgattga ccacaatggt 60

gatgaaattt tggatacccc aacggaagag gatttttaag atg gct ttg gtt ctt 115
Met Ala Leu Val Leu
1 5

gga atc gat agt tcc acc caa tcc tgc aag gct ttg ctt gtc gac gcc 163
Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala Leu Leu Val Asp Ala
10 15 20

gcc acc ggc cag gtt atc gac gaa ggc cgc gcg agt cac ccg agc ggg 211
Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala Ser His Pro Ser Gly
25 30 35

tcg gag gta gat cca cgt gcg tgg atc gct gcg ctg gat caa gct acc 259
Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala Leu Asp Gln Ala Thr
40 45 50

gag ggg ttg tta gaa cgc gcg gac gct gta tct att gca ggc cag cag 307
Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser Ile Ala Gly Gln Gln
55 60 65

cac ggc atg gtg gcg ttg gat gaa aac gat gaa atc gtt cgc ccg gcg 355
His Gly Met Val Ala Leu Asp Glu Asn Asp Glu Ile Val Arg Pro Ala
70 75 80 85

```
ttg tta tgg aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat   403
Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn
                 90                  95                 100

gag gag atc ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg   451
Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val
            105                 110                 115

tat gtt gct tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat   499
Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His
        120                 125                 130

gaa cca gaa aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat   547
Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp
    135                 140                 145

ttc ctc acc tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat   595
Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His
150                 155                 160                 165

ggt gat gct tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg   643
Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp
                170                 175                 180

cgc acc gat cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct   691
Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro
            185                 190                 195

gaa ctc ctg gcc cca aat gcg att gcg gga aca act cca ggt gga gtg   739
Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val
        200                 205                 210

aaa gtt gct gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt   787
Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu
    215                 220                 225

gat ttg cag cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt   835
Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val
230                 235                 240                 245

gcc ggc atg acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc   883
Ala Gly Met Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val
                250                 255                 260

act ggt ttc gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg   931
Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr
            265                 270                 275

ctt aat ggc gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg   979
Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val
        280                 285                 290

gaa tgg gaa gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca   1027
Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser
    295                 300                 305

ggt ggc gtg acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat   1075
Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn
310                 315                 320                 325
```

```
cgt ccc gca gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc   1123
Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr
                330                 335                 340

cgc gag gac ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg   1171
Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu
            345                 350                 355

gat gat gct gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag   1219
Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln
        360                 365                 370

cgc atc cag ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag   1267
Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu
    375                 380                 385

att gcc cct gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct   1315
Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala
390                 395                 400                 405

gaa tat gtg gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg   1363
Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser
                410                 415                 420

ggt gag gcc acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac   1411
Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His
            425                 430                 435

cgc gca cct aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt   1459
Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg
        440                 445                 450

gct gca acg cag ggt tgg tac tagagctcga tattgtcgat caa             1503
Ala Ala Thr Gln Gly Trp Tyr
    455                 460
```

<210> 386
<211> 460
<212> PRT
<213> Corynebacterium glutamicum

<400> 386

```
Met Ala Leu Val Leu Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala
  1               5                  10                  15

Leu Leu Val Asp Ala Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala
             20                  25                  30

Ser His Pro Ser Gly Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala
         35                  40                  45

Leu Asp Gln Ala Thr Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser
     50                  55                  60

Ile Ala Gly Gln Gln His Gly Met Val Ala Leu Asp Glu Asn Asp Glu
 65                  70                  75                  80

Ile Val Arg Pro Ala Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala
                 85                  90                  95
```

Ala Leu Asp Leu Asn Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp
100 105 110

Ala Thr Gly Ser Val Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg
115 120 125

Trp Met Arg Asp His Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val
130 135 140

Met Leu Pro His Asp Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg
145 150 155 160

Lys Val Thr Asp His Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr
165 170 175

Arg Asp Arg Ala Trp Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His
180 185 190

Glu Val Glu Leu Pro Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr
195 200 205

Thr Pro Gly Gly Val Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala
210 215 220

Ala Ala Leu Gly Leu Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile
225 230 235 240

Gly Thr Ser Gly Val Ala Gly Met Thr Val Gln His Ser Val His Asp
245 250 255

Pro Ser Gly Leu Val Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe
260 265 270

Pro Leu Ala Cys Thr Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg
275 280 285

Arg Ile Leu Gly Val Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala
290 295 300

Ala Gln Pro Gly Ser Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly
305 310 315 320

Glu Arg Thr Pro Asn Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu
325 330 335

Asn Cys Ala Thr Thr Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly
340 345 350

Leu Leu Leu Ala Leu Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr
355 360 365

Gly Val Pro Val Gln Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser
370 375 380

Gln Ala Val Arg Glu Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val
385 390 395 400

Val Pro Glu Pro Ala Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala
405 410 415

Ala Trp Ala Leu Ser Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro

Sequence Listing

```
            420                 425                 430

Gly Ser Asp Pro His Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg
        435                 440                 445

Tyr Ala Lys Leu Arg Ala Ala Thr Gln Gly Trp Tyr
    450                 455                 460


<210> 387
<211> 1139
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1116)
<223> FRXA01927

<400> 387
aat gac act cgt tct gcc cag gct gcg ttg gat ctc aat gag gag atc   48
Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile
  1               5                  10                  15

ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg tat gtt gct   96
Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala
             20                  25                  30

tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat gaa cca gaa   144
Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu
         35                  40                  45

aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat ttc ctc acc   192
Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr
     50                  55                  60

tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat ggt gat gct   240
Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala
 65                  70                  75                  80

tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg cgc acc gat   288
Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp
                 85                  90                  95

cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct gaa ctc ctg   336
Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu
            100                 105                 110

gcc cca aat gcg att gcg gga aca act cca ggt gga gtg aaa gtt gct   384
Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala
        115                 120                 125

gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt gat ttg cag   432
Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu Asp Leu Gln
    130                 135                 140

cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt gcc ggc atg   480
Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met
145                 150                 155                 160

acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc act ggt ttc   528
```

```
Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe
                165                 170                 175

gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg ctt aat ggc   576
Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly
            180                 185                 190

gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg gaa tgg gaa   624
Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu
        195                 200                 205

gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca ggt ggc gtg   672
Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val
    210                 215                 220

acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat cgt ccc gca   720
Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala
225                 230                 235                 240

gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc cgc gag gac   768
Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp
                245                 250                 255

ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg gat gat gct   816
Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala
            260                 265                 270

gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag cgc atc cag   864
Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln
        275                 280                 285

ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag att gcc cct   912
Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro
    290                 295                 300

gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct gaa tat gtg   960
Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val
305                 310                 315                 320

gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg ggt gag gcc  1008
Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala
                325                 330                 335

acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac cgc gca cct  1056
Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro
            340                 345                 350

aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt gct gca acg  1104
Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr
        355                 360                 365

cag ggt tgg tac tagagctcga tattgtcgat caa                       1139
Gln Gly Trp Tyr
    370
```

<210> 388
<211> 372
<212> PRT
<213> Corynebacterium glutamicum

<400> 388

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Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile
 1               5                  10                  15

Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala
            20                  25                  30

Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu
        35                  40                  45

Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr
    50                  55                  60

Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala
65                  70                  75                  80

Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp
                85                  90                  95

Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu
            100                 105                 110

Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala
        115                 120                 125

Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu Asp Leu Gln
    130                 135                 140

Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met
145                 150                 155                 160

Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe
                165                 170                 175

Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly
            180                 185                 190

Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu
        195                 200                 205

Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val
    210                 215                 220

Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala
225                 230                 235                 240

Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp
                245                 250                 255

Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala
            260                 265                 270

Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln
        275                 280                 285

Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro
    290                 295                 300

Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val
305                 310                 315                 320
```

09852-0052

```
Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala
                325                 330                 335

Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro
            340                 345                 350

Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr
        355                 360                 365

Gln Gly Trp Tyr
    370
```

<210> 389
<211> 844
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(844)
<223> RXA02729

<400> 389

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gaattaattg caggcacggt acctagcgtg acgaaaacta cgatccccac tgcccttatt 60

catcgtgaat caatcatcaa ctccacttta aggaagaagg atg gac tcc cca atg   115
                                            Met Asp Ser Pro Met
                                              1               5

agt aac tca acc ggt acc gac att gtc gtt gtc gga tcc atc aat gcc   163
Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val Gly Ser Ile Asn Ala
                  10                  15                  20

gat ctc acc gca aaa gtt caa cgc cac cct gaa cct gga gaa acc ctc   211
Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu Pro Gly Glu Thr Leu
              25                  30                  35

ctg ggt agc ggc ggc aca gtg agt gct ggt ggc aaa ggc gcc aac caa   259
Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly Lys Gly Ala Asn Gln
          40                  45                  50

gct gtg gcg gca gcg caa tta ggt gcc aaa gtc acc atg atc ggt gcg   307
Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val Thr Met Ile Gly Ala
      55                  60                  65

gtc gga acc gat caa atg gct ggc gag gcg ctg aca cat ttg cgt caa   355
Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu Thr His Leu Arg Gln
  70                  75                  80                  85

tca gga gca gat atg tcc gcg att gcc act gtg gac ggt ccc act ggt   403
Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val Asp Gly Pro Thr Gly
                  90                  95                 100

ctt gcc atc atc act gtg tct gac gat ggg gaa aac acc atc atc gtt   451
Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu Asn Thr Ile Ile Val
              105                 110                 115

atc cct ggc gct aac gct tct gtc acc gcg gaa ttt gtt gat aaa cac   499
Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu Phe Val Asp Lys His
          120                 125                 130
```

```
tcc caa ctc att gag aac gcc ggc att gtg ttg ctt cag ggt gag atc   547
Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu Leu Gln Gly Glu Ile
    135                 140                 145

cct gcc gat ggt ttc gag cgt gcc gtt gat ctt tca caa gga cgt gtg   595
Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu Ser Gln Gly Arg Val
150                 155                 160                 165

gtg atc aat ctg gct cca gtt gtg ccc gtg gga cat gat cag ctg cgt   643
Val Ile Asn Leu Ala Pro Val Val Pro Val Gly His Asp Gln Leu Arg
                170                 175                 180

cgt gcc gat cca ttg ctg gtc aac gaa cac gaa ggc gct ctg gtg ctg   691
Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu Gly Ala Leu Val Leu
            185                 190                 195

gac atg ctt gga act cca gcg acc acg tct gat ccc caa agt ttg gtc   739
Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp Pro Gln Ser Leu Val
        200                 205                 210

act gaa ttg ctg gag cag ggt ttt act tcc gtg gtg atg aca ctt ggt   787
Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val Val Met Thr Leu Gly
    215                 220                 225

gcc gaa ggt gct ctg gtt ggc acg ccg ggc caa ctc acg gca att cct   835
Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln Leu Thr Ala Ile Pro
230                 235                 240                 245

acc cca aag                                                      844
Thr Pro Lys
```

<210> 390
<211> 248
<212> PRT
<213> Corynebacterium glutamicum

<400> 390

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Met Asp Ser Pro Met Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val
  1               5                  10                  15

Gly Ser Ile Asn Ala Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu
            20                  25                  30

Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly
        35                  40                  45

Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val
    50                  55                  60

Thr Met Ile Gly Ala Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu
65                  70                  75                  80

Thr His Leu Arg Gln Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val
                85                  90                  95

Asp Gly Pro Thr Gly Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu
            100                 105                 110
```

Asn Thr Ile Ile Val Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu
115 120 125

Phe Val Asp Lys His Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu
130 135 140

Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu
145 150 155 160

Ser Gln Gly Arg Val Val Ile Asn Leu Ala Pro Val Val Pro Val Gly
165 170 175

His Asp Gln Leu Arg Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu
180 185 190

Gly Ala Leu Val Leu Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp
195 200 205

Pro Gln Ser Leu Val Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val
210 215 220

Val Met Thr Leu Gly Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln
225 230 235 240

Leu Thr Ala Ile Pro Thr Pro Lys
245

<210> 391
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1003)
<223> RXA02797

<400> 391
acagtctcat gaagccataa taaccacctt ctacaaagat cgacgtagaa tggaataacc 60

ccttatgaaa acgtttgcat aactccgcta aggatgttcc atg aat aat cga att 115
Met Asn Asn Arg Ile
1 5

gtc gta gtc ggc tcc atc aac gct gat ctt aat gtt ctc gtt gac cgc 163
Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn Val Leu Val Asp Arg
10 15 20

cac cca gca cct ggc gaa aca ctg ttg ggc agt ggt gga cac atc act 211
His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly His Ile Thr
25 30 35

gca gga ggc aaa ggc gcc aac cag gca gta gct gcc gct ctt caa ggt 259
Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Leu Gln Gly
40 45 50

gca gac gtc gcc ttt gtc ggc gct gtg ggc aag gat cct tac gct gcc 307
Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys Asp Pro Tyr Ala Ala
55 60 65

```
cca gcc tta gaa ttc ctt cgt tcg tca ggc gtc gac ctt acg gca gta   355
Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val Asp Leu Thr Ala Val
 70                  75                  80                  85

tcc gaa gta gat gac acc acc ggg ctt gca gtt atc acc gtt gcc aaa   403
Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val Ile Thr Val Ala Lys
                90                  95                 100

gac ggc gag aac aat atc gtt gtc atc ccc ggc gcg aat tcc ctg gtc   451
Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly Ala Asn Ser Leu Val
            105                 110                 115

aat tgt gat tat gta agc agc caa tcc gct ctt tta gct gaa gct gga   499
Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu Leu Ala Glu Ala Gly
        120                 125                 130

atc ctg ttg ctg caa ggt gag atc cct gcg gat ggc ttc aaa gag gcc   547
Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Lys Glu Ala
    135                 140                 145

att cac cac acc atg ggt cgc gtc gtg gtg aat cta gcg ccc gtc atc   595
Ile His His Thr Met Gly Arg Val Val Val Asn Leu Ala Pro Val Ile
150                 155                 160                 165

gag gta gag aag tcc gcg tta ctt gag gct gat ccg atc atc gcc aat   643
Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp Pro Ile Ile Ala Asn
                170                 175                 180

gag cac gag gcc ggc ctg att ctg gat caa ttc ggg gca ggc atc gat   691
Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe Gly Ala Gly Ile Asp
            185                 190                 195

tcc atg gat ccc cac gag ctc gcg caa gct ctc ctc gac gcc ggt ttc   739
Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu Leu Asp Ala Gly Phe
        200                 205                 210

gcc tct gtt gtt tta acg ctt gga tcc gca ggc gcg ttg gtc gcc gat   787
Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly Ala Leu Val Ala Asp
    215                 220                 225

gcc acc ggt atc acg gac atc gcc aca cca acg gtg cag gca gtt gac   835
Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr Val Gln Ala Val Asp
230                 235                 240                 245

acc acg gga gcc ggt gac gct ttt gcc gga gcc ttc tgc gca cga cta   883
Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala Phe Cys Ala Arg Leu
                250                 255                 260

att aaa ggc gat tcg ctt atc gac gcc gcc acc cac gca gca cgc gtc   931
Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr His Ala Ala Arg Val
            265                 270                 275

ggc gct tac tcg gtg caa acc gcc gga gcg caa gcg tcc tat ccg gac   979
Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln Ala Ser Tyr Pro Asp
        280                 285                 290

gcg agc gtt tca ctt ccc tct gtt taaaaaaact atttaagaag agg         1026
Ala Ser Val Ser Leu Pro Ser Val
    295                 300
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<210> 392
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 392
Met Asn Asn Arg Ile Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn
1 5 10 15

Val Leu Val Asp Arg His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser
20 25 30

Gly Gly His Ile Thr Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala
35 40 45

Ala Ala Leu Gln Gly Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys
50 55 60

Asp Pro Tyr Ala Ala Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val
65 70 75 80

Asp Leu Thr Ala Val Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val
85 90 95

Ile Thr Val Ala Lys Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly
100 105 110

Ala Asn Ser Leu Val Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu
115 120 125

Leu Ala Glu Ala Gly Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp
130 135 140

Gly Phe Lys Glu Ala Ile His His Thr Met Gly Arg Val Val Val Asn
145 150 155 160

Leu Ala Pro Val Ile Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp
165 170 175

Pro Ile Ile Ala Asn Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe
180 185 190

Gly Ala Gly Ile Asp Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu
195 200 205

Leu Asp Ala Gly Phe Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly
210 215 220

Ala Leu Val Ala Asp Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr
225 230 235 240

Val Gln Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala
245 250 255

Phe Cys Ala Arg Leu Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr
260 265 270

His Ala Ala Arg Val Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln
275 280 285

Ala Ser Tyr Pro Asp Ala Ser Val Ser Leu Pro Ser Val

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290 295 300

<210> 393
<211> 1161
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1138)
<223> RXA02730

<400> 393
ccaacatcgc cttgcacgta ataggttaaa acacaagtga atgtaatcgt ttgcagcaat 60

cgattacata aaggtagata atgagataaa gcgaggcgct atg gcg acg gaa aaa 115
Met Ala Thr Glu Lys
1 5

ttc cga ccg act ctt aaa gat gtc gct cgt caa gca ggt gtc tcc atc 163
Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln Ala Gly Val Ser Ile
10 15 20

gcc aca gca tca cga gca cta gcg gat aat ccg gcg gtt gct gca tcg 211
Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro Ala Val Ala Ala Ser
25 30 35

act cgt gaa aga atc caa caa tta gcc tct gat ctg ggt tac cgg gcc 259
Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp Leu Gly Tyr Arg Ala
40 45 50

aat gct caa gct cgt gcg ctt cgc agt tct cgc agc aac acc att ggt 307
Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg Ser Asn Thr Ile Gly
55 60 65

gtg att gtt ccc agt ttg att aac cat tac ttc gcc gca atg gtt act 355
Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe Ala Ala Met Val Thr
70 75 80 85

gaa att caa agc acc gcc agc aaa gct gga ctt gcc acg att atc acc 403
Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu Ala Thr Ile Ile Thr
90 95 100

aac agc aat gaa gat gcg acc act atg tct ggg tct ttg gag ttt ctc 451
Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly Ser Leu Glu Phe Leu
105 110 115

acc tcg cat ggt gtc gat gga atc atc tgc gta cct aat gag gaa tgc 499
Thr Ser His Gly Val Asp Gly Ile Ile Cys Val Pro Asn Glu Glu Cys
120 125 130

gcg aat caa cta gag gac ttg cag aag caa gga atg cca gtg gtg ttg 547
Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly Met Pro Val Val Leu
135 140 145

gtt gac cga gag ctt cca gga gac tcc acc atc cca acg gcg acc tct 595
Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile Pro Thr Ala Thr Ser
150 155 160 165

aac ccc caa cca gga atc gcc gca gca gta gaa ctc ctg gct cac aac 643

```
Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu Leu Leu Ala His Asn
                170                 175                 180

aac gcg ttg ccg att ggt tac ctc tca ggt ccc atg gac acc tca aca   691
Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro Met Asp Thr Ser Thr
            185                 190                 195

ggt aga gag cga tta gag gat ttc aaa gca gcc tgc gcc aac tcc aaa   739
Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala Cys Ala Asn Ser Lys
        200                 205                 210

att ggc gaa cag ctc gtt ttt ctg ggt ggg tac gaa caa agc gtt gga   787
Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr Glu Gln Ser Val Gly
    215                 220                 225

ttt gaa ggc gct acg aaa ttg ctc gat caa gga gct aaa act ctt ttt   835
Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly Ala Lys Thr Leu Phe
230                 235                 240                 245

gcc ggc gat tct atg atg acg atc ggt gtc att gaa gcc tgc cat aag   883
Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile Glu Ala Cys His Lys
                250                 255                 260

gct ggt ttg gtt atc ggc aag gat gtc agc gtg att ggt ttt gat aca   931
Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val Ile Gly Phe Asp Thr
            265                 270                 275

cat ccg ctt ttt gcc ctg caa cct cat ccg ttg aca gtg att gat caa   979
His Pro Leu Phe Ala Leu Gln Pro His Pro Leu Thr Val Ile Asp Gln
        280                 285                 290

aat gta gaa caa cta gcc caa cga gca gtg tct atc ctc acc gaa tta   1027
Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser Ile Leu Thr Glu Leu
    295                 300                 305

att gca ggc acg gta cct agc gtg acg aaa act acg atc ccc act gcc   1075
Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr Thr Ile Pro Thr Ala
310                 315                 320                 325

ctt att cat cgt gaa tca atc atc aac tcc act tta agg aag aag gat   1123
Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr Leu Arg Lys Lys Asp
                330                 335                 340

gga ctc ccc aat gag taactcaacc ggtaccgaca ttg                    1161
Gly Leu Pro Asn Glu
            345


<210> 394
<211> 346
<212> PRT
<213> Corynebacterium glutamicum

<400> 394
Met Ala Thr Glu Lys Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln
  1               5                  10                  15

Ala Gly Val Ser Ile Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro
             20                  25                  30

Ala Val Ala Ala Ser Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp
```

```
         35                  40                  45

Leu Gly Tyr Arg Ala Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg
     50                  55                  60

Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe
 65                  70                  75                  80

Ala Ala Met Val Thr Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu
                 85                  90                  95

Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly
            100                 105                 110

Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val
        115                 120                 125

Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly
    130                 135                 140

Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile
145                 150                 155                 160

Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu
                165                 170                 175

Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro
            180                 185                 190

Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala
        195                 200                 205

Cys Ala Asn Ser Lys Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr
    210                 215                 220

Glu Gln Ser Val Gly Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly
225                 230                 235                 240

Ala Lys Thr Leu Phe Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile
                245                 250                 255

Glu Ala Cys His Lys Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val
            260                 265                 270

Ile Gly Phe Asp Thr His Pro Leu Phe Ala Leu Gln Pro His Pro Leu
        275                 280                 285

Thr Val Ile Asp Gln Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser
    290                 295                 300

Ile Leu Thr Glu Leu Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr
305                 310                 315                 320

Thr Ile Pro Thr Ala Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr
                325                 330                 335

Leu Arg Lys Lys Asp Gly Leu Pro Asn Glu
            340                 345
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<210> 395

09605420.1

<211> 483
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(460)
<223> RXA02551

<400> 395
gctgcacaaa ttccgcgaaa gggtatcacc atcgacatca cagatgaaga ccgtgagatc 60

ttaaaaaaac accgtcgatt tcatttcctt ctcctattac atg tcc gta tgt gaa 115
Met Ser Val Cys Glu
1 5

gcc cac aac ccc gaa aac tac tca acc ggt ggc ggt aac atc atc ggc 163
Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly Gly Asn Ile Ile Gly
10 15 20

gga gtg gtc agc ccc act ctc gcg gct tcc gaa tgg ggt tgg caa gtt 211
Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu Trp Gly Trp Gln Val
25 30 35

gat ccc ctc ggt ttg cgc atc gtc ctg aac aac tac tgg gag cgc tgg 259
Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn Tyr Trp Glu Arg Trp
40 45 50

cag aag cca ctg ttc atc gtc gaa aac gga cta gga gca aag gac gtg 307
Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val
55 60 65

ctt atc gac gga ccc tcc ggc cca aca gta aac gat gac tac cgc atc 355
Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn Asp Asp Tyr Arg Ile
70 75 80 85

aaa tac ctc gac gac ggc ggc tca gga atc ttg aag cgc tac aag aag 403
Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu Lys Arg Tyr Lys Lys
90 95 100

aag tcc ttt gat tgg tgc cgc gac atc atc gcc acc aat ggc gaa agc 451
Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala Thr Asn Gly Glu Ser
105 110 115

ctg gaa tcc taagaaataa aggtaggtgt cac 483
Leu Glu Ser
120

<210> 396
<211> 120
<212> PRT
<213> Corynebacterium glutamicum

<400> 396
Met Ser Val Cys Glu Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly
1 5 10 15

Gly Asn Ile Ile Gly Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu
20 25 30

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```
Trp Gly Trp Gln Val Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn
          35                  40                  45

Tyr Trp Glu Arg Trp Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu
      50                  55                  60

Gly Ala Lys Asp Val Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn
 65                  70                  75                  80

Asp Asp Tyr Arg Ile Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu
                 85                  90                  95

Lys Arg Tyr Lys Lys Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala
            100                 105                 110

Thr Asn Gly Glu Ser Leu Glu Ser
        115                 120


<210> 397
<211> 795
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(772)
<223> RXA01325

<400> 397
gcgcagcgct cggacgatta cgaacttcag gagaactcgg ggtcattcgt tgcattctac 60

cctggaaatt ttcccacact aagtcaggtc taagtagggt atg gat atg acg att   115
                                            Met Asp Met Thr Ile
                                              1               5

tcc cgc tcc acc atg gcc caa atc ctt gac tac acc ctc ctc gga cca   163
Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr Thr Leu Leu Gly Pro
                 10                  15                  20

gaa gta acc aac tcc gaa ctg gcc gca ttt ata gat tcc gca att gag   211
Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile Asp Ser Ala Ile Glu
            25                  30                  35

ctg gga gtc ggc acg atc tgt gtc ccc aac agc atg gtc aac cta act   259
Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser Met Val Asn Leu Thr
        40                  45                  50

gca aaa gcc caa gaa gct gga att cga gtg gcc acc gtc gca gga ttc   307
Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala Thr Val Ala Gly Phe
    55                  60                  65

ccg cac ggc aaa acc ccc gcg ttg gtg aaa gcc gcc gaa gcg cgc ctt   355
Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala Ala Glu Ala Arg Leu
70                  75                  80                  85

gcc gta cag tcc gga gct tcc gaa gta gat gtt gtt ttg gat att gcg   403
Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val Val Leu Asp Ile Ala
                90                  95                 100

gta gtg aaa gag gga gat gcc aat agg ttg ctg cag gaa att gtg gca   451
```

```
Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu Gln Glu Ile Val Ala
            105                 110                 115

atc agg gag gct gtt cca tct cct gtg gtg ctg aaa ttc atc ctc gaa   499
Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu Lys Phe Ile Leu Glu
        120                 125                 130

aca gct gtt gtg agt gat gaa gca att gtg act gca gtg aat gcg ttg   547
Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr Ala Val Asn Ala Leu
    135                 140                 145

att gct gct ggt gct gac ttc gct aaa act tcc acg gga ttc cac cca   595
Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser Thr Gly Phe His Pro
150                 155                 160                 165

gcg gga ggg gca act gtt gag gct gtt cgg gtg atg gct tcg gct tct   643
Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val Met Ala Ser Ala Ser
                170                 175                 180

cgg gga agg gtt gga att aag gct gcc ggt ggg gtg aaa act tgg gaa   691
Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly Val Lys Thr Trp Glu
            185                 190                 195

gat gcg gtg gcg ttt gtt gaa gca ggg gct act cgc att gga act tct   739
Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr Arg Ile Gly Thr Ser
        200                 205                 210

aat gcg gga gcc att ttg gag ggt gcg ccg gag tagtttggcg ttctaatcgg 792
Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu
    215                 220

gac                                                               795


<210> 398
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 398
Met Asp Met Thr Ile Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr
  1               5                  10                  15

Thr Leu Leu Gly Pro Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile
             20                  25                  30

Asp Ser Ala Ile Glu Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser
         35                  40                  45

Met Val Asn Leu Thr Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala
     50                  55                  60

Thr Val Ala Gly Phe Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala
 65                  70                  75                  80

Ala Glu Ala Arg Leu Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val
                 85                  90                  95

Val Leu Asp Ile Ala Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu
            100                 105                 110
```

```
Gln Glu Ile Val Ala Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu
        115                 120                 125

Lys Phe Ile Leu Glu Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr
    130                 135                 140

Ala Val Asn Ala Leu Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser
145                 150                 155                 160

Thr Gly Phe His Pro Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val
                165                 170                 175

Met Ala Ser Ala Ser Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly
            180                 185                 190

Val Lys Thr Trp Glu Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr
        195                 200                 205

Arg Ile Gly Thr Ser Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu
    210                 215                 220
```

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<210> 399
<211> 684
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(661)
<223> RXA00195

<400> 399
tcgcagtcat catgcaggca taacctgaaa cccatccgtt tggattgccc caaatgggtg 60

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tagtgggtgc gtttacccaa caagtgcaag aatgggagtc gtg act aaa aag atc   115
                                              Val Thr Lys Lys Ile
                                                1               5

ctt att ttg gga agc act ggt tcg att gga act cag gcg ctg gac gtt   163
Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr Gln Ala Leu Asp Val
                10                  15                  20

att gct gat aat tca gac aag ttt gag gtg gtg ggt atc gct gcg ggc   211
Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val Gly Ile Ala Ala Gly
            25                  30                  35

ggt tct cag cca gac ctc gtt att tcg cag gcg cag cag ttg ggg ctg   259
Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala Gln Gln Leu Gly Leu
        40                  45                  50

gct gca gac aag gtt gcg gtt gct gat gca cag gct gcc gca gta att   307
Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln Ala Ala Ala Val Ile
    55                  60                  65

tcg aag gct ctc ggc ggc gag atc atc tct gga acc gat gct gcg aag   355
Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly Thr Asp Ala Ala Lys
70                  75                  80                  85
```

```
att ctg gtg gaa acc aca aag gcc gac act gtg ctt aat gct ctg gtt   403
Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val Leu Asn Ala Leu Val
                 90                  95                 100

ggt tct ttg ggg ctt gcg gca acg ctg gcc act ctg gaa tct ggt gcg   451
Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr Leu Glu Ser Gly Ala
            105                 110                 115

cat ctt gcc ttg gct aac aaa gaa tcg ctg gtt gcc ggt ggt gag ttt   499
His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val Ala Gly Gly Glu Phe
        120                 125                 130

gtt acc tca aag gca aag ctg ggg cag atc att ccg gtc gat tcg gag   547
Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile Pro Val Asp Ser Glu
    135                 140                 145

cac tct gcc atg gcg cag tgt ttg cgt tcg ggt act cgt gat gag gtt   595
His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly Thr Arg Asp Glu Val
150                 155                 160                 165

gcg cgg att gtg ctg aca gct tcg ggc gga cct ttc agg gct gga cca   643
Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro Phe Arg Ala Gly Pro
                170                 175                 180

ggg aga aga tgt ggg agg tgactcccga gcaggcagca gcg                 684
Gly Arg Arg Cys Gly Arg
            185
```

<210> 400
<211> 187
<212> PRT
<213> Corynebacterium glutamicum

<400> 400

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Val Thr Lys Lys Ile Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr
  1               5                  10                  15

Gln Ala Leu Asp Val Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val
             20                  25                  30

Gly Ile Ala Ala Gly Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala
         35                  40                  45

Gln Gln Leu Gly Leu Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln
     50                  55                  60

Ala Ala Ala Val Ile Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly
 65                  70                  75                  80

Thr Asp Ala Ala Lys Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val
                 85                  90                  95

Leu Asn Ala Leu Val Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr
            100                 105                 110

Leu Glu Ser Gly Ala His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val
        115                 120                 125

Ala Gly Gly Glu Phe Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile
```

```
    130                 135                 140

Pro Val Asp Ser Glu His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly
145                 150                 155                 160

Thr Arg Asp Glu Val Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro
                165                 170                 175

Phe Arg Ala Gly Pro Gly Arg Arg Cys Gly Arg
            180                 185
```

<210> 401
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXA00196

<400> 401

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ctgccatggc gcagtgtttg cgttcgggta ctcgtgatga ggttgcgcgg attgtgctga 60

cagcttcggg cggacctttc agggctggac cagggagaag atg tgg gag gtg act   115
                                               Met Trp Glu Val Thr
                                                 1               5

ccc gag cag gca gca gcg cac cca acg tgg gcg atg ggg cag atg aac   163
Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala Met Gly Gln Met Asn
                  10                  15                  20

acg ttg aac tcc gcc acc ctt att aat aaa ggc ctc gaa ctc atc gag   211
Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly Leu Glu Leu Ile Glu
              25                  30                  35

gcg acc ctg ctg ttt gaa acg gat gcg gat ctc att gat gtg acg gtg   259
Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu Ile Asp Val Thr Val
          40                  45                  50

cat ccg cag tcg atc atc cac tcc atg atc acg ttt acg gat ggt gcg   307
His Pro Gln Ser Ile Ile His Ser Met Ile Thr Phe Thr Asp Gly Ala
      55                  60                  65

acc atc gcg cag gcg tcg cca cca tcg atg aaa ctg ccg atc gcg ttg   355
Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys Leu Pro Ile Ala Leu
  70                  75                  80                  85

gcg ctt gat tgg cca cat cgg gtg ccg aag gct cag ccg gcg ctg gat   403
Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala Gln Pro Ala Leu Asp
                  90                  95                 100

ttc acc gct gct cat acc tgg gct ttt gag ccg gtg gat gat gcc gca   451
Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro Val Asp Asp Ala Ala
             105                 110                 115

ttc cct gcg gtg cag ctg gct agg cac gtc gca aag caa aaa ggc acg   499
Phe Pro Ala Val Gln Leu Ala Arg His Val Ala Lys Gln Lys Gly Thr
         120                 125                 130
```

```
tac ccc gcg gtg tat aac gcc gcc aac gag gag gcg gct gag gcg ttt   547
Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu Ala Ala Glu Ala Phe
    135                 140                 145

ttg cgc ggg cga atc aag ttt ccg cag atc gtg gac gtg gtg gac gag   595
Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val Asp Val Val Asp Glu
150                 155                 160                 165

gtc ctc caa gga gct tct cag ttt gct ggt gta gca tca cac gtc gat   643
Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val Ala Ser His Val Asp
                170                 175                 180

gat att ttg gca acc gaa tct gag gca cgc gcg cgt gcg aat gct ttg   691
Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala Arg Ala Asn Ala Leu
            185                 190                 195

atc aac cgg ttg gca acc aac ttg taagctaagg agcttccgcc tcg         738
Ile Asn Arg Leu Ala Thr Asn Leu
        200                 205
```

09529206.090205

<210> 402
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 402

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Met Trp Glu Val Thr Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala
  1               5                  10                  15

Met Gly Gln Met Asn Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly
             20                  25                  30

Leu Glu Leu Ile Glu Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu
         35                  40                  45

Ile Asp Val Thr Val His Pro Gln Ser Ile Ile His Ser Met Ile Thr
     50                  55                  60

Phe Thr Asp Gly Ala Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys
 65                  70                  75                  80

Leu Pro Ile Ala Leu Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala
                 85                  90                  95

Gln Pro Ala Leu Asp Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro
            100                 105                 110

Val Asp Asp Ala Ala Phe Pro Ala Val Gln Leu Ala Arg His Val Ala
        115                 120                 125

Lys Gln Lys Gly Thr Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu
    130                 135                 140

Ala Ala Glu Ala Phe Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val
145                 150                 155                 160

Asp Val Val Asp Glu Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val
                165                 170                 175

Ala Ser His Val Asp Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala
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            180                 185                 190

Arg Ala Asn Ala Leu Ile Asn Arg Leu Ala Thr Asn Leu
        195                 200                 205


<210> 403
<211> 2031
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2008)
<223> RXN01562

<400> 403
gcaggtgcac atttgttttg tcacctgcac aaaagtgtcg ccagcccgat acttgtacaa 60

ccgtccgcat ccgagaagca aaggtgtctg actcgcgcca atg gga att ctg aac   115
                                              Met Gly Ile Leu Asn
                                                1               5

agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg   163
Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu
                10                  15                  20

gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca   211
Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala
            25                  30                  35

gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc   259
Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr
        40                  45                  50

atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt   307
Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe
    55                  60                  65

gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct   355
Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala
70                  75                  80                  85

aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc   403
Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr
                90                  95                  100

tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg   451
Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser
            105                 110                 115

gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat   499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp
        120                 125                 130

ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta   547
Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu
    135                 140                 145

act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa   595
Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys
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150                 155                 160                 165

gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct   643
Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser
                170                 175                 180

cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag   691
Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln
            185                 190                 195

cct ttc tat gat cgc ttc atg gaa aag ggc aag acg tcc ctg aaa tcc   739
Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys Thr Ser Leu Lys Ser
        200                 205                 210

atg ggg tgg gta ggg gag cgt act ttt gaa gcg ctc cat gca ttt aaa   787
Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala Leu His Ala Phe Lys
    215                 220                 225

gaa ggt gtg aag agc acc gtc att ccc acc gaa atg ttc cct gaa ctg   835
Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu Met Phe Pro Glu Leu
230                 235                 240                 245

ggc atg aaa tac gtg ggt ccg gtt gat gga cat aac caa aaa gct gtc   883
Gly Met Lys Tyr Val Gly Pro Val Asp Gly His Asn Gln Lys Ala Val
                250                 255                 260

gac aat gcg ctg aaa tac gct cat gat tat gat ggc ccc atc atc gtg   931
Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp Gly Pro Ile Ile Val
            265                 270                 275

cac atg gtc acc gaa aag ggt cgt ggt tac gcg cct gct gag cag gat   979
His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala Pro Ala Glu Gln Asp
        280                 285                 290

ttg gac gaa ttg atg cac tcc acg ggc gtc atc gat ccg ctc aca gga   1027
Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro Leu Thr Gly
    295                 300                 305

gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg ttc agc gat   1075
Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val Phe Ser Asp
310                 315                 320                 325

gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt gcc atc acc   1123
Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val Ala Ile Thr
                330                 335                 340

gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa gcc aat ttc   1171
Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu Ala Asn Phe
            345                 350                 355

ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac gcg gta act   1219
Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His Ala Val Thr
        360                 365                 370

tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg gtg gct att   1267
Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val Val Ala Ile
    375                 380                 385

tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc atg gat gtg   1315
Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu Met Asp Val
390                 395                 400                 405
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09852-0020US1

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ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc tca ggt gtc   1363
Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg Ser Gly Val
                410                 415                 420

acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat atg gcg ctg   1411
Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp Met Ala Leu
            425                 430                 435

acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt gat gag gat   1459
Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg Asp Glu Asp
        440                 445                 450

tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat gat ggc ccc   1507
Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp Asp Gly Pro
    455                 460                 465

aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca att gtt gct   1555
Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro Ile Val Ala
470                 475                 480                 485

atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat gaa gac gcc   1603
Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr Glu Asp Ala
                490                 495                 500

act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc atc att gcg   1651
Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu Ile Ile Ala
            505                 510                 515

gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc agg att aaa   1699
Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser Arg Ile Lys
        520                 525                 530

cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg att gtc ccc   1747
Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp Ile Val Pro
    535                 540                 545

atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac ctc gtg atc   1795
Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp Leu Val Ile
550                 555                 560                 565

acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc ttg ctc tct   1843
Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser Leu Leu Ser
                570                 575                 580

gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga caa atc gcc   1891
Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg Gln Ile Ala
            585                 590                 595

gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa gtg ctc gcc   1939
Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu Val Leu Ala
        600                 605                 610

gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt gtt gga tgg   1987
Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val Val Gly Trp
    615                 620                 625

ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg ccg            2031
Leu Asp Ser Leu Phe Gly Glu
630                 635
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<210> 404
<211> 636
<212> PRT
<213> Corynebacterium glutamicum

<400> 404

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Met Gly Ile Leu Asn Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu
  1               5                  10                  15

Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu
             20                  25                  30

Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
         35                  40                  45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
     50                  55                  60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile
 65                  70                  75                  80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
                 85                  90                  95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
            100                 105                 110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys
        115                 120                 125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val
    130                 135                 140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn
145                 150                 155                 160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Val Asn Asp Asn
                165                 170                 175

Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala
            180                 185                 190

Gly Leu Arg Met Gln Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys
        195                 200                 205

Thr Ser Leu Lys Ser Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala
    210                 215                 220

Leu His Ala Phe Lys Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu
225                 230                 235                 240

Met Phe Pro Glu Leu Gly Met Lys Tyr Val Gly Pro Val Asp Gly His
                245                 250                 255

Asn Gln Lys Ala Val Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp
            260                 265                 270

Gly Pro Ile Ile Val His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala
        275                 280                 285
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Pro Ala Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile
    290                 295                 300

Asp Pro Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr
305                 310                 315                 320

Ser Val Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn
                325                 330                 335

Val Val Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys
            340                 345                 350

Phe Glu Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu
        355                 360                 365

Gln His Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His
    370                 375                 380

Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln
385                 390                 395                 400

Leu Leu Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu
                405                 410                 415

Asp Arg Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val
            420                 425                 430

Trp Asp Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala
        435                 440                 445

Pro Arg Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser
    450                 455                 460

Ile Asp Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro
465                 470                 475                 480

Thr Pro Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu
                485                 490                 495

Ala Tyr Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser
            500                 505                 510

Val Leu Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val
        515                 520                 525

Ala Ser Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro
    530                 535                 540

Arg Trp Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp
545                 550                 555                 560

His Asp Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val
                565                 570                 575

Gly Ser Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro
            580                 585                 590

Arg Arg Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg
        595                 600                 605

Asn Glu Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr
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    610                 615                 620

Thr Val Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
625                 630                 635


<210> 405
<211> 1061
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1038)
<223> FRXA01562

<400> 405
gag cag gat ttg gac gaa ttg atg cac tcc acg ggc gtc atc gat ccg   48
Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro
  1               5                  10                  15

ctc aca gga gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg   96
Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val
            20                  25                  30

ttc agc gat gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt   144
Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val
        35                  40                  45

gcc atc acc gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa   192
Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu
    50                  55                  60

gcc aat ttc ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac   240
Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His
65                  70                  75                  80

gcg gta act tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg   288
Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val
                85                  90                  95

gtg gct att tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc   336
Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu
            100                 105                 110

atg gat gtg ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc   384
Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg
        115                 120                 125

tca ggt gtc acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat   432
Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp
    130                 135                 140

atg gcg ctg acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt   480
Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg
145                 150                 155                 160

gat gag gat tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat   528
Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp
                165                 170                 175
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gat ggc ccc aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca   576
Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro
            180                 185                 190

att gtt gct atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat   624
Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr
        195                 200                 205

gaa gac gcc act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc   672
Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu
    210                 215                 220

atc att gcg gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc   720
Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser
225                 230                 235                 240

agg att aaa cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg   768
Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp
                245                 250                 255

att gtc ccc atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac   816
Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp
            260                 265                 270

ctc gtg atc acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc   864
Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser
        275                 280                 285

ttg ctc tct gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga   912
Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg
    290                 295                 300

caa atc gcc gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa   960
Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu
305                 310                 315                 320

gtg ctc gcc gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt  1008
Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val
                325                 330                 335

gtt gga tgg ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg    1058
Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
            340                 345

ccg                                                              1061
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<210> 406
<211> 346
<212> PRT
<213> Corynebacterium glutamicum

<400> 406

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Glu Gln Asp Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro
  1               5                  10                  15

Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val
             20                  25                  30

Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val
         35                  40                  45
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Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu
     50                  55                  60

Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His
 65                  70                  75                  80

Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val
                 85                  90                  95

Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu
            100                 105                 110

Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg
        115                 120                 125

Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp
    130                 135                 140

Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg
145                 150                 155                 160

Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp
                165                 170                 175

Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro
            180                 185                 190

Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr
        195                 200                 205

Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu
    210                 215                 220

Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser
225                 230                 235                 240

Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp
                245                 250                 255

Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp
            260                 265                 270

Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser
        275                 280                 285

Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg
    290                 295                 300

Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu
305                 310                 315                 320

Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val
                325                 330                 335

Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
            340                 345
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<210> 407
<211> 703

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> FRXA01705

<400> 407
gcaggtgcac atttgttttg tcacctgcac aaaagtgtcg ccagcccgat acttgtacaa 60

ccgtccgcat ccgagaagca aaggtgtctg actcgcgcca atg gga att ctg aac 115
Met Gly Ile Leu Asn
1 5

agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg 163
Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu
10 15 20

gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca 211
Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala
25 30 35

gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc 259
Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr
40 45 50

atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt 307
Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe
55 60 65

gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct 355
Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala
70 75 80 85

aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc 403
Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr
90 95 100

tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg 451
Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser
105 110 115

gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat 499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp
120 125 130

ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta 547
Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu
135 140 145

act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa 595
Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys
150 155 160 165

gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct 643
Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser
170 175 180

cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag 691
Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln

185 190 195

cct ttc tat gat 703
Pro Phe Tyr Asp
200

<210> 408
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 408
Met Gly Ile Leu Asn Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu
1 5 10 15

Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu
20 25 30

Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
35 40 45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
50 55 60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile
65 70 75 80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
85 90 95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
100 105 110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys
115 120 125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val
130 135 140

Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn
145 150 155 160

Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Val Asn Asp Asn
165 170 175

Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala
180 185 190

Gly Leu Arg Met Gln Pro Phe Tyr Asp
195 200

<210> 409
<211> 2241
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2218)

<223> RXN00879

<400> 409

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atgctgtgcc cacacgctat tagtggcata atgttgtgtt gtg act gct cgc aga   115
                                          Val Thr Ala Arg Arg
                                            1               5

ttt ttg aat gaa ctc gcc gat ctc tac ggc gta gca act tcc tac act   163
Phe Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr
                10                  15                  20

gat tac aaa ggt gcc cat att gag gtc agc gat gac aca tta gtg aaa   211
Asp Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys
            25                  30                  35

atc ctg cgt gct ctg ggt gtg aat tta gat aca agc aac ctc ccc aac   259
Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn
        40                  45                  50

gat gac gct atc caa cgc caa att gcc ctc ttc cat gat cga gag ttc   307
Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe
    55                  60                  65

act cgc cca ctg cct cca tcg gtg gtt gca gtt gaa ggt gat gaa cta   355
Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu
70                  75                  80                  85

gtt ttc ccg gtg cat gtg cac gac ggt tcc cct gca gat gtc cac atc   403
Val Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile
                90                  95                  100

gaa ttg gaa gac ggc acg cag cgg gat gtt tct cag gtg gaa aac tgg   451
Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp
            105                 110                 115

aca gcg cca cgg gaa att gat ggg att agg tgg ggc gag gca tcg ttt   499
Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe
        120                 125                 130

aag att cct ggt gat ctc ccc ttg ggt tgg cac aag ctt cac ctt aaa   547
Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys
    135                 140                 145

tcc aat gaa cgc tca gct gag tgc ggt ttg atc atc acc ccg gct cgt   595
Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg
150                 155                 160                 165

ctg tct act gct gat aag tat ctt gat tcc cct cgc agt ggt gtc atg   643
Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met
                170                 175                 180

gcg cag atc tac tct gtg cgt tcc acg ttg tcg tgg ggc atg ggt gat   691
Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp
            185                 190                 195

ttc aat gat tta gga aac ttg gca agt gtg gtt gcc cag gat gga gca   739
Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala
        200                 205                 210
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gac ttc ctg ctc atc aac ccc atg cac gct gca gag ccg ctg cct cct   787
Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro
    215                 220                 225

act gag gac tct cct tat ctg ccc aca acc agg cgc ttt atc aac ccg   835
Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro
230                 235                 240                 245

atc tac att cgg gta gaa gat att ccg gag ttt aat cag ctt gag att   883
Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile
                250                 255                 260

gat cta cgc gat gat atc gca gag atg gct gcg gaa ttc cgc gaa cgc   931
Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg
            265                 270                 275

aat ctg acc tca gac atc att gag cgc aat gac gtc tac gct gca aag   979
Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys
        280                 285                 290

ctt caa gtg ctg cgc gcc att ttt gaa atg cct cgt tcc agc gaa cgt   1027
Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg
    295                 300                 305

gaa gcc aac ttt gtc tcc ttc gtg caa cgg gaa ggc caa ggt ctt att   1075
Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile
310                 315                 320                 325

gat ttc gcc acc tgg tgc gcg gac cgc gaa act gca cag tct gaa tct   1123
Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser
                330                 335                 340

gtc cac gga act gag cca gac cgc gat gag ctg acc atg ttc tac atg   1171
Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met
            345                 350                 355

tgg ttg cag tgg cta tgt gat gag cag ctg gcg gca gct caa aag cgc   1219
Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg
        360                 365                 370

gct gtc gat gcc gga atg tcg atc ggc atc atg gca gac ctg gca gtt   1267
Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val
    375                 380                 385

ggt gtg cat cca ggt ggt gct gat gcc cag aac ctc agc cac gta ctt   1315
Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu
390                 395                 400                 405

gct ccg gat gcg tca gtg ggc gcc cca cca gat gga tac aac cag cag   1363
Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln
                410                 415                 420

ggc caa gac tgg tcc cag cca cca tgg cat cca gtg cgt ctt gca gag   1411
Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu
            425                 430                 435

gaa ggc tac att ccg tgg cgt aat ctg ctg cgc act gtg ctg cgt cac   1459
Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His
        440                 445                 450

tcc ggc gga atc cgc gtg gac cac gtt ctt ggt ttg ttc agg ctc ttt   1507
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Ser Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe
    455                 460                 465

gtc atg cca cgc atg caa tcc cct gct acg ggc acc tat atc cgc ttc   1555
Val Met Pro Arg Met Gln Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe
470                 475                 480                 485

gac cat aat gcg ttg gta ggc att cta gcc cta gaa gca gaa ctc gca   1603
Asp His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala
                490                 495                 500

ggc gcc gtt gtc att ggt gaa gat ctg gga acg ttt gag cct tgg gta   1651
Gly Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val
            505                 510                 515

caa gat gca ttg gct cag cgt ggc atc atg ggc acc tcg atc cta tgg   1699
Gln Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp
        520                 525                 530

ttc gag cat tcc cca agc cag ccg ggt cct cgc cgc cag gaa gag tat   1747
Phe Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr
    535                 540                 545

cgt ccg ctg gcc ttg acc act gtg acc act cat gat ctc cct ccg act   1795
Arg Pro Leu Ala Leu Thr Thr Val Thr Thr His Asp Leu Pro Pro Thr
550                 555                 560                 565

gct ggt tat ttg gag ggc gag cac att gct ctt cgt gag cga ttg ggg   1843
Ala Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly
                570                 575                 580

gtg ctc aac act gat cct gct gca gaa ctc gct gag gat ctg cag tgg   1891
Val Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp
            585                 590                 595

caa gcg gag atc ctt gat gtc gca gca tct gcc aac gca ttg cca gcc   1939
Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala
        600                 605                 610

cgg gaa tac gtg gga ctc gaa cgc gat cag cgc ggt gag ttg gct gag   1987
Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu
    615                 620                 625

ctg ttg gaa ggc ctg cac act ttc gtt gcg aaa acc cct tca gca ctg   2035
Leu Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu
630                 635                 640                 645

acc tgt gtc tgc ttg gta gac atg gtc ggt gaa aag cgg gca cag aat   2083
Thr Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn
                650                 655                 660

cag ccg ggc aca acg agg gat atg tat ccc aac tgg tgt atc cca ctg   2131
Gln Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu
            665                 670                 675

tgt gac agc gaa ggc aac tcc gtg ctc att gaa tcg ctg cgt gaa aat   2179
Cys Asp Ser Glu Gly Asn Ser Val Leu Ile Glu Ser Leu Arg Glu Asn
        680                 685                 690

gag ctg tat cac cgt gtg gca aag gca agc aag cga gat taggtccgct    2228
Glu Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp
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695 700 705

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Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His Ile Glu Val Ser Asp
             20                  25                  30

Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr
         35                  40                  45

Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe
     50                  55                  60

His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val
 65                  70                  75                  80

Glu Gly Asp Glu Leu Val Phe Pro Val His Val His Asp Gly Ser Pro
                 85                  90                  95

Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser
            100                 105                 110

Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp
        115                 120                 125

Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His
    130                 135                 140

Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile
145                 150                 155                 160

Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro
                165                 170                 175

Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser
            180                 185                 190

Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val
        195                 200                 205

Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala
    210                 215                 220

Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg
225                 230                 235                 240

Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe
                245                 250                 255

Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala
            260                 265                 270
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09252010

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Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp
        275                 280                 285

Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro
    290                 295                 300

Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu
305                 310                 315                 320

Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr
                325                 330                 335

Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu
            340                 345                 350

Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala
        355                 360                 365

Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met
    370                 375                 380

Ala Asp Leu Ala Val Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn
385                 390                 395                 400

Leu Ser His Val Leu Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp
                405                 410                 415

Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro
            420                 425                 430

Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg
        435                 440                 445

Thr Val Leu Arg His Ser Gly Gly Ile Arg Val Asp His Val Leu Gly
    450                 455                 460

Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln Ser Pro Ala Thr Gly
465                 470                 475                 480

Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val Gly Ile Leu Ala Leu
                485                 490                 495

Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly Glu Asp Leu Gly Thr
            500                 505                 510

Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln Arg Gly Ile Met Gly
        515                 520                 525

Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser Gln Pro Gly Pro Arg
    530                 535                 540

Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr Thr Val Thr Thr His
545                 550                 555                 560

Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly Glu His Ile Ala Leu
                565                 570                 575

Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala
            580                 585                 590
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US 2005/0260186 A1

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Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala
        595                 600                 605

Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg
    610                 615                 620

Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His Thr Phe Val Ala Lys
625                 630                 635                 640

Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val Asp Met Val Gly Glu
                645                 650                 655

Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn
            660                 665                 670

Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn Ser Val Leu Ile Glu
        675                 680                 685

Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val Ala Lys Ala Ser Lys
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Arg Asp
705
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US20050153417A1

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<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(2200)
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attagtggca taatgttgtg ttgtgactgc tcgcagattt ttg aat gaa ctc gcc   115
                                          Leu Asn Glu Leu Ala
                                            1               5

gat ctc tac ggc gta gca act tcc tac act gat tac aaa ggt gcc cat   163
Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr Asp Tyr Lys Gly Ala His
                10                  15                  20

att gag gtc agc gat gac aca tta gtg aaa atc ctg cgt gct ctg ggt   211
Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly
            25                  30                  35

gtg aat tta gat aca agc aac ctc ccc aac gat gac gct atc caa cgc   259
Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg
        40                  45                  50

caa att gcc ctc ttc cat gat cga gag ttc act cgc cca ctg cct cca   307
Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro
    55                  60                  65

tcg gtg gtt gca gtt gaa ggt gat gaa cta gtt ttc ccg gtg cat gtg   355
Ser Val Val Ala Val Glu Gly Asp Glu Leu Val Phe Pro Val His Val
70                  75                  80                  85
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cac gac ggt tcc cct gca gat gtc cac atc gaa ttg gaa gac ggc acg   403
His Asp Gly Ser Pro Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr
                 90                  95                 100

cag cgg gat gtt tct cag gtg gaa aac tgg aca gcg cca cgg gaa att   451
Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile
            105                 110                 115

gat ggg att agg tgg ggc gag gca tcg ttt aag att cct ggt gat ctc   499
Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu
        120                 125                 130

ccc ttg ggt tgg cac aag ctt cac ctt aaa tcc aat gaa cgc tca gct   547
Pro Leu Gly Trp His Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala
    135                 140                 145

gag tgc ggt ttg atc atc acc ccg gct cgt ctg tct act gct gat aag   595
Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys
150                 155                 160                 165

tat ctt gat tcc cct cgc agt ggt gtc atg gcg cag atc tac tct gtg   643
Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val
                170                 175                 180

cgt tcc acg ttg tcg tgg ggc atg ggt gat ttc aat gat tta gga aac   691
Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn
            185                 190                 195

ttg gca agt gtg gtt gcc cag gat gga gca gac ttc ctg ctc atc aac   739
Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn
        200                 205                 210

ccc atg cac gct gca gag ccg ctg cct cct act gag gac tct cct tat   787
Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr
    215                 220                 225

ctg ccc aca acc agg cgc ttt atc aac ccg atc tac att cgg gta gaa   835
Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu
230                 235                 240                 245

gat att ccg gag ttt aat cag ctt gag att gat cta cgc gat gat atc   883
Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile
                250                 255                 260

gca gag atg gct gcg gaa ttc cgc gaa cgc aat ctg acc tca gac atc   931
Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile
            265                 270                 275

att gag cgc aat gac gtc tac gct gca aag ctt caa gtg ctg cgc gcc   979
Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala
        280                 285                 290

att ttt gaa atg cct cgt tcc agc gaa cgt gaa gcc aac ttt gtc tcc   1027
Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser
    295                 300                 305

ttc gtg caa cgg gaa ggc caa ggt ctt att gat ttc gcc acc tgg tgc   1075
Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys
310                 315                 320                 325
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gcg gac cgc gaa act gca cag tct gaa tct gtc cac gga act gag cca   1123
Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro
                330                 335                 340

gac cgc gat gag ctg acc atg ttc tac atg tgg ttg cag tgg cta tgt   1171
Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys
            345                 350                 355

gat gag cag ctg gcg gca gct caa aag cgc gct gtc gat gcc gga atg   1219
Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met
        360                 365                 370

tcg atc ggc atc atg gca gac ctg gca gtt ggt gtg cat cca ggt ggt   1267
Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly Val His Pro Gly Gly
    375                 380                 385

gct gat gcc cag aac ctc agc cac gta ctt gct ccg gat gcg tca gtg   1315
Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala Pro Asp Ala Ser Val
390                 395                 400                 405

ggc gcc cca cca gat gga tac aac cag cag ggc caa gac tgg tcc cag   1363
Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln
                410                 415                 420

cca cca tgg cat cca gtg cgt ctt gca gag gaa ggc tac att ccg tgg   1411
Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp
            425                 430                 435

cgt aat ctg ctg cgc act gtg ctg cgt cac tcc ggc gga atc cgc gtg   1459
Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser Gly Gly Ile Arg Val
        440                 445                 450

gac cac gtt ctt ggt ttg ttc agg ctc ttt gtc atg cca cgc atg caa   1507
Asp His Val Leu Gly Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln
    455                 460                 465

tcc cct gct acg ggc acc tat atc cgc ttc gac cat aat gcg ttg gta   1555
Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val
470                 475                 480                 485

ggc att cta gcc cta gaa gca gaa ctc gca ggc gcc gtt gtc att ggt   1603
Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly
                490                 495                 500

gaa gat ctg gga acg ttt gag cct tgg gta caa gat gca ttg gct cag   1651
Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln
            505                 510                 515

cgt ggc atc atg ggc acc tcg atc cta tgg ttc gag cat tcc cca agc   1699
Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser
        520                 525                 530

cag ccg ggt cct cgc cgc cag gaa gag tat cgt ccg ctg gcc ttg acc   1747
Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr
    535                 540                 545

act gtg acc act cat gat ctc cct ccg act gct ggt tat ttg gag ggc   1795
Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly
550                 555                 560                 565

gag cac att gct ctt cgt gag cga ttg ggg gtg ctc aac act gat cct   1843
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09850120.090502

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Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro
                570                 575                 580

gct gca gaa ctc gct gag gat ctg cag tgg caa gcg gag atc ctt gat   1891
Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp
            585                 590                 595

gtc gca gca tct gcc aac gca ttg cca gcc cgg gaa tac gtg gga ctc   1939
Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu
        600                 605                 610

gaa cgc gat cag cgc ggt gag ttg gct gag ctg ttg gaa ggc ctg cac   1987
Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His
    615                 620                 625

act ttc gtt gcg aaa acc cct tca gca ctg acc tgt gtc tgc ttg gta   2035
Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val
630                 635                 640                 645

gac atg gtc ggt gaa aag cgg gca cag aat cag ccg ggc aca acg agg   2083
Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg
                650                 655                 660

gat atg tat ccc aac tgg tgt atc cca ctg tgt gac agc gaa ggc aac   2131
Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn
            665                 670                 675

tcc gtg ctc att gaa tcg ctg cgt gaa aat gag ctg tat cac cgt gtg   2179
Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val
        680                 685                 690

gca aag gca agc aag cga gat taggtccgct tcagttgtgg tgg             2223
Ala Lys Ala Ser Lys Arg Asp
    695                 700


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Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile
             20                  25                  30

Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp
         35                  40                  45

Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr
     50                  55                  60

Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu Val
 65                  70                  75                  80

Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile Glu
                 85                  90                  95

Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr
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            100                 105                 110

Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys
        115                 120                 125

Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys Ser
    130                 135                 140

Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu
145                 150                 155                 160

Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala
                165                 170                 175

Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe
            180                 185                 190

Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp
        195                 200                 205

Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr
    210                 215                 220

Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile
225                 230                 235                 240

Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp
                245                 250                 255

Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn
            260                 265                 270

Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu
        275                 280                 285

Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu
    290                 295                 300

Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp
305                 310                 315                 320

Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val
                325                 330                 335

His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp
            340                 345                 350

Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala
        355                 360                 365

Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly
    370                 375                 380

Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala
385                 390                 395                 400

Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly
                405                 410                 415

Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu
            420                 425                 430
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09699-0126WO1

Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser
435 440 445

Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe Val
450 455 460

Met Pro Arg Met Gln Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp
465 470 475 480

His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly
485 490 495

Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln
500 505 510

Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe
515 520 525

Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg
530 535 540

Pro Leu Ala Leu Thr Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala
545 550 555 560

Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val
565 570 575

Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln
580 585 590

Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg
595 600 605

Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu
610 615 620

Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr
625 630 635 640

Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln
645 650 655

Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys
660 665 670

Asp Ser Glu Gly Asn Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu
675 680 685

Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp
690 695 700

<210> 413
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1264)

<223> RXN00043

<400> 413

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aacagcaggc ctcaagtccg aagataatta acctaaatcc gtagacataa gacatcatac 60

gtcctatgct tgctggaagg aagcaaataa cctcagaaag atg gca gaa gtg gtg   115
                                              Met Ala Glu Val Val
                                                1               5

cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga   163
His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg
                  10                  15                  20

att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac   211
Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn
              25                  30                  35

ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga   259
Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly
          40                  45                  50

ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat   307
Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His
      55                  60                  65

aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag   355
Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln
  70                  75                  80                  85

gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg   403
Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met
                  90                  95                 100

ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg   451
Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val
              105                 110                 115

gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac   499
Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His
          120                 125                 130

ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg   547
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro
      135                 140                 145

gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat   595
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His
  150                 155                 160                 165

gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac   643
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp
                  170                 175                 180

aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct   691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala
              185                 190                 195

tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att   739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile
          200                 205                 210
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gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc   787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe
    215                 220                 225

aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct   835
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala
230                 235                 240                 245

ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc   883
Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala
                250                 255                 260

gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac   931
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn
            265                 270                 275

aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac   979
Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp
        280                 285                 290

ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc   1027
Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val
    295                 300                 305

gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta   1075
Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu
310                 315                 320                 325

gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac   1123
Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp
                330                 335                 340

gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc   1171
Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser
            345                 350                 355

gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac   1219
Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp
        360                 365                 370

tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att       1264
Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile
    375                 380                 385

taaatacgag caaaactttc ctg                                        1287
```

<210> 414
<211> 388
<212> PRT
<213> Corynebacterium glutamicum

<400> 414

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Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys
  1               5                  10                  15

Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe
             20                  25                  30

Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala
         35                  40                  45
```

```
Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
     50                  55                  60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr
 65                  70                  75                  80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
                 85                  90                  95

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala
            100                 105                 110

Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
        115                 120                 125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys
    130                 135                 140

Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu
145                 150                 155                 160

Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val
                165                 170                 175

Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala
            180                 185                 190

His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr
        195                 200                 205

Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr
    210                 215                 220

Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro
225                 230                 235                 240

Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr
                245                 250                 255

Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp
            260                 265                 270

Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala
        275                 280                 285

Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr
    290                 295                 300

Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly
305                 310                 315                 320

Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly
                325                 330                 335

Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys
            340                 345                 350

Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn
        355                 360                 365
```

Doc No. 1000

```
Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp
    370                 375                 380

His Gln Val Ile
385
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<210> 415
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1264)
<223> FRXA00043

<400> 415

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gtcctatgct tgctggaagg aagcaaataa cctcagaaag atg gca gaa gtg gtg   115
                                              Met Ala Glu Val Val
                                                1               5

cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga   163
His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg
                10                  15                  20

att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac   211
Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn
            25                  30                  35

ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga   259
Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly
        40                  45                  50

ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat   307
Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His
    55                  60                  65

aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag   355
Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln
70                  75                  80                  85

gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg   403
Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met
                90                  95                  100

ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg   451
Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val
            105                 110                 115

gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac   499
Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His
        120                 125                 130

ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg   547
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro
    135                 140                 145

gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat   595
```

```
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His
150                 155                 160                 165

gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac   643
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp
                170                 175                 180

aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct   691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala
            185                 190                 195

tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att   739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile
        200                 205                 210

gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc   787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe
    215                 220                 225

aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct   835
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala
230                 235                 240                 245

ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc   883
Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala
                250                 255                 260

gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac   931
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn
            265                 270                 275

aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac   979
Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp
        280                 285                 290

ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc   1027
Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val
    295                 300                 305

gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta   1075
Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu
310                 315                 320                 325

gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac   1123
Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp
                330                 335                 340

gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc   1171
Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser
            345                 350                 355

gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac   1219
Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp
        360                 365                 370

tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att       1264
Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile
    375                 380                 385

taaatacgag caaaactttc ctg                                        1287
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<210> 416
<211> 388
<212> PRT
<213> Corynebacterium glutamicum

<400> 416

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Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys
  1               5                  10                  15

Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe
            20                  25                  30

Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala
        35                  40                  45

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
    50                  55                  60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr
65                  70                  75                  80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
                85                  90                  95

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala
            100                 105                 110

Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
        115                 120                 125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys
    130                 135                 140

Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu
145                 150                 155                 160

Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val
                165                 170                 175

Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala
            180                 185                 190

His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr
        195                 200                 205

Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr
    210                 215                 220

Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro
225                 230                 235                 240

Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr
                245                 250                 255

Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp
            260                 265                 270

Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala
        275                 280                 285
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09825400-090705

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Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr
    290                 295                 300

Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly
305                 310                 315                 320

Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly
                325                 330                 335

Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys
            340                 345                 350

Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn
        355                 360                 365

Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp
    370                 375                 380

His Gln Val Ile
385
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<210> 417
<211> 1584
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1561)
<223> RXN01752

<400> 417

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ttggccgtca gatcgtggca gaacaacagg tggggaggtc atg atg gaa caa gat   115
                                            Met Met Glu Gln Asp
                                              1               5

ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa   163
Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys
                  10                  15                  20

aag gct gca ctg att gat gcc att gaa ggg tta agg gtg cgc gat ccg   211
Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro
              25                  30                  35

cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc   259
Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe
          40                  45                  50

att gct gtg gtg gtg ggc ttt atc ttg atg ctc att ttt gct cgg caa   307
Ile Ala Val Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln
      55                  60                  65

gca gca ctt att gga ctg tca gca acg tgt acg ttc atg tac ctc att   355
Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile
  70                  75                  80                  85

aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa   403
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu
```

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                  90                  95                 100

tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac   451
Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp
            105                 110                 115

aag ctg aaa acc tac acg gtg ttg gtg ccc gcc tat ggc gaa cct gag   499
Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala Tyr Gly Glu Pro Glu
        120                 125                 130

gtg att gcg cag ctg ctg gca tcc atg cac gct ttt gat tac ccc aag   547
Val Ile Ala Gln Leu Leu Ala Ser Met His Ala Phe Asp Tyr Pro Lys
    135                 140                 145

cat ctt ctg cag gta ttg ctc atg ttg gag gaa gat gat ctg ccc acg   595
His Leu Leu Gln Val Leu Leu Met Leu Glu Glu Asp Asp Leu Pro Thr
150                 155                 160                 165

atc gcc gcg gca gag gca gcg gga gtg gat cag gtg gca acg atc att   643
Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln Val Ala Thr Ile Ile
                170                 175                 180

aag gtg ccg cca gcg cag ccc cgc acc aag ccg aag gcc tgt aac tat   691
Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro Lys Ala Cys Asn Tyr
            185                 190                 195

gga ttg cac ttt gcc acg ggg gaa att gtc acg atc ttt gac gcg gaa   739
Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr Ile Phe Asp Ala Glu
        200                 205                 210

gac atg cca gat ccc ctc caa ctg cgt cgc gtg gtg gtg gca ttt gaa   787
Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val Val Val Ala Phe Glu
    215                 220                 225

cgc tcg gct tcc aat acg gtg tgc gtc cag tca agg ttg tcg tat cga   835
Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser Arg Leu Ser Tyr Arg
230                 235                 240                 245

aac gcc agg cag aat ctg cta act gcg tgg ttc acc att gaa tat gac   883
Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe Thr Ile Glu Tyr Asp
                250                 255                 260

gtg tgg ttt aac ttc ctg ctg cca ggc gtc atg cgc atg aac gca cct   931
Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met Arg Met Asn Ala Pro
            265                 270                 275

gtc cca ttg ggc ggt acc tcc aac cat ctg ctc acg ggt gtc ctg aaa   979
Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys
        280                 285                 290

gat ctc ggc gcg tgg gat cct ttc aat gtc aca gaa aat gcc gac ctc   1027
Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr Glu Asn Ala Asp Leu
    295                 300                 305

ggc gta ccc atc gcg gca aaa gga tat tcc acc gcg gtg ttg gat tcg   1075
Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser
310                 315                 320                 325

gtg acg tgg gag gaa gca aac tcc gac acc atc aac tgg ttg cgc cag   1123
Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln
                330                 335                 340
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US 2009/0162360 A1

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cgt tct cgc tgg tac aag ggc tat ctg caa aca tgg ctt gtg tat atg   1171
Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met
            345                 350                 355

cgc agg cca aag tgg tta gtc caa gag ctt ggc atc att cct gct gtg   1219
Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val
        360                 365                 370

cgt ttt acc ttc ctc atg gca ggc acc ccg atc att gcg gtg ctc aat   1267
Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn
    375                 380                 385

ctg ctc ttt tgg tac ttg tcg ctc acg tgg att ctg ggc cag ccc ggc   1315
Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly
390                 395                 400                 405

acc att gag cag atg ttc cca cct gcg gtg tac tac cca gcg ttg gtg   1363
Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val
                410                 415                 420

tgt ttg gtg gtg gcc aat gct gcg acc atc ttt atg aat ctc att ggc   1411
Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly
            425                 430                 435

tgc cgg gaa ggc cgc gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc   1459
Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe
        440                 445                 450

ccg ctg tat tgg ctg ctc atg agc att gca gcg ttg aaa ggc acg tgg   1507
Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp
    455                 460                 465

caa ttg atc acg cga cca tcc tat tgg gag aaa act gcc cac gga ttg   1555
Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu
470                 475                 480                 485

gag gcg taagcggtgc ccatcgtcaa acc                                 1584
Glu Ala
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<210> 418
<211> 487
<212> PRT
<213> Corynebacterium glutamicum

<400> 418

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Met Met Glu Gln Asp Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala
  1               5                  10                  15

Ser Glu Glu Lys Lys Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu
            20                  25                  30

Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly
        35                  40                  45

Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu
    50                  55                  60

Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr
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65 70 75 80

Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg
85 90 95

Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu
100 105 110

Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala
115 120 125

Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala
130 135 140

Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu
145 150 155 160

Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln
165 170 175

Val Ala Thr Ile Ile Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro
180 185 190

Lys Ala Cys Asn Tyr Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr
195 200 205

Ile Phe Asp Ala Glu Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val
210 215 220

Val Val Ala Phe Glu Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser
225 230 235 240

Arg Leu Ser Tyr Arg Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe
245 250 255

Thr Ile Glu Tyr Asp Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met
260 265 270

Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu
275 280 285

Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr
290 295 300

Glu Asn Ala Asp Leu Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr
305 310 315 320

Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile
325 330 335

Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr
340 345 350

Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly
355 360 365

Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile
370 375 380

Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile
385 390 395 400

Sequence Listing

```
Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr
                405                 410                 415

Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe
            420                 425                 430

Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile
        435                 440                 445

Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala
    450                 455                 460

Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys
465                 470                 475                 480

Thr Ala His Gly Leu Glu Ala
                485
```

<210> 419
<211> 689
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (19)..(666)
<223> FRXA01839

<400> 419

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ttcctgctgc caggtgtcatg cgc atg aac gca cct gtc cca ttg ggc ggt    51
                     Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly
                       1               5                  10

acc tcc aac cat ctg ctc acg ggt gtc ctg aaa gat ctc ggc gcg tgg    99
Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp
             15                  20                  25

gat cct ttc aat gtc aca gaa gat gcg gac ctc ggc gta cgc atc gcg   147
Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala
         30                  35                  40

gca aag gga tat tcc acc gcg gtg ttg gat tcg gtg acg tgg gag gaa   195
Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu
     45                  50                  55

gca aac tcc gac acc atc aac tgg ttg cgc cag cgt tct cgc tgg tac   243
Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr
 60                  65                  70                  75

aag ggc tat ctg caa aca tgg ctt gtg tat atg cgc agg cca aag tgg   291
Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp
                 80                  85                  90

tta gtc caa gag ctt ggc atc att cct gct gtg cgt ttt acc ttc ctc   339
Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu
             95                  100                 105

atg gca ggc acc ccg atc att gcg gtg ctc aat ctg ctc ttt tgg tac   387
Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr
```

```
        110                 115                 120

ttg tcg ctc acg tgg att ctg ggc cag ccc ggc acc att gag cag atg   435
Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met
    125                 130                 135

ttc cca cct gcg gtg tac tac cca gcg ttg gtg tgt ttg gtg gtg gcc   483
Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala
140                 145                 150                 155

aat gct gcg acc atc ttt atg aat ctc att ggc tgc cgg gaa ggc cgc   531
Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg
                160                 165                 170

gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc ccg ctg tat tgg ctg   579
Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu
            175                 180                 185

ctc atg agc att gca gcg ttg aaa ggc acg tgg caa ttg atc acg cga   627
Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg
        190                 195                 200

cca tcc tat tgg gag aaa act gcc cac gga ttg gag gcg taagcggtgc    676
Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu Glu Ala
    205                 210                 215

ccatcgtcaa acc                                                   689
```

<210> 420
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 420

```
Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu
  1               5                  10                  15

Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val
             20                  25                  30

Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala Ala Lys Gly Tyr Ser
         35                  40                  45

Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr
     50                  55                  60

Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln
 65                  70                  75                  80

Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu
                 85                  90                  95

Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro
            100                 105                 110

Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp
        115                 120                 125

Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val
    130                 135                 140
```

```
Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile
145                 150                 155                 160

Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu
                165                 170                 175

Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala
            180                 185                 190

Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu
        195                 200                 205

Lys Thr Ala His Gly Leu Glu Ala
    210                 215
```

<210> 421
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1027)
<223> RXA01859

<400> 421

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tacgcccagg gtttccatat tggtaaatct aagccgattg atgaatttat agctacttat 60

ctcgagacga accaaaccgc tacctggggg taggaagaat atg aaa aag aag agc   115
                                              Met Lys Lys Lys Ser
                                                1               5

ttt cca atc gca aga gtc atc ggt atc ggc gtc ctt ggc atc gcc ggg   163
Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val Leu Gly Ile Ala Gly
                10                  15                  20

atg gga ata ttg ttg cta tgg ctt gca gtt acc ctg tct gat cca gca   211
Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr Leu Ser Asp Pro Ala
            25                  30                  35

tca ccg ggt gcc aaa gaa acc gaa gtc ttt gat agg tgg aaa gtg ctc   259
Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp Arg Trp Lys Val Leu
        40                  45                  50

ttt gat gac tat att cca cca gtc agg gta ttg gtt gct gcg att atc   307
Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu Val Ala Ala Ile Ile
    55                  60                  65

gtt gca tta att ttc gtc ttt atc gct gcc aca gtg gaa cga acc gta   355
Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr Val Glu Arg Thr Val
70                  75                  80                  85

acc aac cgc tac cga agc tcc gta gac ggc gaa aga gtg cca tta gcg   403
Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu Arg Val Pro Leu Ala
                90                  95                  100

ccg aag att gtg atg gca gaa acc cga ggg gta ttt cat gga ccg att   451
Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val Phe His Gly Pro Ile
            105                 110                 115
```

```
acc att aac gtg ctc gtg cca gca cac aat gag gcg gaa aga att act   499
Thr Ile Asn Val Leu Val Pro Ala His Asn Glu Ala Glu Arg Ile Thr
        120                 125                 130

gga aca att cag gca ttg aaa tca caa cat gag cct cca gaa cgc atc   547
Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu Pro Pro Glu Arg Ile
    135                 140                 145

gtt gta gtt gcc gat aat tgc act gat gaa act acg gaa tta gcc cgt   595
Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr Thr Glu Leu Ala Arg
150                 155                 160                 165

gct gag gga gtg gag gtc ttg gaa aca gtc aat aat aag ttt aag aag   643
Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn Asn Lys Phe Lys Lys
                170                 175                 180

gcc gga gga ctc aat cag gct ttg agc cgg atg ctt ccc aca ttg ggg   691
Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met Leu Pro Thr Leu Gly
            185                 190                 195

gag aat gac att gtg atg atc gtt gac gct gat aca gca ctt gat caa   739
Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp Thr Ala Leu Asp Gln
        200                 205                 210

ggt ttc ctc aag gaa gca cgg cgc cgc ttt gag tct gat cgc gct cta   787
Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu Ser Asp Arg Ala Leu
    215                 220                 225

atg gcc gtg ggc gga ttg ttc tac ggt gag tca ggc tcc gga tgg ctt   835
Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser Gly Ser Gly Trp Leu
230                 235                 240                 245

ggc caa tat cag cgc aac gaa tac acc cgt tat agc cgt gac atc tat   883
Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr Ser Arg Asp Ile Tyr
                250                 255                 260

cga cgc cgc gga cgt gtg ttt gtt ttg act gga aca gcg tcg gct ttt   931
Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly Thr Ala Ser Ala Phe
            265                 270                 275

cgg cca cgc ggc ctg cgg aca gta gcg gaa tca cgc ggg aca ttg atc   979
Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser Arg Gly Thr Leu Ile
        280                 285                 290

ccc gga cgt aaa gcc gat gtt tat gac acc gcg ggc gtt gac cga aga   1027
Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala Gly Val Asp Arg Arg
    295                 300                 305

taatgagttg accctggctt tga                                       1050


<210> 422
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 422
Met Lys Lys Lys Ser Phe Pro Ile Ala Arg Val Ile Gly Ile Gly Val
  1               5                  10                  15
```

Leu Gly Ile Ala Gly Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr
20 25 30

Leu Ser Asp Pro Ala Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp
35 40 45

Arg Trp Lys Val Leu Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu
50 55 60

Val Ala Ala Ile Ile Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr
65 70 75 80

Val Glu Arg Thr Val Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu
85 90 95

Arg Val Pro Leu Ala Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val
100 105 110

Phe His Gly Pro Ile Thr Ile Asn Val Leu Val Pro Ala His Asn Glu
115 120 125

Ala Glu Arg Ile Thr Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu
130 135 140

Pro Pro Glu Arg Ile Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr
145 150 155 160

Thr Glu Leu Ala Arg Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn
165 170 175

Asn Lys Phe Lys Lys Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met
180 185 190

Leu Pro Thr Leu Gly Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp
195 200 205

Thr Ala Leu Asp Gln Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu
210 215 220

Ser Asp Arg Ala Leu Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser
225 230 235 240

Gly Ser Gly Trp Leu Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr
245 250 255

Ser Arg Asp Ile Tyr Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly
260 265 270

Thr Ala Ser Ala Phe Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser
275 280 285

Arg Gly Thr Leu Ile Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala
290 295 300

Gly Val Asp Arg Arg
305

<210> 423
<211> 882
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(859)
<223> RXA00042

<400> 423
gtggtctttg actcaaacgg ccagttacaa caggtccatt tagaccatca agtaatttaa 60

atacgagcaa aactttcctg ataataaaag gagtccgacc atg gac atc atc atc 115
Met Asp Ile Ile Ile
1 5

tgc aaa gac gag caa gaa gtc ggc aaa gca gcg gca gcc ctg atc gca 163
Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala Ala Ala Leu Ile Ala
10 15 20

ccc ttc gca act aag ggc gga acc ttg ggg ctt gca act gga tcg tca 211
Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu Ala Thr Gly Ser Ser
25 30 35

cct ttg agc acc tac caa gag ctc att cgc atg tat gaa gct ggg gaa 259
Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met Tyr Glu Ala Gly Glu
40 45 50

gtg tca ttc aag aac tgc aag gca ttc ttg ttg gat gaa tac gtg gga 307
Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu Asp Glu Tyr Val Gly
55 60 65

tta acg cgc gac gat gaa aac agc tac ttc aaa acc att cgt aaa gag 355
Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys Thr Ile Arg Lys Glu
70 75 80 85

ttc act gac cac atc gac atc gtt gat gaa gag gtc tac agc cca gat 403
Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu Val Tyr Ser Pro Asp
90 95 100

ggt gca aac cct gat cca tac gaa gca gct gca gag tat gag gca aag 451
Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala Glu Tyr Glu Ala Lys
105 110 115

atc gct gca gaa tcc gtt gat gtt caa atc ctt ggc atc ggc gga aac 499
Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu Gly Ile Gly Gly Asn
120 125 130

ggc cac atc gct ttc aat gag cca tca tct tct ctg tca gga ctg aca 547
Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser Leu Ser Gly Leu Thr
135 140 145

aag gtc cag gcg ctg cac cct aaa act gtg gag gac aac gct cga ttc 595
Lys Val Gln Ala Leu His Pro Lys Thr Val Glu Asp Asn Ala Arg Phe
150 155 160 165

ttc aac acc atc gaa gag gtc cca acc cac gcc ctc acc cag ggt ttg 643
Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala Leu Thr Gln Gly Leu
170 175 180

ggc act ttg tcc cgc gcg caa aac atc gtg ttg gtg gca act ggt gaa 691
Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu Val Ala Thr Gly Glu
185 190 195

```
gga aaa gcc gac gcc atc cgc gga act gtg gaa ggc cca ctg acc gcc   739
Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu Gly Pro Leu Thr Ala
        200                 205                 210

atg tgc cca ggt tcc atc ctg cag atg cac aac aat gcc acc atc atc   787
Met Cys Pro Gly Ser Ile Leu Gln Met His Asn Asn Ala Thr Ile Ile
    215                 220                 225

gtt gat gaa gca gca gca tcc aag ctg gaa aac gct gat cac tac cgt   835
Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn Ala Asp His Tyr Arg
230                 235                 240                 245

ctc atg gag caa tta aag ctg cgc tagaaacaaa aaggaaagta gtg         882
Leu Met Glu Gln Leu Lys Leu Arg
                250
```

<210> 424
<211> 253
<212> PRT
<213> Corynebacterium glutamicum

<400> 424

```
Met Asp Ile Ile Ile Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala
  1               5                  10                  15

Ala Ala Leu Ile Ala Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu
            20                  25                  30

Ala Thr Gly Ser Ser Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met
        35                  40                  45

Tyr Glu Ala Gly Glu Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu
    50                  55                  60

Asp Glu Tyr Val Gly Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys
65                  70                  75                  80

Thr Ile Arg Lys Glu Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu
                85                  90                  95

Val Tyr Ser Pro Asp Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala
            100                 105                 110

Glu Tyr Glu Ala Lys Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu
        115                 120                 125

Gly Ile Gly Gly Asn Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser
    130                 135                 140

Leu Ser Gly Leu Thr Lys Val Gln Ala Leu His Pro Lys Thr Val Glu
145                 150                 155                 160

Asp Asn Ala Arg Phe Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala
                165                 170                 175

Leu Thr Gln Gly Leu Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu
            180                 185                 190

Val Ala Thr Gly Glu Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu
```

```
        195                 200                 205

Gly Pro Leu Thr Ala Met Cys Pro Gly Ser Ile Leu Gln Met His Asn
    210                 215                 220

Asn Ala Thr Ile Ile Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn
225                 230                 235                 240

Ala Asp His Tyr Arg Leu Met Glu Gln Leu Lys Leu Arg
                245                 250


<210> 425
<211> 1998
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1975)
<223> RXA01482

<400> 425
ttgcgtgctg caacttaatt atggtcctcc agctcagtg tgctgtgtgg attgtttatt 60

ctcgtccatt aagtgatcga gaaaaagttg ttgtaaagtc atg cgc atg tgt gga   115
                                            Met Arg Met Cys Gly
                                              1               5

att gtt gga tat att ggc caa gcg ggc gac tcc cgt gat tac ttt gct   163
Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser Arg Asp Tyr Phe Ala
                10                  15                  20

cta gat gta gtt gtt gaa gga cta cgt cgc ctg gaa tac cgc gga tat   211
Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr
            25                  30                  35

gac tcc gca ggt att gct att cac gcc aat ggt gag att agc tac cga   259
Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly Glu Ile Ser Tyr Arg
        40                  45                  50

aag aag gcc gga aag gtt gct gca cta gat gca gaa atc gct aaa gca   307
Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala Glu Ile Ala Lys Ala
    55                  60                  65

cct ctt cca gat tct att ttg gga att gga cac acc cgt tgg gca act   355
Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His Thr Arg Trp Ala Thr
70                  75                  80                  85

cat ggt ggc cca acc gat gtc aac gct cac ccc cac gtt gtt tcc aat   403
His Gly Gly Pro Thr Asp Val Asn Ala His Pro His Val Val Ser Asn
                90                  95                  100

ggc aag ctt gcc gta gta cac aac ggc atc atc gaa aac ttt gcg gaa   451
Gly Lys Leu Ala Val Val His Asn Gly Ile Ile Glu Asn Phe Ala Glu
            105                 110                 115

ctg cgc tct gag ctt tcc gct aag ggc tac aac ttt gta tcc gat acc   499
Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn Phe Val Ser Asp Thr
        120                 125                 130
```

```
gat acc gaa gtt gct gct tct ttg ctt gct gaa att tac aat act cag   547
Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu Ile Tyr Asn Thr Gln
    135                 140                 145

gca aac ggt gac ctc acc ctt gct atg cag ctg acc ggt cag cgc ctt   595
Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu Thr Gly Gln Arg Leu
150                 155                 160                 165

gag ggt gct ttc acc ctg cta gct att cat gct gat cac gat gac cgc   643
Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala Asp His Asp Asp Arg
                170                 175                 180

atc gtt gca gct cgt cgt aac tct cct ttg gtt atc ggc gtc ggc gag   691
Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val Ile Gly Val Gly Glu
            185                 190                 195

ggc gag aac ttc ctc gga tct gac gtt tct ggc ttt att gat tac acc   739
Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly Phe Ile Asp Tyr Thr
        200                 205                 210

cgc aag gct gta gag ctg gct aat gac cag gtt gtt acc atc acc gct   787
Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val Val Thr Ile Thr Ala
    215                 220                 225

gat gat tac gcc atc acc aac ttt gat gga tca gaa gca gtt ggc aag   835
Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser Glu Ala Val Gly Lys
230                 235                 240                 245

cct ttc gac gtg gag tgg gac gct gca gct gct gaa aag ggt ggc ttc   883
Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala Glu Lys Gly Gly Phe
                250                 255                 260

ggt tcc ttc atg gag aag gaa atc cac gat cag cca gca gct gtt cgc   931
Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln Pro Ala Ala Val Arg
            265                 270                 275

gat acc ctg atg ggc cgt ctt gat gaa gat ggc aag ctc gtt ctt gat   979
Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly Lys Leu Val Leu Asp
        280                 285                 290

gag ctg cgc atc gat gaa gct att ctg cgt agt gtc gac aag atc gtc   1027
Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser Val Asp Lys Ile Val
    295                 300                 305

att gtt gct tgt ggt act gca gct tat gca ggc cag gtt gct cgt tac   1075
Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly Gln Val Ala Arg Tyr
310                 315                 320                 325

gcc att gag cac tgg tgc cgc atc cca acc gag gtg gag ctg gct cac   1123
Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu Val Glu Leu Ala His
                330                 335                 340

gag ttc cgt tac cgc gac cca atc ctc aac gag aag acc ctt gtt gtg   1171
Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu Lys Thr Leu Val Val
            345                 350                 355

gca ttg tcc cag tcc ggc gag acc atg gat acc ctc atg gct gtt cgc   1219
Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr Leu Met Ala Val Arg
        360                 365                 370

cac gca cgt gag cag ggt gcc aag gtt gtt gct att tgt aac act gtt   1267
```

```
His Ala Arg Glu Gln Gly Ala Lys Val Val Ala Ile Cys Asn Thr Val
    375                 380                 385

gga tcc act ctt cca cgt gaa gca gat gcg tcc ctg tac acc tac gct   1315
Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser Leu Tyr Thr Tyr Ala
390                 395                 400                 405

ggc cct gag atc gct gtg gcg tcc acc aag gcg ttc ttg gct cag atc   1363
Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala Phe Leu Ala Gln Ile
                410                 415                 420

act gct tct tac ttg ctt ggc ctg tac ttg gct cag ctg cgc ggc aac   1411
Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala Gln Leu Arg Gly Asn
            425                 430                 435

aag ttc gct gat gag gtt tct tcc att ctg gac agc ctg cgt gag atg   1459
Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp Ser Leu Arg Glu Met
        440                 445                 450

cct gag aag att cag cag gtc atc gat gca gaa gag cag atc aag aag   1507
Pro Glu Lys Ile Gln Gln Val Ile Asp Ala Glu Glu Gln Ile Lys Lys
    455                 460                 465

ctt ggc caa gat atg gca gat gct aag tct gtg ctg ttc ctg ggc cgc   1555
Leu Gly Gln Asp Met Ala Asp Ala Lys Ser Val Leu Phe Leu Gly Arg
470                 475                 480                 485

cac gtt ggt ttc cca gtt gcg ctt gag ggt gcg ttg aag ctc aag gag   1603
His Val Gly Phe Pro Val Ala Leu Glu Gly Ala Leu Lys Leu Lys Glu
                490                 495                 500

atc gca tac ctg cac gct gaa ggt ttc gct gca ggc gag ctc aag cac   1651
Ile Ala Tyr Leu His Ala Glu Gly Phe Ala Ala Gly Glu Leu Lys His
            505                 510                 515

ggc cca att gct ttg gtt gag gaa ggc cag ccg atc ttc gtt atc gtg   1699
Gly Pro Ile Ala Leu Val Glu Glu Gly Gln Pro Ile Phe Val Ile Val
        520                 525                 530

cct tca cct cgt ggt cgc gat tcc ctg cac tcc aag gtt gtc tcc aac   1747
Pro Ser Pro Arg Gly Arg Asp Ser Leu His Ser Lys Val Val Ser Asn
    535                 540                 545

att cag gag atc cgt gca cgt ggc gct gtc acc atc gtg att gca gag   1795
Ile Gln Glu Ile Arg Ala Arg Gly Ala Val Thr Ile Val Ile Ala Glu
550                 555                 560                 565

gaa ggc gat gag gct gtc aac gat tac gcc aac ttc atc atc cgc att   1843
Glu Gly Asp Glu Ala Val Asn Asp Tyr Ala Asn Phe Ile Ile Arg Ile
                570                 575                 580

cct cag gcc cca acc ctg atg cag cct ctg ctg tcc acc gtg cct ctg   1891
Pro Gln Ala Pro Thr Leu Met Gln Pro Leu Leu Ser Thr Val Pro Leu
            585                 590                 595

cag atc ttt gcg tgc gct gtg gca acc gca aag ggc tac aac gtg gat   1939
Gln Ile Phe Ala Cys Ala Val Ala Thr Ala Lys Gly Tyr Asn Val Asp
        600                 605                 610

cag cct cgt aac ctg gca aag tct gtc acc gtc gaa taaaaagatt        1985
Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
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615 620 625

tcgcttctcg acg 1998

<210> 426
<211> 625
<212> PRT
<213> Corynebacterium glutamicum

<400> 426
Met Arg Met Cys Gly Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser
1 5 10 15

Arg Asp Tyr Phe Ala Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu
20 25 30

Glu Tyr Arg Gly Tyr Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly
35 40 45

Glu Ile Ser Tyr Arg Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala
50 55 60

Glu Ile Ala Lys Ala Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His
65 70 75 80

Thr Arg Trp Ala Thr His Gly Gly Pro Thr Asp Val Asn Ala His Pro
85 90 95

His Val Val Ser Asn Gly Lys Leu Ala Val Val His Asn Gly Ile Ile
100 105 110

Glu Asn Phe Ala Glu Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn
115 120 125

Phe Val Ser Asp Thr Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu
130 135 140

Ile Tyr Asn Thr Gln Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu
145 150 155 160

Thr Gly Gln Arg Leu Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala
165 170 175

Asp His Asp Asp Arg Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val
180 185 190

Ile Gly Val Gly Glu Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly
195 200 205

Phe Ile Asp Tyr Thr Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val
210 215 220

Val Thr Ile Thr Ala Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser
225 230 235 240

Glu Ala Val Gly Lys Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala
245 250 255

Glu Lys Gly Gly Phe Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln
260 265 270

Pro Ala Ala Val Arg Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly
275 280 285

Lys Leu Val Leu Asp Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser
290 295 300

Val Asp Lys Ile Val Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly
305 310 315 320

Gln Val Ala Arg Tyr Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu
325 330 335

Val Glu Leu Ala His Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu
340 345 350

Lys Thr Leu Val Val Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr
355 360 365

Leu Met Ala Val Arg His Ala Arg Glu Gln Gly Ala Lys Val Val Ala
370 375 380

Ile Cys Asn Thr Val Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser
385 390 395 400

Leu Tyr Thr Tyr Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala
405 410 415

Phe Leu Ala Gln Ile Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala
420 425 430

Gln Leu Arg Gly Asn Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp
435 440 445

Ser Leu Arg Glu Met Pro Glu Lys Ile Gln Gln Val Ile Asp Ala Glu
450 455 460

Glu Gln Ile Lys Lys Leu Gly Gln Asp Met Ala Asp Ala Lys Ser Val
465 470 475 480

Leu Phe Leu Gly Arg His Val Gly Phe Pro Val Ala Leu Glu Gly Ala
485 490 495

Leu Lys Leu Lys Glu Ile Ala Tyr Leu His Ala Glu Gly Phe Ala Ala
500 505 510

Gly Glu Leu Lys His Gly Pro Ile Ala Leu Val Glu Glu Gly Gln Pro
515 520 525

Ile Phe Val Ile Val Pro Ser Pro Arg Gly Arg Asp Ser Leu His Ser
530 535 540

Lys Val Val Ser Asn Ile Gln Glu Ile Arg Ala Arg Gly Ala Val Thr
545 550 555 560

Ile Val Ile Ala Glu Glu Gly Asp Glu Ala Val Asn Asp Tyr Ala Asn
565 570 575

Phe Ile Ile Arg Ile Pro Gln Ala Pro Thr Leu Met Gln Pro Leu Leu
580 585 590

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```
Ser Thr Val Pro Leu Gln Ile Phe Ala Cys Ala Val Ala Thr Ala Lys
        595                 600                 605

Gly Tyr Asn Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
    610                 615                 620

Glu
625
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<210> 427
<211> 666
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(666)
<223> RXN03179

<400> 427

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gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca   48
Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
  1               5                  10                  15

gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc   96
Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
             20                  25                  30

ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac   144
Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
         35                  40                  45

gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga   192
Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
     50                  55                  60

cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc   240
Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65                  70                  75                  80

gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat   288
Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
                 85                  90                  95

cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac   336
Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
            100                 105                 110

acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc   384
Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
        115                 120                 125

gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca   432
Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
    130                 135                 140

atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg   480
Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
145                 150                 155                 160
```

```
gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat   528
Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
                165                 170                 175

gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct   576
Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
            180                 185                 190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt tcg cgg aaa tgt   624
Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys
        195                 200                 205

cca aga aga cgg ctg gtc atg acc atc cac cag gtg tgt acc           666
Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr
    210                 215                 220
```

<210> 428
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 428

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Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
  1               5                  10                  15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
            20                  25                  30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
        35                  40                  45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
    50                  55                  60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
65                  70                  75                  80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
                85                  90                  95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
            100                 105                 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
        115                 120                 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
    130                 135                 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
145                 150                 155                 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
                165                 170                 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
            180                 185                 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys
        195                 200                 205
```

```
Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr
    210                 215                 220


<210> 429
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(672)
<223> FRXA02872

<400> 429
gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca   48
Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
  1               5                  10                  15

gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc   96
Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
             20                  25                  30

ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac   144
Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
         35                  40                  45

gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga   192
Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
     50                  55                  60

cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc   240
Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65                  70                  75                  80

gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat   288
Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
                 85                  90                  95

cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac   336
Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
            100                 105                 110

acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc   384
Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
        115                 120                 125

gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca   432
Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
    130                 135                 140

atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg   480
Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
145                 150                 155                 160

gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat   528
Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
                165                 170                 175

gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct   576
```

```
Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
            180                 185                 190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt ttc gcg gaa atg   624
Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met
        195                 200                 205

tcc caa gaa gac ggc ctg gtc atg acc atc cac cca ggt gtg tac cgc   672
Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg
    210                 215                 220
```

<210> 430
<211> 224
<212> PRT
<213> Corynebacterium glutamicum

<400> 430

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Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
  1               5                  10                  15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
             20                  25                  30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
         35                  40                  45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
     50                  55                  60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65                  70                  75                  80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
                 85                  90                  95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
            100                 105                 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
        115                 120                 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
    130                 135                 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
145                 150                 155                 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
                165                 170                 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
            180                 185                 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met
        195                 200                 205

Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg
    210                 215                 220
```

09529180 - 060208

<210> 431
<211> 533
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(510)
<223> RXN03180

<400> 431

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ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg   48
Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
  1               5                  10                  15

ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca   96
Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
            20                  25                  30

gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc  144
Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
        35                  40                  45

gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac  192
Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
    50                  55                  60

ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc  240
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
65                  70                  75                  80

att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga  288
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
                85                  90                  95

ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc  336
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
            100                 105                 110

cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat  384
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
        115                 120                 125

gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa  432
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
    130                 135                 140

atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac  480
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
145                 150                 155                 160

gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga     530
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
                165                 170

tgt                                                              533
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<210> 432
<211> 170
<212> PRT
<213> Corynebacterium glutamicum

<400> 432
Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
1 5 10 15

Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
20 25 30

Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
35 40 45

Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
50 55 60

Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
65 70 75 80

Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
85 90 95

Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
100 105 110

Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
115 120 125

Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
130 135 140

Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
145 150 155 160

Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
165 170

<210> 433
<211> 533
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(510)
<223> FRXA02873

<400> 433
ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg 48
Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
1 5 10 15

ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96
Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
20 25 30

gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144
Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg

```
         35                  40                  45

gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac   192
Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
     50                  55                  60

ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc   240
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
 65                  70                  75                  80

att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga   288
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
                 85                  90                  95

ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc   336
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
            100                 105                 110

cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat   384
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
        115                 120                 125

gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa   432
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
    130                 135                 140

atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac   480
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
145                 150                 155                 160

gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga     530
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
                165                 170

tgt                                                               533


<210> 434
<211> 170
<212> PRT
<213> Corynebacterium glutamicum

<400> 434
Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
  1               5                  10                  15

Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
            20                  25                  30

Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
        35                  40                  45

Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
     50                  55                  60

Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
 65                  70                  75                  80

Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
                 85                  90                  95
```

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```
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
            100                 105                 110

Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
        115                 120                 125

Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
    130                 135                 140

Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
145                 150                 155                 160

Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
                165                 170
```

<210> 435
<211> 798
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(775)
<223> RXA02292

<400> 435

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tgcaccacgc cagctgcaac cctgcgcggt ggtctgggaa gttggtggag gggatcgtcg 60

aaaagcgtag gcactaaagt tctcctgcac aatggaggat atg gac aat gac ttt   115
                                              Met Asp Asn Asp Phe
                                                1               5

gaa tct atc gag aaa atg agc agc ggc gat tgg tac gtg gct acc ggc   163
Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp Tyr Val Ala Thr Gly
                10                  15                  20

gcg gaa cgt gaa gaa gtg gca caa aaa aca gcg tta ctt ttc cac gaa   211
Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala Leu Leu Phe His Glu
            25                  30                  35

tac aac caa att gga cct aca gac ccc gca cga act gcc gaa ata cta   259
Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg Thr Ala Glu Ile Leu
        40                  45                  50

aga act gta cta aat cct gcc agc gga acc tgc acg atc aaa gcg cca   307
Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys Thr Ile Lys Ala Pro
    55                  60                  65

gcc atc att gaa tac ggc ttc aac acc acg atc ggc gag cat gtg ttc   355
Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile Gly Glu His Val Phe
70                  75                  80                  85

atc aac ttt ggc ctc acc att tta gat atc gca ccg gtt cgc atc ggg   403
Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala Pro Val Arg Ile Gly
                90                  95                  100

gca cgc agc atg ctc ggg cca aac tgt cag ctc ttc acc gca ggt cac   451
Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu Phe Thr Ala Gly His
            105                 110                 115
```

```
ccg gtc gat gac tgg gaa atg cgc tcc ggt ggg tgg gaa aat ggc gca   499
Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly Trp Glu Asn Gly Ala
        120                 125                 130

ccc att tcc att ggc gag gat acg tgg ctg ggt gga aat gtc acc gtc   547
Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly Gly Asn Val Thr Val
    135                 140                 145

gtt ggt ggc gtg agc att ggc gat agg tgt gtg att ggc gcg ggg ccc   595
Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val Ile Gly Ala Gly Pro
150                 155                 160                 165

gtg gtg acc aag gat att ccg gat gat tct att gct gtg ggc aac cct   643
Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile Ala Val Gly Asn Pro
                170                 175                 180

gcg cga gta gtg cgg aaa cgt gat gat agc cgg ctc gaa cgt tcg cag   691
Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg Leu Glu Arg Ser Gln
            185                 190                 195

ctg cca gaa ggt gct tcc gtg gat gcg ttg ggg att ctt cct aca aaa   739
Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly Ile Leu Pro Thr Lys
        200                 205                 210

tca cct agg ctg tca gaa aat att gcc gaa aaa tat taaatacgca        785
Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys Tyr
    215                 220                 225

ggcactaaga aga                                                   798
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09501.seq

<210> 436
<211> 225
<212> PRT
<213> Corynebacterium glutamicum

<400> 436

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Met Asp Asn Asp Phe Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp
  1               5                  10                  15

Tyr Val Ala Thr Gly Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala
             20                  25                  30

Leu Leu Phe His Glu Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg
         35                  40                  45

Thr Ala Glu Ile Leu Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys
     50                  55                  60

Thr Ile Lys Ala Pro Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile
 65                  70                  75                  80

Gly Glu His Val Phe Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala
                 85                  90                  95

Pro Val Arg Ile Gly Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu
            100                 105                 110

Phe Thr Ala Gly His Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly
        115                 120                 125
```

```
Trp Glu Asn Gly Ala Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly
    130                 135                 140

Gly Asn Val Thr Val Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val
145                 150                 155                 160

Ile Gly Ala Gly Pro Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile
                165                 170                 175

Ala Val Gly Asn Pro Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg
            180                 185                 190

Leu Glu Arg Ser Gln Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly
        195                 200                 205

Ile Leu Pro Thr Lys Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys
    210                 215                 220

Tyr
225
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[redacted]

<210> 437
<211> 891
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(868)
<223> RXA02666

<400> 437

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gctcggcgac gaggaagaga agaaggacgc attcgacgac ttcgacgatt ccgacgtgga 60

tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga   115
                                            Met Ser Ser Thr Arg
                                              1               5

atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc   163
Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly Arg Gly Thr Arg Leu
                 10                  15                  20

ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt   211
Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu
             25                  30                  35

tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa   259
Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu
         40                  45                  50

atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg   307
Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu
     55                  60                  65

ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg   355
Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg
 70                  75                  80                  85

ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt   403
Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu
```

```
                90                  95                 100

cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc   451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile
            105                 110                 115

cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg   499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val
        120                 125                 130

gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca   547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro
    135                 140                 145

gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc   595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val
150                 155                 160                 165

gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc   643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly
                170                 175                 180

ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac   691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp
            185                 190                 195

ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg   739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp
        200                 205                 210

tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa   787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys
    215                 220                 225

gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa   835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu
230                 235                 240                 245

gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atcccccgcg 888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp
                250                 255

tag                                                               891


<210> 438
<211> 256
<212> PRT
<213> Corynebacterium glutamicum

<400> 438
Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly
  1               5                  10                  15

Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu
            20                  25                  30

Arg Glu Arg Thr Leu Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser
        35                  40                  45

Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr
```

```
     50                  55                  60

Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu
 65                  70                  75                  80

Gly Val Arg Val Arg Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser
                85                  90                  95

Val Trp Ala Gly Leu Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp
            100                 105                 110

Ala Ile Val Leu Ile His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly
        115                 120                 125

Met Ile Ala Arg Val Val Arg Lys Val His Glu Gly Ala Thr Ala Val
    130                 135                 140

Ile Pro Val Leu Pro Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp
145                 150                 155                 160

Gly Gly Val Val Val Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val
                165                 170                 175

Gln Thr Pro Gln Gly Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu
            180                 185                 190

Lys Phe Phe Ala Asp Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala
        195                 200                 205

Ser Leu Met Glu Trp Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp
    210                 215                 220

Pro Met Ala Phe Lys Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln
225                 230                 235                 240

Arg Ile Thr Asp Glu Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp
                245                 250                 255
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09054-0020US1

<210> 439
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1042)
<223> RXA00202

<400> 439
ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60

aaacaaaacc tctaagtaat tcctgaaagg aaattttcac atg tac gct cgt aaa 115
                                        Met Tyr Ala Arg Lys
                                          1   5

ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163
Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala

```
                10                  15                  20

tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat   211
Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp
            25                  30                  35

ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg   259
Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val
        40                  45                  50

cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc   307
Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr
    55                  60                  65

ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag   355
Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln
70                  75                  80                  85

ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca   403
Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro
                90                  95                  100

act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct   451
Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala
            105                 110                 115

gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg   499
Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val
        120                 125                 130

gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct   547
Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala
    135                 140                 145

gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg   595
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu
150                 155                 160                 165

caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt   643
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe
                170                 175                 180

gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag   691
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln
            185                 190                 195

acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg   739
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu
        200                 205                 210

ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag   787
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu
    215                 220                 225

atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat   835
Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp
230                 235                 240                 245

gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt   883
Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val
                250                 255                 260
```

09653600 - 09653600

```
gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg   931
Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu
            265                 270                 275

gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac   979
Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp
        280                 285                 290

gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac   1027
Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn
    295                 300                 305

gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt                    1065
Val Ala Asp Phe Lys
310
```

<210> 440
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 440

```
Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala
  1               5                  10                  15

Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
            20                  25                  30

Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
        35                  40                  45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
    50                  55                  60

Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
65                  70                  75                  80

Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
                85                  90                  95

Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
            100                 105                 110

Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
        115                 120                 125

Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
    130                 135                 140

Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
145                 150                 155                 160

Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
                165                 170                 175

Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
            180                 185                 190

Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
```

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```
        195                 200                 205

Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
    210                 215                 220

Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
225                 230                 235                 240

Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
                245                 250                 255

Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
            260                 265                 270

Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
        275                 280                 285

Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr
    290                 295                 300

Val Lys Leu Asp Asn Val Ala Asp Phe Lys
305                 310
```

US09/852,915

<210> 441
<211> 963
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(940)
<223> RXA02440

<400> 441

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gctgttaatc acgggttgtt cagctaccgg gggagcacca cgggcaacag atggggcatc 60

aggcggagga accgtcgata cgcctcggtt ggttgtcgcg atg gtg agc cac ggc   115
                                              Met Val Ser His Gly
                                                1               5

gcg ccg ggc gat act ttt tgg gat ttg gtc cga aaa ggt gct gaa gac   163
Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg Lys Gly Ala Glu Asp
                10                  15                  20

gcc gcc caa aaa gac aac gtt gaa ctc cgc tat tcc tct aat ccg gaa   211
Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr Ser Ser Asn Pro Glu
            25                  30                  35

atc cct gaa caa tcc aac ctc gtg caa aat gcc atc gat tca cgc gtc   259
Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala Ile Asp Ser Arg Val
        40                  45                  50

gac ggc atc gcc atg acc atg cct aat gct caa tca cta gga ccg gtc   307
Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln Ser Leu Gly Pro Val
    55                  60                  65

gct caa aag gcc gtg gat gcg ggc att cct gtg gtt ggt ctc aac gct   355
Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val Val Gly Leu Asn Ala
70                  75                  80                  85
```

```
gga atg aac gaa tac caa gat tat gga atg aca gga ttc ttt ggt caa   403
Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr Gly Phe Phe Gly Gln
                 90                  95                 100

gat gaa tcc gtc gca gga gca tcc gca gga gcg cgc ctt gcc gag gaa   451
Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala Arg Leu Ala Glu Glu
            105                 110                 115

aac gca caa aaa gtt ttg tgt gtg atc cat gaa cag ggc aac tcc tcc   499
Asn Ala Gln Lys Val Leu Cys Val Ile His Glu Gln Gly Asn Ser Ser
        120                 125                 130

cag gaa gct cgc tgt ggt ggc gtg tct gaa ggt ttg ggc aaa caa gta   547
Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly Leu Gly Lys Gln Val
    135                 140                 145

gaa acc ctg tat gtc aac ggc atg gat ctc acc tca gtg aac tcc acc   595
Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr Ser Val Asn Ser Thr
150                 155                 160                 165

ctg cag gca aaa ctt gct caa gac cgc agc att gat tgg gtt gtg gga   643
Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile Asp Trp Val Val Gly
                170                 175                 180

ctc cag gct ggt gta tca atg gct att tct gat gcg gca gac gct gcg   691
Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp Ala Ala Asp Ala Ala
            185                 190                 195

aac tca gaa gta aag atc gcc acc ttt gat aca aac gca cag ctc atg   739
Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr Asn Ala Gln Leu Met
        200                 205                 210

acc gct att cgt gat ggc aag atc caa ttc gcc att gat cag caa cca   787
Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala Ile Asp Gln Gln Pro
    215                 220                 225

tat ctg cag ggc tac atg gcc gtg gat tcg ctg tgg ttg gcg cac cga   835
Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu Trp Leu Ala His Arg
230                 235                 240                 245

aac ggc acc act gtt ggt ggc gga cga ccc gtg tac aca gga cca gcc   883
Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val Tyr Thr Gly Pro Ala
                250                 255                 260

att gtg gat gcc acc aac gtt gat gtc att gct gaa gcc gtt ggg gag   931
Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala Glu Ala Val Gly Glu
            265                 270                 275

ggt ctg cga tgacaaaaat caagagtggg gag                            963
Gly Leu Arg
        280
```

<210> 442
<211> 280
<212> PRT
<213> Corynebacterium glutamicum

<400> 442

```
Met Val Ser His Gly Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg
  1               5                  10                  15
```

```
Lys Gly Ala Glu Asp Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr
            20                  25                  30

Ser Ser Asn Pro Glu Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala
        35                  40                  45

Ile Asp Ser Arg Val Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln
    50                  55                  60

Ser Leu Gly Pro Val Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val
65                  70                  75                  80

Val Gly Leu Asn Ala Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr
                85                  90                  95

Gly Phe Phe Gly Gln Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala
            100                 105                 110

Arg Leu Ala Glu Glu Asn Ala Gln Lys Val Leu Cys Val Ile His Glu
        115                 120                 125

Gln Gly Asn Ser Ser Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly
    130                 135                 140

Leu Gly Lys Gln Val Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr
145                 150                 155                 160

Ser Val Asn Ser Thr Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile
                165                 170                 175

Asp Trp Val Val Gly Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp
            180                 185                 190

Ala Ala Asp Ala Ala Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr
        195                 200                 205

Asn Ala Gln Leu Met Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala
    210                 215                 220

Ile Asp Gln Gln Pro Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu
225                 230                 235                 240

Trp Leu Ala His Arg Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val
                245                 250                 255

Tyr Thr Gly Pro Ala Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala
            260                 265                 270

Glu Ala Val Gly Glu Gly Leu Arg
        275                 280
```

<210> 443
<211> 1482
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1459)

<223> RXN01569

<400> 443

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aaggcctaga gcagaccatc gattggtacc gcgaaaacga ggcctggtgg cgccctgcca 60

agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa   115
                                            Met Glu Tyr Gly Lys
                                              1               5

caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat   163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp
                  10                  15                  20

ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag   211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln
              25                  30                  35

cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa   259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln
          40                  45                  50

aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac   307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His
      55                  60                  65

gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc   355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe
  70                  75                  80                  85

gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc   403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val
                  90                  95                 100

gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt   451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly
             105                 110                 115

gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac   499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr
         120                 125                 130

ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac   547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn
     135                 140                 145

ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa   595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys
150                 155                 160                 165

gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc   643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg
                 170                 175                 180

aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc   691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg
             185                 190                 195

gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc   739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile
         200                 205                 210
```

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```
acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc   787
Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile
    215                 220                 225

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc   835
Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg
230                 235                 240                 245

gca gca gcg tgg gac atc aac gca gcg gca gtg gct aac ctc gcg acc   883
Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val Ala Asn Leu Ala Thr
                250                 255                 260

atc gcg cgc gac aac aac ctc acc ctc gtg cac gtg tcc tca gat tat   931
Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His Val Ser Ser Asp Tyr
            265                 270                 275

gtc ttc gac ggt gcg gcc gaa tcc tac gat gaa aac gca ccg ttt tcc   979
Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu Asn Ala Pro Phe Ser
        280                 285                 290

cca ctc ggc gtg tac ggc caa tcc aaa gca gcc ggc gac atc gga gac   1027
Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala Gly Asp Ile Gly Asp
    295                 300                 305

acc acc gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc   1075
Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly
310                 315                 320                 325

gat ggc aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc   1123
Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly
                330                 335                 340

atc gca cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc   1171
Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr
            345                 350                 355

gaa gac atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca   1219
Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala
        360                 365                 370

tat ggc acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc   1267
Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala
    375                 380                 385

gat gtt gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg   1315
Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val
390                 395                 400                 405

agc acc gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg   1363
Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu
                410                 415                 420

aac tcc gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca   1411
Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala
            425                 430                 435

ccg acc tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag   1459
Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
        440                 445                 450

tgaaaggcat catcctcgca ggt                                        1482
```

<210> 444
<211> 453
<212> PRT
<213> Corynebacterium glutamicum

<400> 444

```
Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly
  1               5                  10                  15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe
            20                  25                  30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
        35                  40                  45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
    50                  55                  60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
65                  70                  75                  80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
                85                  90                  95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
            100                 105                 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
        115                 120                 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
    130                 135                 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
145                 150                 155                 160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
                165                 170                 175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
            180                 185                 190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
        195                 200                 205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
    210                 215                 220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
225                 230                 235                 240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val
                245                 250                 255

Ala Asn Leu Ala Thr Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His
            260                 265                 270

Val Ser Ser Asp Tyr Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu
        275                 280                 285
```

```
Asn Ala Pro Phe Ser Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala
    290                 295                 300

Gly Asp Ile Gly Asp Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr
305                 310                 315                 320

Ser Trp Val Ile Gly Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser
                325                 330                 335

Leu Asp Glu Arg Gly Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly
            340                 345                 350

Arg Leu Ser Phe Thr Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu
        355                 360                 365

Glu Val Gly Ala Ala Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu
    370                 375                 380

Pro Ala Ser Trp Ala Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr
385                 390                 395                 400

Lys Val Thr Gly Val Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala
                405                 410                 415

Ala Pro Arg Pro Leu Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala
            420                 425                 430

Thr Gly Phe Ser Ala Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu
        435                 440                 445

Lys Glu Leu Ser Lys
    450
```

US 2005/0196848 A1

<210> 445
<211> 449
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(426)
<223> FRXA01569

<400> 445

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gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc gat ggc   48
Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly
  1               5                  10                  15

aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc atc gca   96
Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala
             20                  25                  30

cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc gaa gac  144
Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp
         35                  40                  45

atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca tat ggc  192
Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly
     50                  55                  60
```

```
acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc gat gtt   240
Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val
 65                  70                  75                  80

gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg agc acc   288
Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr
                85                  90                  95

gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg aac tcc   336
Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser
            100                 105                 110

gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca ccg acc   384
Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr
        115                 120                 125

tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag           426
Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
    130                 135                 140

tgaaaggcat catcctcgca ggt                                        449
```

<210> 446
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 446

```
Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly
  1               5                  10                  15

Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala
             20                  25                  30

Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp
         35                  40                  45

Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly
     50                  55                  60

Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val
 65                  70                  75                  80

Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr
                85                  90                  95

Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser
            100                 105                 110

Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr
        115                 120                 125

Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
    130                 135                 140
```

<210> 447
<211> 1028
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1021)
<223> FRXA02055

<400> 447
aaggcctaga gcagaccatc gattggtacc gcgaaaacga ggcctggtgg cgccctgcca 60

agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115
Met Glu Tyr Gly Lys
1 5

caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163
Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp
10 15 20

ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211
Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln
25 30 35

cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259
Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln
40 45 50

aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307
Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His
55 60 65

gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355
Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe
70 75 80 85

gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc 403
Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val
90 95 100

gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt 451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly
105 110 115

gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac 499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr
120 125 130

ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac 547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn
135 140 145

ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa 595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys
150 155 160 165

gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc 643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg
170 175 180

aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc 691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg
185 190 195

```
gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc   739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile
        200                 205                 210

acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc   787
Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile
    215                 220                 225

ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc   835
Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg
230                 235                 240                 245

gca gca gcg tgg gac att aac gca gcg gca gtg gct acc tcg cga cca   883
Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val Ala Thr Ser Arg Pro
                250                 255                 260

tcg cgc gcg aca aca acc tca ccc tcg tgc acg tgt cct cag att atg   931
Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr Cys Pro Gln Ile Met
            265                 270                 275

tct tcg acg gtg cgg gcg aat cct acg atg aaa acg cac cgt ttt ccc   979
Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys Thr His Arg Phe Pro
        280                 285                 290

cac tcg gcg tgt acg gcc aat cca aag cag ccg gcg aca tcg          1021
His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro Ala Thr Ser
    295                 300                 305

taagcac                                                         1028
```

<210> 448
<211> 307
<212> PRT
<213> Corynebacterium glutamicum

<400> 448

```
Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly
  1               5                  10                  15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe
            20                  25                  30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
        35                  40                  45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
    50                  55                  60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
65                  70                  75                  80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
                85                  90                  95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
            100                 105                 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
        115                 120                 125
```

09825.1.ST25

```
Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
    130                 135                 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
145                 150                 155                 160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
                165                 170                 175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
            180                 185                 190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
        195                 200                 205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
    210                 215                 220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
225                 230                 235                 240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val
                245                 250                 255

Ala Thr Ser Arg Pro Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr
            260                 265                 270

Cys Pro Gln Ile Met Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys
        275                 280                 285

Thr His Arg Phe Pro His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro
    290                 295                 300

Ala Thr Ser
305
```

US 2009/0298136 A1

<210> 449
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXA00825

<400> 449
cccgttcatg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60

```
tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt   115
                                              Met Arg Thr Val Val
                                                1               5

acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc   163
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile
                10                  15                  20

aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc   211
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg
```

```
            25                  30                  35

ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg   259
Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val
        40                  45                  50

gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac   307
Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His
    55                  60                  65

aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac   355
Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His
70                  75                  80                  85

tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc   403
Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr
                90                  95                  100

atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc   451
Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val
            105                 110                 115

ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca   499
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro
        120                 125                 130

gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc   547
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser
    135                 140                 145

aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc   595
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly
150                 155                 160                 165

tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa   643
Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln
                170                 175                 180

gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt   691
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu
            185                 190                 195

ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc   739
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg
        200                 205                 210

gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct   787
Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser
    215                 220                 225

ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa   835
Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu
230                 235                 240                 245

acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc   883
Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser
                250                 255                 260

aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc   931
Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg
            265                 270                 275
```

US 2006/0160090 A1

```
agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct   979
Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro
        280                 285                 290

gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc   1027
Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg
    295                 300                 305

act cac taggggaaaa tccaccacaa atc                                 1056
Thr His
310
```

<210> 450
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 450

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Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu
  1               5                  10                  15

Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn
             20                  25                  30

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly
         35                  40                  45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
     50                  55                  60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
 65                  70                  75                  80

Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
                 85                  90                  95

Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
            100                 105                 110

Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu
        115                 120                 125

Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
    130                 135                 140

Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
145                 150                 155                 160

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
                165                 170                 175

Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile
            180                 185                 190

Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp
        195                 200                 205

Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala
    210                 215                 220
```

```
Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile
225                 230                 235                 240

Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala
                245                 250                 255

Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu
            260                 265                 270

Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val
        275                 280                 285

Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr
    290                 295                 300

Val Glu Tyr Phe Arg Thr His
305                 310


<210> 451
<211> 1140
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1117)
<223> RXA02054

<400> 451
cctaatgaac agccggagca ccctggtcgt ttgcagaata ggcgcatcga caacagctac 60

taactctgcc agctcgcccg gacgaactaa ggtagacggc atg act tct ttg ctt   115
                                            Met Thr Ser Leu Leu
                                              1               5

gtg acc gga ggt gcc gga ttt atc ggc gcc aac ttc gtc cgc caa acc   163
Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn Phe Val Arg Gln Thr
                  10                  15                  20

gta gag cag cac cct gaa tac acc cac atc acg gtg ctg gat aaa ctc   211
Val Glu Gln His Pro Glu Tyr Thr His Ile Thr Val Leu Asp Lys Leu
              25                  30                  35

acc tac gca gga aac gcc gac aat ctc aaa ggc ctc ccc gac agc aaa   259
Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly Leu Pro Asp Ser Lys
          40                  45                  50

gta acc ctc atc gaa ggc gat atc tgc gat gct gaa tta gtc gac tcc   307
Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala Glu Leu Val Asp Ser
      55                  60                  65

ctg gtc aaa gac cac gac atc aca gtc cac ttc gca gca gaa tcc cac   355
Leu Val Lys Asp His Asp Ile Thr Val His Phe Ala Ala Glu Ser His
  70                  75                  80                  85

aac gac aac tcc ctc aac gac ccc tcc ccg ttt gtt cac act aac ctc   403
Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe Val His Thr Asn Leu
                  90                  95                 100
```

```
atc ggc acc ttt gtc ctg cta gaa gca gtc cgc aag cac aac aaa cgc   451
Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg Lys His Asn Lys Arg
            105                 110                 115

ttc cac cac atc tcc acc gat gaa gtc ttc ggc gat cta gag ctg gat   499
Phe His His Ile Ser Thr Asp Glu Val Phe Gly Asp Leu Glu Leu Asp
        120                 125                 130

gat cca aac cgc ttc act gaa acc acc gcc tac aag cca tcg tct cca   547
Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr Lys Pro Ser Ser Pro
    135                 140                 145

tat tct gca acc aag gca ggg tct gat cac ttg gta cac gca tgg atc   595
Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu Val His Ala Trp Ile
150                 155                 160                 165

cgc tcc ttc gga atc cag gca acc atg tct aac tgc tcc aac aat tac   643
Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn Cys Ser Asn Asn Tyr
                170                 175                 180

ggt ccc tac cag cac att gaa aag ttc atc ccc cgc cag atc acc aat   691
Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro Arg Gln Ile Thr Asn
            185                 190                 195

att ctg gcc ggc ctg aca cca aaa ctt tat gga acc ggc gag cag gtc   739
Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly Thr Gly Glu Gln Val
        200                 205                 210

cgc gac tgg atc cac gtc gat gat cac aat gac gcc gtc cac ctg atc   787
Arg Asp Trp Ile His Val Asp Asp His Asn Asp Ala Val His Leu Ile
    215                 220                 225

ctg agt aag ggc aag atc ggc gaa acc tac atc atc ggc gcc gac aac   835
Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile Ile Gly Ala Asp Asn
230                 235                 240                 245

gat cat gtg aat aac aag cag gtc atc gag ctt att tgt gaa ctc atg   883
Asp His Val Asn Asn Lys Gln Val Ile Glu Leu Ile Cys Glu Leu Met
                250                 255                 260

ggc ctc gac aaa aac gca tac gag cac gtc gca gac cgc ccc ggc cac   931
Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala Asp Arg Pro Gly His
            265                 270                 275

gat atg cgt tac gcc atg gat tcc acc aag ctg cgc acc gag ctc ggc   979
Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu Arg Thr Glu Leu Gly
        280                 285                 290

tgg gca cct aaa tac acc gac gtt gat tcc ggc atg cgc aaa ggc cta   1027
Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly Met Arg Lys Gly Leu
    295                 300                 305

gag cag acc atc gat tgg tac cgc gaa aac gag gcc tgg tgg cgc cct   1075
Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu Ala Trp Trp Arg Pro
310                 315                 320                 325

gcc aag aac aac gtc gaa gct acc tac gct aag cag gga caa           1117
Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys Gln Gly Gln
                330                 335

taatggaata cggtaaacaa ctc                                        1140
```

Sequence Listing

<210> 452
<211> 339
<212> PRT
<213> Corynebacterium glutamicum

<400> 452
Met Thr Ser Leu Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn
1 5 10 15

Phe Val Arg Gln Thr Val Glu Gln His Pro Glu Tyr Thr His Ile Thr
20 25 30

Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly
35 40 45

Leu Pro Asp Ser Lys Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala
50 55 60

Glu Leu Val Asp Ser Leu Val Lys Asp His Asp Ile Thr Val His Phe
65 70 75 80

Ala Ala Glu Ser His Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe
85 90 95

Val His Thr Asn Leu Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg
100 105 110

Lys His Asn Lys Arg Phe His His Ile Ser Thr Asp Glu Val Phe Gly
115 120 125

Asp Leu Glu Leu Asp Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr
130 135 140

Lys Pro Ser Ser Pro Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu
145 150 155 160

Val His Ala Trp Ile Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn
165 170 175

Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro
180 185 190

Arg Gln Ile Thr Asn Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly
195 200 205

Thr Gly Glu Gln Val Arg Asp Trp Ile His Val Asp Asp His Asn Asp
210 215 220

Ala Val His Leu Ile Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile
225 230 235 240

Ile Gly Ala Asp Asn Asp His Val Asn Asn Lys Gln Val Ile Glu Leu
245 250 255

Ile Cys Glu Leu Met Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala
260 265 270

Asp Arg Pro Gly His Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu
275 280 285

09252010

```
Arg Thr Glu Leu Gly Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly
    290                 295                 300

Met Arg Lys Gly Leu Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu
305                 310                 315                 320

Ala Trp Trp Arg Pro Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys
                325                 330                 335

Gln Gly Gln
```

<210> 453
<211> 909
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(886)
<223> RXN00427

<400> 453

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gcggtcattg tgacccacaa tcgtgtggaa ttgctgcggc attccctcga ggttgttgcc 60

aatcaaacct atccggtgaa acacattgtg gtggtggata atg ggg cgg atc cta   115
                                              Met Gly Arg Ile Leu
                                                1               5

gta ttc tat agt gtc act tta gag gtg gcg gga gac cgt ccc gtt tac   163
Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly Asp Arg Pro Val Tyr
                10                  15                  20

acg cct tcg cgc acc aat ttg ggc gac ggt ggc ggt ttt gct ttt ggt   211
Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly Gly Phe Ala Phe Gly
            25                  30                  35

ttt ttg acg gcg ttg gcg ctg ggg gcg aac gcg gtg tgg tgc aca gac   259
Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala Val Trp Cys Thr Asp
        40                  45                  50

gat gac ggc cgg ccg gag ggg cca ggg gtg ttg aag acg ctt atc gac   307
Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu Lys Thr Leu Ile Asp
    55                  60                  65

gcc gct tct cgg cat aat ctg gag gag gtt tct ccg gtg gta tgc aat   355
Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser Pro Val Val Cys Asn
70                  75                  80                  85

gct gat gat ccg gag cgg ttg gca ttt ccg ctg cgt cgg ggc ttg gag   403
Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu Arg Arg Gly Leu Glu
                90                  95                  100

tgg cgt cgg atg cgc agt gag ttg att gat cca gcc aac ccg gag gat   451
Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro Ala Asn Pro Glu Asp
            105                 110                 115

gat ttg ctg ccg ggc atc gcc tcc ttg ttc aat ggt gcc ctg atc agc   499
Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser
```

```
        120                 125                 130

gct tat gca atg gag cgc att ggc gtg ccg gac tat cga ctg ttt att   547
Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile
    135                 140                 145

cgc ggc gat gag gtg gag tat cac cgc cgt ttg gtg cgt tcc ggt ttg   595
Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu
150                 155                 160                 165

ccg ttt ggt acg tgt ttg acc acg gcg tat ttg cac ccg gat ggt tct   643
Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser
                170                 175                 180

gat gag ttc aag ccg att ctg ggt ggg cgg atg cat acg cag tat ccg   691
Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro
            185                 190                 195

gat aat gat ttc aag agg ttt ttc acc tac cgc aac cgt ggc tac ctg   739
Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu
        200                 205                 210

atg agc cag ccg gga atg cgc aag ctt ctc cct cag gaa tat gcg cgc   787
Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg
    215                 220                 225

ttt gcg tgg ttc ttc ctg gtt cag aaa cgg gat gtg aag gga ttc cgg   835
Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg
230                 235                 240                 245

gag tgg ctg cgc ctg cac aaa ctg ggc cgc gac gag aaa ttc aat agg   883
Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg
                250                 255                 260

ccc tagatcagtt ttagtagttc ctc                                    909
Pro
```

09825420.1

<210> 454
<211> 262
<212> PRT
<213> Corynebacterium glutamicum

<400> 454

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Met Gly Arg Ile Leu Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly
  1               5                  10                  15

Asp Arg Pro Val Tyr Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly
             20                  25                  30

Gly Phe Ala Phe Gly Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala
         35                  40                  45

Val Trp Cys Thr Asp Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu
     50                  55                  60

Lys Thr Leu Ile Asp Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser
 65                  70                  75                  80

Pro Val Val Cys Asn Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu
```

```
                85                  90                  95

Arg Arg Gly Leu Glu Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro
            100                 105                 110

Ala Asn Pro Glu Asp Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn
        115                 120                 125

Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp
    130                 135                 140

Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu
145                 150                 155                 160

Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu
                165                 170                 175

His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met
            180                 185                 190

His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg
        195                 200                 205

Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro
    210                 215                 220

Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp
225                 230                 235                 240

Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp
                245                 250                 255

Glu Lys Phe Asn Arg Pro
            260
```

09825120.3-2605

<210> 455
<211> 555
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(532)
<223> FRXA00427

<400> 455
tgctgatgat ccggagcggt tggcatttcc gctgcgtcgg ggcttggagt ggcgtcggat 60

gcgcagtgag ttgattgatc cagccaaccc ggaggatgat ttg ctg ccg ggc atc 115
                                              Leu Leu Pro Gly Ile
                                                1   5

gcc tcc ttg ttc aat ggt gcc ctg atc agc gct tat gca atg gag cgc 163
Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg
                10   15   20

att ggc gtg ccg gac tat cga ctg ttt att cgc ggc gat gag gtg gag 211
Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu
            25   30   35

```
tat cac cgc cgt ttg gtg cgt tcc ggt ttg ccg ttt ggt acg tgt ttg   259
Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu
         40                  45                  50

acc acg gcg tat ttg cac ccg gat ggt tct gat gag ttc aag ccg att   307
Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile
     55                  60                  65

ctg ggt ggg cgg atg cat acg cag tat ccg gat aat gat ttc aag agg   355
Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg
 70                  75                  80                  85

ttt ttc acc tac cgc aac cgt ggc tac ctg atg agc cag ccg gga atg   403
Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met
                 90                  95                 100

cgc aag ctt ctc cct cag gaa tat gcg cgc ttt gcg tgg ttc ttc ctg   451
Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu
            105                 110                 115

gtt cag aaa cgg gat gtg aag gga ttc cgg gag tgg ctg cgc ctg cac   499
Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His
        120                 125                 130

aaa ctg ggc cgc gac gag aaa ttc aat agg ccc tagatcagtt ttagtagttc 552
Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro
    135                 140

ctc                                                               555
```

09502120 - 09502120

<200> 456
<211> 144
<212> PRT
<213> Corynebacterium glutamicum

<400> 456

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Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala
  1               5                  10                  15

Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg
             20                  25                  30

Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro
         35                  40                  45

Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp
     50                  55                  60

Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp
 65                  70                  75                  80

Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met
                 85                  90                  95

Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe
            100                 105                 110

Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu
        115                 120                 125
```

```
Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro
    130                 135                 140
```

<210> 457
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> RXA00327

<400> 457

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aacgattttc gccgtcgcaa ccgtgatcac cggtcgcttt ccggcatcgt gtcgtcgcgg 60

ctaggggccc aggcgcggga tgattgggtt tgtcacgccg atg att cag gcg gcg   115
                                            Met Ile Gln Ala Ala
                                              1               5

ttg tgg atc gtg ctc ttt tta ttc gct gat cgc ctg tcc aat ccg ctg   163
Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg Leu Ser Asn Pro Leu
                 10                  15                  20

gtt ttt gtc agc gcc atc atg ttc gcg att tcc ttt agc tcc ccc gtg   211
Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser Phe Ser Ser Pro Val
             25                  30                  35

gcg aac ttc ggt ttc gat acg atc tgc gaa aaa ctc gac cgc cgc gtc   259
Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys Leu Asp Arg Arg Val
         40                  45                  50

atg gtc gcc ggc acc ggc atg gcc aac atg agc gcc tac att tgc gcg   307
Met Val Ala Gly Thr Gly Met Ala Asn Met Ser Ala Tyr Ile Cys Ala
     55                  60                  65

atg ctg gcc aca caa atc atc gga ttt tta ctc gac tgg aac gcc gac   355
Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu Asp Trp Asn Ala Asp
 70                  75                  80                  85

ggc cac gcc tac acc tgg tcg aat ttc cag gtg gcg tgg ctt ggt ctg   403
Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val Ala Trp Leu Gly Leu
                 90                  95                 100

ggc gcg gtg tgg ctg gca ggc atg atc ggg ctt gca gtc tgc ctc ctg   451
Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu Ala Val Cys Leu Leu
             105                 110                 115

ctg cag cgt cga aaa aat att gct ttt cga cgc taaaacccga ccgtaaccgc 504
Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg
         120                 125

tag                                                               507
```

<210> 458
<211> 128

<212> PRT
<213> Corynebacterium glutamicum

<400> 458
Met Ile Gln Ala Ala Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg
1 5 10 15

Leu Ser Asn Pro Leu Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser
20 25 30

Phe Ser Ser Pro Val Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys
35 40 45

Leu Asp Arg Arg Val Met Val Ala Gly Thr Gly Met Ala Asn Met Ser
50 55 60

Ala Tyr Ile Cys Ala Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu
65 70 75 80

Asp Trp Asn Ala Asp Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val
85 90 95

Ala Trp Leu Gly Leu Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu
100 105 110

Ala Val Cys Leu Leu Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg
115 120 125

<210> 459
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXA00328

<400> 459
gtcacgggat ttgttgtagc ccgactcaag ggtggaccgg gccgcagatt actcgcccag 60

attaggtcta ccaaggactt ttaaagatcg ggtaaaacct gtg ggc gtt gaa agg 115
Val Gly Val Glu Arg
1 5

ggc aag gtc tct gcc aag gca cta gtt gtc tgg ttg acg gca atg tgc 163
Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp Leu Thr Ala Met Cys
10 15 20

gtg tac atc gtg gcc att gct ggt cga aca tca ttt ggt gtc gcc gga 211
Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser Phe Gly Val Ala Gly
25 30 35

gtg cat gcg atc gat cgc ttt gat atc gac gcc tcc cgg ttg gcc gtg 259
Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala Ser Arg Leu Ala Val
40 45 50

```
ttc act tct gtt cag gtt gga gtc tat gtt ctc gcg cag att ccc atg   307
Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu Ala Gln Ile Pro Met
     55                  60                  65

ggc atg ctg gtg gac agg ttc gac gcc cgg aaa ctc ttg ctg gct ggc   355
Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys Leu Leu Leu Ala Gly
 70                  75                  80                  85

gct tta att ttg gca gct ggc cag ctc att ttg ggt ttc act gat tct   403
Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser
                 90                  95                 100

tat atg atc gcc att ttt gcc cga gtg ctc atc agt gtt ggc gat tct   451
Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile Ser Val Gly Asp Ser
            105                 110                 115

tct gca ttt ttg tcc gtg atg cga ctg ttg ccc aac tgg ttc ccg atg   499
Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro Asn Trp Phe Pro Met
        120                 125                 130

tct tgg aca cct gtg ttg cag cag ctc acg ggc gct ttt ggc ttt gtg   547
Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly Ala Phe Gly Phe Val
    135                 140                 145

ggg cag ttt tct ccg cgg tgc cgt ttt tgc aca tac tca aca cct       592
Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr Tyr Ser Thr Pro
150                 155                 160

tagggtggac aattcctttc gca                                       615
```

Sequence Listing

<210> 460
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 460

```
Val Gly Val Glu Arg Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp
  1               5                  10                  15

Leu Thr Ala Met Cys Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser
             20                  25                  30

Phe Gly Val Ala Gly Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala
         35                  40                  45

Ser Arg Leu Ala Val Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu
     50                  55                  60

Ala Gln Ile Pro Met Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys
 65                  70                  75                  80

Leu Leu Leu Ala Gly Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu
                 85                  90                  95

Gly Phe Thr Asp Ser Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile
            100                 105                 110

Ser Val Gly Asp Ser Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro
        115                 120                 125
```

```
Asn Trp Phe Pro Met Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly
    130                 135                 140

Ala Phe Gly Phe Val Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr
145                 150                 155                 160

Tyr Ser Thr Pro
```

<210> 461
<211> 1347
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1324)
<223> RXA00329

<400> 461

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tgtgaagaac aatgatcaac ggccttcgcc aagaccgcat cccagagaga aagtaactac 60

ccgcgccctc atagtttggg cagcagcctg tcttgtgtat atg gca gcc att acc   115
                                              Met Ala Ala Ile Thr
                                                1               5

agc cgc acc agc ttt ggt gtg gct gga gtg gag gcc att gat cgt ttt   163
Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu Ala Ile Asp Arg Phe
                10                  15                  20

cag gta gac gcc aca cgc att gca gta ttc act tct gtt cag gtt ggt   211
Gln Val Asp Ala Thr Arg Ile Ala Val Phe Thr Ser Val Gln Val Gly
            25                  30                  35

gtg tac gcg ttt gct cag att ccg atg ggc att ttg atc gat aag ttt   259
Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile Leu Ile Asp Lys Phe
        40                  45                  50

ggt cct cgg aag ctc ctt gcc att ggt gct ttg gtg atg ggt atc ggc   307
Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu Val Met Gly Ile Gly
    55                  60                  65

cag ctc att ttg ggc ttt acg gat agc tat tcc atc gcg att att gcc   355
Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser Ile Ala Ile Ile Ala
70                  75                  80                  85

cgc gtg ttt atc ggc gcc ggc gat gca tcg atc ttc ctt tcg gtt atg   403
Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile Phe Leu Ser Val Met
                90                  95                  100

cgc atc ctg ccg ttt tgg ttc cca ctg aag cac acc cct att ttc acg   451
Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His Thr Pro Ile Phe Thr
            105                 110                 115

cag tta act acc tgc ctt ggc cag ttg ggc cag ttc ttt tct gcg gtg   499
Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln Phe Phe Ser Ala Val
        120                 125                 130

cct ttc atg gcg ttg ttg ggt gcg cag ggt tgg cct gtg gcg ttt gtc   547
Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp Pro Val Ala Phe Val
```

```
    135                 140                 145

agc ctt ggt tcc gtg gtg gca ctc att gcg atc gca gcg ctg gtg gcc   595
Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile Ala Ala Leu Val Ala
150                 155                 160                 165

gtt cgg gat act cca gat cct cag cca aaa cct gtc gaa tca gct cag   643
Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro Val Glu Ser Ala Gln
                170                 175                 180

gaa gca gat aaa cca agc ctg cgc gcg agt ttg aag ttg att gtc cgc   691
Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu Lys Leu Ile Val Arg
            185                 190                 195

aat ccg att acg tgg cag ggt ttc ttc att cac tac gta ttg atg gtg   739
Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His Tyr Val Leu Met Val
        200                 205                 210

tgg cag acc gtg ttc tcc atg atg tgg ggc gtc ccg ctg atg act ttg   787
Trp Gln Thr Val Phe Ser Met Met Trp Gly Val Pro Leu Met Thr Leu
    215                 220                 225

ggc atg gga ctg tct gca acg acg gct ggt ttg gtg ttg agc atc aac   835
Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu Val Leu Ser Ile Asn
230                 235                 240                 245

acg ctg tgc atg gtg gta tcg gcg cca atc atc gga ata att tcc gca   883
Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile Gly Ile Ile Ser Ala
                250                 255                 260

cgc ctt ggg tat cgc cgt gac gtg gtc gcc att gcg ctg tcg ttt gtt   931
Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile Ala Leu Ser Phe Val
            265                 270                 275

caa tcc gca gta tgg ctg gtg ttc ttg gcc tcc gat gca cct cgt ggt   979
Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser Asp Ala Pro Arg Gly
        280                 285                 290

ttg atg gct atc atc ttg gtc aac atc gtc atg ggt ctg act act gcg  1027
Leu Met Ala Ile Ile Leu Val Asn Ile Val Met Gly Leu Thr Thr Ala
    295                 300                 305

gct tct ggt tat ggc ttt gac acc att cgt gag cgc cta gat cgc aag  1075
Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu Arg Leu Asp Arg Lys
310                 315                 320                 325

att ttg gct gcg ggc acg gga ctg gca aac atg ggt gga ttc ttg tca  1123
Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met Gly Gly Phe Leu Ser
                330                 335                 340

tcg atg gtt gca gcg cag gtt atg ggg ttc ctt ctt gat cac agc gcg  1171
Ser Met Val Ala Ala Gln Val Met Gly Phe Leu Leu Asp His Ser Ala
            345                 350                 355

cat ggt agc acc tat act tgg gtg gac ttc cgt ttt ggt ttc ctt gcg  1219
His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg Phe Gly Phe Leu Ala
        360                 365                 370

att ctt gtc aca tgg gcc gtc gga gtc acg gga ttt gtt gta gcc cga  1267
Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly Phe Val Val Ala Arg
    375                 380                 385
```

09852-0126

```
ctc aag ggt gga ccg ggc cgc aga tta ctc gcc cag att agg tct acc   1315
Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala Gln Ile Arg Ser Thr
390                 395                 400                 405

aag gac ttt taaagatcgg gtaaaacctg tgg                            1347
Lys Asp Phe
```

<210> 462
<211> 408
<212> PRT
<213> Corynebacterium glutamicum

<400> 462

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Met Ala Ala Ile Thr Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu
  1               5                  10                  15

Ala Ile Asp Arg Phe Gln Val Asp Ala Thr Arg Ile Ala Val Phe Thr
            20                  25                  30

Ser Val Gln Val Gly Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile
        35                  40                  45

Leu Ile Asp Lys Phe Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu
    50                  55                  60

Val Met Gly Ile Gly Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser
65                  70                  75                  80

Ile Ala Ile Ile Ala Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile
                85                  90                  95

Phe Leu Ser Val Met Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His
            100                 105                 110

Thr Pro Ile Phe Thr Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln
        115                 120                 125

Phe Phe Ser Ala Val Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp
    130                 135                 140

Pro Val Ala Phe Val Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile
145                 150                 155                 160

Ala Ala Leu Val Ala Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro
                165                 170                 175

Val Glu Ser Ala Gln Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu
            180                 185                 190

Lys Leu Ile Val Arg Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His
        195                 200                 205

Tyr Val Leu Met Val Trp Gln Thr Val Phe Ser Met Met Trp Gly Val
    210                 215                 220

Pro Leu Met Thr Leu Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu
225                 230                 235                 240
```

```
Val Leu Ser Ile Asn Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile
                245                 250                 255

Gly Ile Ile Ser Ala Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile
            260                 265                 270

Ala Leu Ser Phe Val Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser
        275                 280                 285

Asp Ala Pro Arg Gly Leu Met Ala Ile Ile Leu Val Asn Ile Val Met
    290                 295                 300

Gly Leu Thr Thr Ala Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu
305                 310                 315                 320

Arg Leu Asp Arg Lys Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met
                325                 330                 335

Gly Gly Phe Leu Ser Ser Met Val Ala Ala Gln Val Met Gly Phe Leu
            340                 345                 350

Leu Asp His Ser Ala His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg
        355                 360                 365

Phe Gly Phe Leu Ala Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly
    370                 375                 380

Phe Val Val Ala Arg Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala
385                 390                 395                 400

Gln Ile Arg Ser Thr Lys Asp Phe
                405
```

09625480 - 090502

<210> 463
<211> 2265
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2242)
<223> RXN01554

<400> 463

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tggcttaaac cttatttgta gttgtcaata aatatgaaat tccttagcaa cttgtttaaa 60

tagacgtata aacaagtttg aaaaaggaag gttatccatc ttg aaa aag cat gtg   115
                                            Leu Lys Lys His Val
                                              1               5

acc tca gcc gtt acc gcc gtg gtg acg gct ttt tca acg gct gcg ctt   163
Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe Ser Thr Ala Ala Leu
                 10                  15                  20

ggt tta agt att gcc gtt tct cct gct gtt gcc caa gtg gct aat cca   211
Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala Gln Val Ala Asn Pro
             25                  30                  35

gct cca gat ctt tct gcg ccg tat aca tgg gtg gaa gag ttt gat tcc   259
Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val Glu Glu Phe Asp Ser
```

```
         40                  45                  50

gag gat gct ctc aaa ggg tgg aac att ttc cgc cag cca gat tat ggc   307
Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg Gln Pro Asp Tyr Gly
     55                  60                  65

agc gac aaa gtt ctc tat acc gaa gat gct tta agt atc gaa gat ggc   355
Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu Ser Ile Glu Asp Gly
 70                  75                  80                  85

aag ctc acc atc acc act cag cgc cac tgc gtt gac gaa gac ttc gcg   403
Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val Asp Glu Asp Phe Ala
                 90                  95                 100

atc agt gat cct gtc aac cgc gga aag ctc aat gac agc acc gcg caa   451
Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn Asp Ser Thr Ala Gln
            105                 110                 115

gtt gaa cct tgt gct cca ggt cag ttt gaa aag ttc acc agt gcg cgc   499
Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys Phe Thr Ser Ala Arg
        120                 125                 130

atc gtc act ccg aaa att gct cgt gga gag ttc gac ctt tct gtc act   547
Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe Asp Leu Ser Val Thr
    135                 140                 145

gca act ctt aac acc ggt ggc gtc gaa ggt gtc cga agt gcc att tgg   595
Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val Arg Ser Ala Ile Trp
150                 155                 160                 165

atg caa aac ggt gaa cag gcg tgt tcc tca gca acc aac aat ggc ctc   643
Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala Thr Asn Asn Gly Leu
                170                 175                 180

tac gga gaa cta gac ctg gta gag cac ttt tct tac gat ctt cgc tcg   691
Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser Tyr Asp Leu Arg Ser
            185                 190                 195

cca tgg tct cca tca aac acc cac ttg ggt tgt gat cct gaa agt gtc   739
Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys Asp Pro Glu Ser Val
        200                 205                 210

aac ggc acc aac cgt gca cct cgt gaa ctt aaa cta gat gag tca ctc   787
Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys Leu Asp Glu Ser Leu
    215                 220                 225

gat ggc gtg gag cac acc tgg act gtg agc acc acc cgc gac ggc gtt   835
Asp Gly Val Glu His Thr Trp Thr Val Ser Thr Thr Arg Asp Gly Val
230                 235                 240                 245

gag tac ttc att gat gat gag gcg att aac cgc cag tca tgg cgc aac   883
Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg Gln Ser Trp Arg Asn
                250                 255                 260

gat gtc act ttg ggg cat gcc gaa att gat gat ttc ggg atc tcc gcg   931
Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp Phe Gly Ile Ser Ala
            265                 270                 275

cag acg ttt gat gag atc gtc gac cgc gaa tgg act ctc act ctt aat   979
Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp Thr Leu Thr Leu Asn
        280                 285                 290
```

```
caa aag gta gaa agc gcc gac tgg gca aaa cca cgt tcc tct gag gaa   1027
Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro Arg Ser Ser Glu Glu
    295                 300                 305

gat ttc cca gtc cgg tcc atg gtg att gac cgc atc gag gtc acc gga   1075
Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg Ile Glu Val Thr Gly
310                 315                 320                 325

tct ccc gca gta tct gaa gac acc ccc atg cca gat acc acc cag ctt   1123
Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro Asp Thr Thr Gln Leu
                330                 335                 340

ttg acc caa gac act ctg gaa tac ctc ggt cgc atg cca gtg ctg gaa   1171
Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg Met Pro Val Leu Glu
            345                 350                 355

cgc tac gag cca gca agt gct gat ttt gcc gat ggc cgc agg cct tcc   1219
Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp Gly Arg Arg Pro Ser
        360                 365                 370

tgg aac tac ttc aat ttg aag gaa tcg tgg cag aat cca gaa ctc gag   1267
Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln Asn Pro Glu Leu Glu
    375                 380                 385

caa cgc cca gaa gct gtc gaa ttc gtt gat gga cgc atg gat atc gtg   1315
Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly Arg Met Asp Ile Val
390                 395                 400                 405

acc cgt cgc cac tgt ctg gcc acc act gat gac atc gcc act ccg gaa   1363
Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp Ile Ala Thr Pro Glu
                410                 415                 420

aac gca cag gag gaa ccg tgc gcg ccg ggt gag gtg aca cgc tac agc   1411
Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser
            425                 430                 435

tca gcg cgt gtc cac ctt cca gag atc ccc gcc ggc aac ttc cgg ctc   1459
Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu
        440                 445                 450

acc gtg cgc gca cgg gcg cag tcc gaa gag ctt gtc gac ggc gtc cgc   1507
Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg
    455                 460                 465

ccc gct atc tgg atg cag aac aat acc aac ttc tgt gct gac aac gat   1555
Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp
470                 475                 480                 485

gga cgc cct tat ggt gaa ctg gat att act gag ttc tac agc tct cgt   1603
Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg
                490                 495                 500

gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc   1651
Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg
            505                 510                 515

cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg   1699
Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly
        520                 525                 530
```

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```
gat tgg cat gac tgg ggc gtc gaa gtc ttc gac ggc cag atc gta ttc   1747
Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe
    535                 540                 545

acc att gac ggc aag gca gta act tcc tct ggc aaa gat gtc ttt ggc   1795
Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly
550                 555                 560                 565

aac tct gtt acc cca gcc gct gca cct ctt cgc ccc gcg cac ttc aag   1843
Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg Pro Ala His Phe Lys
                570                 575                 580

ttg tcg gaa gag gaa tac cgt gaa gtc atc ggg cag cct tgg cac ctt   1891
Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly Gln Pro Trp His Leu
            585                 590                 595

att ttg aac acc atg gtg gag cag tct ggc aaa gac agc tgg att aca   1939
Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr
        600                 605                 610

gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac   1987
Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp
    615                 620                 625

cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct   2035
His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro
630                 635                 640                 645

gac gct gcg aat gaa atc cca gac aat gtt ggt att gaa gac tct gat   2083
Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp
                650                 655                 660

gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag   2131
Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu
            665                 670                 675

acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc   2179
Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe
        680                 685                 690

aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc   2227
Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe
    695                 700                 705

atg aga cag ttc aag taatccttgt gggcgctttg tct                    2265
Met Arg Gln Phe Lys
710
```

<210> 464
<211> 714
<212> PRT
<213> Corynebacterium glutamicum

<400> 464

```
Leu Lys Lys His Val Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe
  1               5                  10                  15

Ser Thr Ala Ala Leu Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala
             20                  25                  30
```

```
Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val
         35                  40                  45

Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg
     50                  55                  60

Gln Pro Asp Tyr Gly Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu
 65                  70                  75                  80

Ser Ile Glu Asp Gly Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val
                 85                  90                  95

Asp Glu Asp Phe Ala Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn
            100                 105                 110

Asp Ser Thr Ala Gln Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys
        115                 120                 125

Phe Thr Ser Ala Arg Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe
    130                 135                 140

Asp Leu Ser Val Thr Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val
145                 150                 155                 160

Arg Ser Ala Ile Trp Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala
                165                 170                 175

Thr Asn Asn Gly Leu Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser
            180                 185                 190

Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys
        195                 200                 205

Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys
    210                 215                 220

Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr
225                 230                 235                 240

Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg
                245                 250                 255

Gln Ser Trp Arg Asn Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp
            260                 265                 270

Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp
        275                 280                 285

Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro
    290                 295                 300

Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg
305                 310                 315                 320

Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro
                325                 330                 335

Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg
            340                 345                 350

Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp
```

```
        355                 360                 365

Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln
    370                 375                 380

Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly
385                 390                 395                 400

Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp
                405                 410                 415

Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu
            420                 425                 430

Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala
        435                 440                 445

Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu
    450                 455                 460

Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe
465                 470                 475                 480

Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu
                485                 490                 495

Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly
            500                 505                 510

Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu
        515                 520                 525

Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp
    530                 535                 540

Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly
545                 550                 555                 560

Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg
                565                 570                 575

Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly
            580                 585                 590

Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys
        595                 600                 605

Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His
    610                 615                 620

Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val
625                 630                 635                 640

Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly
                645                 650                 655

Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly
            660                 665                 670

Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu
        675                 680                 685
```

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```
Ser Ser Leu Val Phe Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn
    690                 695                 700

Leu Ile Asn Gln Phe Met Arg Gln Phe Lys
705                 710
```

<210> 465
<211> 389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(382)
<223> RXN03015

<400> 465

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ccgggtttgc ctgaggtttt ggagcgcaat ctggaaaatg gtcgcctgaa cttcactact 60

gattatgcgg aggctgcggc tttcgcgcag gtgcatttct ttg ggc gtg ggt act   115
                                              Leu Gly Val Gly Thr
                                                1               5

cct cag cag aag ggt act tat gcg gcg gat ctg acg tat gtt cgt cag   163
Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu Thr Tyr Val Arg Gln
               10                  15                  20

gtt gtt gag gat ttg gtg ccg ctg ctt gag ggc gag cac att att ttc   211
Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly Glu His Ile Ile Phe
           25                  30                  35

ggc aag tct acg gtt ccg gtt ggt act gct gag cag ttg cag gag ctt   259
Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu Gln Leu Gln Glu Leu
       40                  45                  50

gct gat tct ctg gtc aag cct ggt tcg cac gtg gag atc gcg tgg aat   307
Ala Asp Ser Leu Val Lys Pro Gly Ser His Val Glu Ile Ala Trp Asn
   55                  60                  65

ccg gag ttc ttg cgt gag ggc tac gcg gtc aaa gac acc atc act ccg   355
Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys Asp Thr Ile Thr Pro
70                  75                  80                  85

gac cgc atc gtg gtg ggt gtg cgt gaa taagaca                      389
Asp Arg Ile Val Val Gly Val Arg Glu
               90
```

<210> 466
<211> 94
<212> PRT
<213> Corynebacterium glutamicum

<400> 466

```
Leu Gly Val Gly Thr Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu
  1               5                  10                  15

Thr Tyr Val Arg Gln Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly
            20                  25                  30
```

```
Glu His Ile Ile Phe Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu
         35                  40                  45

Gln Leu Gln Glu Leu Ala Asp Ser Leu Val Lys Pro Gly Ser His Val
     50                  55                  60

Glu Ile Ala Trp Asn Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys
 65                  70                  75                  80

Asp Thr Ile Thr Pro Asp Arg Ile Val Val Gly Val Arg Glu
                 85                  90
```

<210> 467
<211> 801
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> RXN03056

<400> 467

```
ttactatcac tggttttgca gatgagatcg cacatgatct cgacgaacag atttccttac 60

ttaataaact gaagaacagc tcgcggaagc taaagccaaa ttg gat gcc gca gga   115
                                        Leu Asp Ala Ala Gly
                                          1               5

att tca ctt tca gcc gtt gga tcc gac ttc ggc aag atc aac atc acc   163
Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly Lys Ile Asn Ile Thr
                 10                  15                  20

gat cct ttt gaa gat cac ttg gag cgc gca cgc cac ggt gtt gag gtc   211
Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg His Gly Val Glu Val
             25                  30                  35

gct aag ctc ttc ggc gcg aaa tac atc cgc atg ttc tcc ttc ttt att   259
Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met Phe Ser Phe Phe Ile
         40                  45                  50

gca gaa ggc gac aac cct gaa agc ttc cgc aaa gaa gta ctc tcc cgc   307
Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys Glu Val Leu Ser Arg
     55                  60                  65

acc cac gca atg gtc gaa ctc gca gaa gcc ggc ggc atc acc ctc ctc   355
Thr His Ala Met Val Glu Leu Ala Glu Ala Gly Gly Ile Thr Leu Leu
 70                  75                  80                  85

cac gaa aat gaa aag gga atc tat ggc gac tcc ccg cag cgc gtg aag   403
His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser Pro Gln Arg Val Lys
                 90                  95                 100

gat tta atc acc agc atc gac tcc cct aac tac cgc gca atc tac gac   451
Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr Arg Ala Ile Tyr Asp
            105                 110                 115

gca gct aac tac gtg caa acc gga ttc aag cct ttt gat gag gca tgg   499
Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro Phe Asp Glu Ala Trp
```

```
        120                 125                 130

ccg atc gtt aag gac tac gtc gac tac gtc cac atc aag gac gcg acc   547
Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His Ile Lys Asp Ala Thr
    135                 140                 145

att cca gat gca gag cac ccc atc gga atc atc aag cca gca gga caa   595
Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile Lys Pro Ala Gly Gln
150                 155                 160                 165

ggc gac ggc caa tac cca gag ctc ctt gcc gcg cta aac gcc gac ggt   643
Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala Leu Asn Ala Asp Gly
                170                 175                 180

tac aac gga ttc gtc tcc atc gag cct cac ctg ggt gac ttc gat gaa   691
Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu Gly Asp Phe Asp Glu
            185                 190                 195

ttc ggc gga ctc tgc gga cct gac ctg tgg acc agc gca tgc gac gct   739
Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr Ser Ala Cys Asp Ala
        200                 205                 210

ctc gca gga atc ctg aac aac atc aac gcc gag tac aac taaggacaac   788
Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu Tyr Asn
    215                 220                 225

tgataatgac aaa                                                  801


<210> 468
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 468
Leu Asp Ala Ala Gly Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly
  1               5                  10                  15

Lys Ile Asn Ile Thr Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg
            20                  25                  30

His Gly Val Glu Val Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met
        35                  40                  45

Phe Ser Phe Phe Ile Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys
    50                  55                  60

Glu Val Leu Ser Arg Thr His Ala Met Val Glu Leu Ala Glu Ala Gly
65                  70                  75                  80

Gly Ile Thr Leu Leu His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser
                85                  90                  95

Pro Gln Arg Val Lys Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr
            100                 105                 110

Arg Ala Ile Tyr Asp Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro
        115                 120                 125

Phe Asp Glu Ala Trp Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His
    130                 135                 140
```

```
Ile Lys Asp Ala Thr Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile
145                 150                 155                 160

Lys Pro Ala Gly Gln Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala
                165                 170                 175

Leu Asn Ala Asp Gly Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu
            180                 185                 190

Gly Asp Phe Asp Glu Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr
        195                 200                 205

Ser Ala Cys Asp Ala Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu
    210                 215                 220

Tyr Asn
225
```

<210> 469
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXN03030

<400> 469
gaagatgaag cagaaaagat cattggtgcg ccagaggttt ctgcattggg caacaaagca 60

```
cagcttgatt ccgtcacctt gctgcgtaac aaccccatcc gtg ctg cca ctg gat   115
                                            Val Leu Pro Leu Asp
                                              1               5

cct gca gca agc ctg aag atc tac cca ttg gtt act ggc cgt acc aag   163
Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val Thr Gly Arg Thr Lys
                  10                  15                  20

atc gac gag gtt caa cta cag ctg gaa gca gcc att cgc gca gaa ctc   211
Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala Ile Arg Ala Glu Leu
              25                  30                  35

cca ggg gta acc ttg gtg tct tcc gag tca gaa gca gat ctt gca atc   259
Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu Ala Asp Leu Ala Ile
          40                  45                  50

gtg tgg gct cgc cct gaa att gca ctg ttt gaa gat gac ctc gaa ggt   307
Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu Asp Asp Leu Glu Gly
      55                  60                  65

gtt tcc ctc tct gtt gac cct cgt gcc aat ggt gtc gat gtg gaa cgc   355
Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly Val Asp Val Glu Arg
  70                  75                  80                  85

gtt cag gct gtg gaa gct gca gtc cca acc atc ttg gct gtg aac ttc   403
Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile Leu Ala Val Asn Phe
                  90                  95                 100
```

```
acc aac cct tgg gtg ctg tct gag atc gag cct ggt gcc gct gcc gtg   451
Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro Gly Ala Ala Ala Val
            105                 110                 115

gtg ggc act ttt gag atc aag cca gag ttc ctt ctc aag gct ttg act   499
Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu Leu Lys Ala Leu Thr
        120                 125                 130

ggt caa gag gga gga cca aag ggc aag ctg cca ttg act gtt cct gct   547
Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro Leu Thr Val Pro Ala
    135                 140                 145

tcc atg cag gcg att gct gat tcc cct cgc gat atc cca ggc aag ttc   595
Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp Ile Pro Gly Lys Phe
150                 155                 160                 165

ctc gat gag tct tac acc tac gtg gac tcc gca ggg atg gcc tac aag   643
Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala Gly Met Ala Tyr Lys
                170                 175                 180

tac ggt cac gga ctt aat ttc tagattgtag gtagtctcgt ggg             687
Tyr Gly His Gly Leu Asn Phe
            185
```

<210> 470
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 470

```
Val Leu Pro Leu Asp Pro Ala Ala Ser Leu Lys Ile Tyr Pro Leu Val
  1               5                  10                  15

Thr Gly Arg Thr Lys Ile Asp Glu Val Gln Leu Gln Leu Glu Ala Ala
            20                  25                  30

Ile Arg Ala Glu Leu Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu
        35                  40                  45

Ala Asp Leu Ala Ile Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu
    50                  55                  60

Asp Asp Leu Glu Gly Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly
65                  70                  75                  80

Val Asp Val Glu Arg Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile
                85                  90                  95

Leu Ala Val Asn Phe Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro
            100                 105                 110

Gly Ala Ala Ala Val Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu
        115                 120                 125

Leu Lys Ala Leu Thr Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro
    130                 135                 140

Leu Thr Val Pro Ala Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp
145                 150                 155                 160
```

```
Ile Pro Gly Lys Phe Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala
                165                 170                 175

Gly Met Ala Tyr Lys Tyr Gly His Gly Leu Asn Phe
            180                 185
```

<210> 471
<211> 1062
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1039)
<223> RXN00401

<400> 471

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cttttaagca tttcaacatg ccaaactaat cttggacagg tatcactggc tcctcttaga 60

ctccaaagtg tcttagaaaa cactcaccca aggagccctc atg gca cgc ttt tca   115
                                              Met Ala Arg Phe Ser
                                                1               5

cca caa gat ctc gca gac cac ctc aag gat gga ctg ctc tct ttc ccg   163
Pro Gln Asp Leu Ala Asp His Leu Lys Asp Gly Leu Leu Ser Phe Pro
                10                  15                  20

gcc acc gct ttc caa gat gac ctc gaa gta gat gaa gct gct tat gtc   211
Ala Thr Ala Phe Gln Asp Asp Leu Glu Val Asp Glu Ala Ala Tyr Val
            25                  30                  35

gag cac att gaa tgg cag tcc agc tac cca gtc gcc ggc ctc ttc gca   259
Glu His Ile Glu Trp Gln Ser Ser Tyr Pro Val Ala Gly Leu Phe Ala
        40                  45                  50

gct ggc ggt act ggc gaa gga ttc agc ctt acc gtt gag gaa aac cac   307
Ala Gly Gly Thr Gly Glu Gly Phe Ser Leu Thr Val Glu Glu Asn His
    55                  60                  65

cgt gtc act caa ctt gca gtt cag gcg tcc agc ccg gaa gtt ccc gtg   355
Arg Val Thr Gln Leu Ala Val Gln Ala Ser Ser Pro Glu Val Pro Val
70                  75                  80                  85

ttg ggg tct gct act ggc tca act aag tct gcc atc gca aac gca cag   403
Leu Gly Ser Ala Thr Gly Ser Thr Lys Ser Ala Ile Ala Asn Ala Gln
                90                  95                  100

ggc gca gag gca gca ggc gct gaa ggt gtc ctc ctg ctt cct ccc tac   451
Gly Ala Glu Ala Ala Gly Ala Glu Gly Val Leu Leu Leu Pro Pro Tyr
            105                 110                 115

ctc acc gaa tgc gac gca gaa ggc ctg tac aac cat gca gcc gca gtc   499
Leu Thr Glu Cys Asp Ala Glu Gly Leu Tyr Asn His Ala Ala Ala Val
        120                 125                 130

tgt gaa tcc act tct ctt ggt gtc atc gtg tac aac cgt gcc aat gcc   547
Cys Glu Ser Thr Ser Leu Gly Val Ile Val Tyr Asn Arg Ala Asn Ala
    135                 140                 145

atc tac tcc cca gag gtt atc gct cga ctc tct gag cgc tac ccc aac   595
```

```
Ile Tyr Ser Pro Glu Val Ile Ala Arg Leu Ser Glu Arg Tyr Pro Asn
150                 155                 160                 165

ttc att gga ttt aaa gat ggc acc gga aac atc gag cac cta gca aag   643
Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile Glu His Leu Ala Lys
                170                 175                 180

atc acc acg cta tgc gga gat cgc ctg ttc tac ctc ggt gga ctt ccc   691
Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr Leu Gly Gly Leu Pro
            185                 190                 195

acc gct gag acc ttt gca cta cca ctg ctt cag atg ggc atg agc acc   739
Thr Ala Glu Thr Phe Ala Leu Pro Leu Leu Gln Met Gly Met Ser Thr
        200                 205                 210

tac tcc tct gca atg ttc aac ttc att cca gat ttc gca ctg agc ttc   787
Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp Phe Ala Leu Ser Phe
    215                 220                 225

tac gcc gat gtt cgt gcg cag gac agc gca gca gta aag cag aag ctg   835
Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala Val Lys Gln Lys Leu
230                 235                 240                 245

agc gat ttt gtg ctc ccc tac ttg gat atc cgc gat cgc gca caa ggc   883
Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg Asp Arg Ala Gln Gly
                250                 255                 260

tac ggt gtc tcc att ggt aag ggc gga ctc aag gct gtt ggc cgc aac   931
Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys Ala Val Gly Arg Asn
            265                 270                 275

gct ggc ggc gtt cgc cca cca ctg cgt aac ctt tcc gag caa gat atc   979
Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu Ser Glu Gln Asp Ile
        280                 285                 290

gcg gac ctg tcg gat ttg ctt gcc acc tct ggc gca ggt tcc tac cgc   1027
Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly Ala Gly Ser Tyr Arg
    295                 300                 305

ctt cag ttg agg tgaaagcatg atcaccgcaa ccg                        1062
Leu Gln Leu Arg
310
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<210> 472
<211> 313
<212> PRT
<213> Corynebacterium glutamicum

<400> 472

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Met Ala Arg Phe Ser Pro Gln Asp Leu Ala Asp His Leu Lys Asp Gly
  1               5                  10                  15

Leu Leu Ser Phe Pro Ala Thr Ala Phe Gln Asp Asp Leu Glu Val Asp
             20                  25                  30

Glu Ala Ala Tyr Val Glu His Ile Glu Trp Gln Ser Ser Tyr Pro Val
         35                  40                  45

Ala Gly Leu Phe Ala Ala Gly Gly Thr Gly Glu Gly Phe Ser Leu Thr
     50                  55                  60
```

```
Val Glu Glu Asn His Arg Val Thr Gln Leu Ala Val Gln Ala Ser Ser
 65                  70                  75                  80

Pro Glu Val Pro Val Leu Gly Ser Ala Thr Gly Ser Thr Lys Ser Ala
                 85                  90                  95

Ile Ala Asn Ala Gln Gly Ala Glu Ala Ala Gly Ala Glu Gly Val Leu
            100                 105                 110

Leu Leu Pro Pro Tyr Leu Thr Glu Cys Asp Ala Glu Gly Leu Tyr Asn
        115                 120                 125

His Ala Ala Ala Val Cys Glu Ser Thr Ser Leu Gly Val Ile Val Tyr
    130                 135                 140

Asn Arg Ala Asn Ala Ile Tyr Ser Pro Glu Val Ile Ala Arg Leu Ser
145                 150                 155                 160

Glu Arg Tyr Pro Asn Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile
                165                 170                 175

Glu His Leu Ala Lys Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr
            180                 185                 190

Leu Gly Gly Leu Pro Thr Ala Glu Thr Phe Ala Leu Pro Leu Leu Gln
        195                 200                 205

Met Gly Met Ser Thr Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp
    210                 215                 220

Phe Ala Leu Ser Phe Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala
225                 230                 235                 240

Val Lys Gln Lys Leu Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg
                245                 250                 255

Asp Arg Ala Gln Gly Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys
            260                 265                 270

Ala Val Gly Arg Asn Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu
        275                 280                 285

Ser Glu Gln Asp Ile Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly
    290                 295                 300

Ala Gly Ser Tyr Arg Leu Gln Leu Arg
305                 310


<210> 473
<211> 924
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(901)
<223> RXN02125

<400> 473
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Doc No. 5650120

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gacctaaaat tcatcacctc accgttttta aggcttagaa aaatagcagt gttgggatgt 60

gaatatccat ttatgctgct gtagtcggct atgtggacgc atg gtg gca acc tct   115
                                            Met Val Ala Thr Ser
                                              1               5

cag ttt atc gat gac agc gag gct gcc cag gcg gta cgc gca gct att   163
Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala Val Arg Ala Ala Ile
                 10                  15                  20

gtt gca gga tac cga aac att gat act gcc cta gcg tat gga aac gag   211
Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu Ala Tyr Gly Asn Glu
             25                  30                  35

cgc ggc gtt ggc gaa ggc att cgc acc gct gga gtg ccc cgc gag gag   259
Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly Val Pro Arg Glu Glu
         40                  45                  50

ctc ttt att tcc acc aag cta gct gca gaa atc aaa gat tac gat gga   307
Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile Lys Asp Tyr Asp Gly
     55                  60                  65

gca gtc gcc gcg att gat gag tct ttg gcg aaa att ggc ttg gat tat   355
Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys Ile Gly Leu Asp Tyr
 70                  75                  80                  85

gtc gat ctg atg ctc att cac tcc cca caa cca tgg agt gat ttc cgt   403
Val Asp Leu Met Leu Ile His Ser Pro Gln Pro Trp Ser Asp Phe Arg
                 90                  95                 100

ggt ggg gac tat tca gag gga aac cgt gaa gcg tgg cgc gcg ctg gaa   451
Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala Trp Arg Ala Leu Glu
             105                 110                 115

gat gcc tac aaa gcc gga aag att cga tcc att ggt gtc tcg aac ttc   499
Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile Gly Val Ser Asn Phe
         120                 125                 130

ctg gag gcc gat ctg gag aat atc tta gac tcc gcg acg gtt gct cct   547
Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser Ala Thr Val Ala Pro
     135                 140                 145

cac gtt aat cag ctt ctt gtg cat gtt gga aac acc cca agc gag tta   595
His Val Asn Gln Leu Leu Val His Val Gly Asn Thr Pro Ser Glu Leu
 150                 155                 160                 165

atc agt ttc tgc gat tcc aag ggc att ctg gtc gaa gca tat tca ccc   643
Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val Glu Ala Tyr Ser Pro
                 170                 175                 180

atc gcc cac gga gag atg ctg aag aac cag cag gtc aag gcg att gct   691
Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln Val Lys Ala Ile Ala
             185                 190                 195

gac aag tac aac gtg agc att ccg cag cta tgc att cgg tac aca att   739
Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys Ile Arg Tyr Thr Ile
         200                 205                 210

caa ctg gga acg gtg tct ttg cca aag act gcc aac cca gat cat atg   787
Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala Asn Pro Asp His Met
     215                 220                 225
```

```
agc tcc aat gcg cag atc gac ttt gaa att tcc gag gaa gac atg gcg   835
Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser Glu Glu Asp Met Ala
230                 235                 240                 245

gca ctt caa gaa gtg acc gcc cgc gat tat ggc gag cac agc ggt ttt   883
Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly Glu His Ser Gly Phe
                250                 255                 260

cct gtg tat tcc ggc aag tagaaagatt tttatcatgg gac                924
Pro Val Tyr Ser Gly Lys
            265
```

<210> 474
<211> 267
<212> PRT
<213> Corynebacterium glutamicum

<400> 474

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Met Val Ala Thr Ser Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala
  1               5                  10                  15

Val Arg Ala Ala Ile Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu
            20                  25                  30

Ala Tyr Gly Asn Glu Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly
        35                  40                  45

Val Pro Arg Glu Glu Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile
    50                  55                  60

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys
65                  70                  75                  80

Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro
                85                  90                  95

Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala
            100                 105                 110

Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile
        115                 120                 125

Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser
    130                 135                 140

Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn
145                 150                 155                 160

Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val
                165                 170                 175

Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln
            180                 185                 190

Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys
        195                 200                 205

Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala
    210                 215                 220
```

```
Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser
225                 230                 235                 240

Glu Glu Asp Met Ala Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly
                245                 250                 255

Glu His Ser Gly Phe Pro Val Tyr Ser Gly Lys
            260                 265


<210> 475
<211> 3561
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3538)
<223> RXN00200

<400> 475
aacccggagt catttgatca gatgtggcag accaagcaag tgggaccttt cgtggtggta 60

acgcacaatg agtaattcct caccaaacga cccaagccct atg cgc caa gtc ggt   115
                                            Met Arg Gln Val Gly
                                              1               5

ggt aat ggg ggc cat caa cta gac tcg atc aac gtg tca gat gta gtt   163
Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn Val Ser Asp Val Val
                10                  15                  20

gag tcg aag aaa cta aag ggt tct gcg caa gaa ccc ccg cag gtt gcc   211
Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu Pro Pro Gln Val Ala
            25                  30                  35

ccg ggc tgg ctg aag aaa ctg gct atc tca tca ggt ctg ctt ggc ctg   259
Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser Gly Leu Leu Gly Leu
        40                  45                  50

ttg atg ttt gtg ctg ttg cct ttc ctg cca gtg aac cag gtg cag tct   307
Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val Asn Gln Val Gln Ser
    55                  60                  65

tcg ctg tca tgg cca caa aat ggt gag ctt tcc agc gtt aac gcc ccg   355
Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser Ser Val Asn Ala Pro
70                  75                  80                  85

ctg att tcc tac gca ccg cag tcg atg gat gcg tcc atc cct gtg tcc   403
Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala Ser Ile Pro Val Ser
                90                  95                  100

gcg ctg gac agt ctc aat gac aat cag tcg ttg gtg atg ggc acg ttg   451
Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu Val Met Gly Thr Leu
            105                 110                 115

cct ctg gac agt acg gac gcc acc aac cgt ggt ctg ttt gtg cgc acc   499
Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly Leu Phe Val Arg Thr
        120                 125                 130

atc gac ggt aac ctt gac gtg att gtt cgc ggt gag gtg ctg ttg gat   547
```

```
Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly Glu Val Leu Leu Asp
    135                 140                 145

ctt tca cca aca gag gtg aac cgt ctg cca gat gat gcg atc cta gag   595
Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp Asp Ala Ile Leu Glu
150                 155                 160                 165

att tcc tcc acc gag gaa acc acc agc gcg gaa atc acc ggc acg gca   643
Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu Ile Thr Gly Thr Ala
                170                 175                 180

ttc agc ggc gag acc gaa ggc gat gag cgg cct cag gtc acc ggc gtt   691
Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro Gln Val Thr Gly Val
            185                 190                 195

tac acc gag ctt gtc gac gac ccc tcc acc gca tcg gcc ctg gcc tca   739
Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala Ser Ala Leu Ala Ser
        200                 205                 210

gcg ggc tta aac gtt gat att gag atc aac tcc cgc ttc act tca tcc   787
Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser Arg Phe Thr Ser Ser
    215                 220                 225

ccc agc ctt cta aag tac gca gcc atc ttc att ggc ctt gcg tct gtg   835
Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile Gly Leu Ala Ser Val
230                 235                 240                 245

ttg gtc tcc ctg tgg aca ctg cac cgc atg gat att ttg gat ggt cga   883
Leu Val Ser Leu Trp Thr Leu His Arg Met Asp Ile Leu Asp Gly Arg
                250                 255                 260

aaa gca cac cgc ttc ctg cct gcc aac tgg tac aag ctg aag cca ctt   931
Lys Ala His Arg Phe Leu Pro Ala Asn Trp Tyr Lys Leu Lys Pro Leu
            265                 270                 275

gat ggt gtt gtc gta gcg att ttg gtg ttc tgg cac ttc ctt ggc gcc   979
Asp Gly Val Val Val Ala Ile Leu Val Phe Trp His Phe Leu Gly Ala
        280                 285                 290

aac acc tct gac gac ggc ttc atc atg acc atg gcc cgc gtg tcc cag   1027
Asn Thr Ser Asp Asp Gly Phe Ile Met Thr Met Ala Arg Val Ser Gln
    295                 300                 305

aac gcg gat tat atg gcc aac tac tac cgc tgg ttc ggt gtc cca gaa   1075
Asn Ala Asp Tyr Met Ala Asn Tyr Tyr Arg Trp Phe Gly Val Pro Glu
310                 315                 320                 325

tca cca ttc ggc gca cca tat tac gac ttg ctg gct ctg atg gcc tac   1123
Ser Pro Phe Gly Ala Pro Tyr Tyr Asp Leu Leu Ala Leu Met Ala Tyr
                330                 335                 340

atc tca acc tca tca atc tgg ctt cgt cta ccc gca ttg ctc gct gga   1171
Ile Ser Thr Ser Ser Ile Trp Leu Arg Leu Pro Ala Leu Leu Ala Gly
            345                 350                 355

ctg atc atg tgg ttc gtg atc acc aga gag gtc atg cca cgg ttt ggc   1219
Leu Ile Met Trp Phe Val Ile Thr Arg Glu Val Met Pro Arg Phe Gly
        360                 365                 370

tca ttg gtt aac ggt cgc cgc gtt gcg cac tgg tct gca gcc atg gtg   1267
Ser Leu Val Asn Gly Arg Arg Val Ala His Trp Ser Ala Ala Met Val
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```
    375                 380                 385

ttc ctg gcg ttc tgg ctt cca tac aac aac ggc act cgc cca gag cca   1315
Phe Leu Ala Phe Trp Leu Pro Tyr Asn Asn Gly Thr Arg Pro Glu Pro
390                 395                 400                 405

atc atc gcg atg gga gct cta ctt gcg tgg gtt tcc ttc gag cgc gct   1363
Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val Ser Phe Glu Arg Ala
                410                 415                 420

atc gct acc tcc agg ttg ttg ccc gct gcc att ggt gtc att atc gcc   1411
Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile Gly Val Ile Ile Ala
            425                 430                 435

acc att tcc ctg gca tca ggc ccc acc ggt cta atg gca gtt gct gcg   1459
Thr Ile Ser Leu Ala Ser Gly Pro Thr Gly Leu Met Ala Val Ala Ala
        440                 445                 450

ttg ctg gtc agt ttg tcc gcg ttg att cgc att ctt tat agg cgc ttg   1507
Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile Leu Tyr Arg Arg Leu
    455                 460                 465

ccg ctt att ggg gcg tcg agg ggg gcg tcg aaa agc aaa gtc ttt ggc   1555
Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys Ser Lys Val Phe Gly
470                 475                 480                 485

gct tcg atg gct atg ctt gcc cca ttc ctt gcg tct ggc acc gcg att   1603
Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala Ser Gly Thr Ala Ile
                490                 495                 500

ctc atc gcc gtt ttt ggc gat cag act ctg tca acc gtc atg gaa tcc   1651
Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser Thr Val Met Glu Ser
            505                 510                 515

atc agc gtg cgc tcc gcg aag ggc ccg gca ctg acc tgg tac cac gaa   1699
Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu Thr Trp Tyr His Glu
        520                 525                 530

tat gtg cgc tac caa acc gtc atg gaa caa acc gtt gat ggt tcc ttc   1747
Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr Val Asp Gly Ser Phe
    535                 540                 545

acc cgc cgt ttt gct gtg ctg atg ctc atg gcg tgt ctg gct att gtg   1795
Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala Cys Leu Ala Ile Val
550                 555                 560                 565

gtc atc gcg atc ctg cgt tac ggc cgc att cca ggc gct gcg aag gga   1843
Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro Gly Ala Ala Lys Gly
                570                 575                 580

cca tca ctg cgt ttg atg atg gtc att ttc ggc acc atg ttc ttc atg   1891
Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly Thr Met Phe Phe Met
            585                 590                 595

atg ttc acc cca acc aag tgg act cac cac ttc ggt gtc tac gca gga   1939
Met Phe Thr Pro Thr Lys Trp Thr His His Phe Gly Val Tyr Ala Gly
        600                 605                 610

ctt gcc ggc gca ttg gcc gga ctt gct gcc gtg ggg ctg tcc tat gtt   1987
Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val Gly Leu Ser Tyr Val
    615                 620                 625
```

US 2002/0164570 A1

```
gcg gtg aaa tca cca cgc atg cgc acc att tcc atc ggt gcg ttc ctc   2035
Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser Ile Gly Ala Phe Leu
630                 635                 640                 645

ttc ctg ctg gcg ctg gct ctc gca ggc gtg aac gga ttc tgg tac acc   2083
Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn Gly Phe Trp Tyr Thr
                650                 655                 660

tcc agc tac gcc gtg cca tgg tgg gat aaa acc atc cag atc aag ggc   2131
Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr Ile Gln Ile Lys Gly
            665                 670                 675

atc gaa gca tcc acc gta gtg ctc gtg atc gcc gtg atc gtg ctg atc   2179
Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala Val Ile Val Leu Ile
        680                 685                 690

atc ggt gtt att caa tcc ttt gtc cac gat gtg aaa acc gcg caa gcc   2227
Ile Gly Val Ile Gln Ser Phe Val His Asp Val Lys Thr Ala Gln Ala
    695                 700                 705

gaa acc aat cac tcc atg ggc gaa ctc gtg gcg gaa gat gaa gca aag   2275
Glu Thr Asn His Ser Met Gly Glu Leu Val Ala Glu Asp Glu Ala Lys
710                 715                 720                 725

cgc gag cgt gcc tcc agg ttc acc ggc ctt gcg gcc tcc cct atc gca   2323
Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala Ala Ser Pro Ile Ala
                730                 735                 740

gga gtg tcc gcc ctc gtt gtg ctg att acc tgc gca tcc atg ggc aaa   2371
Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys Ala Ser Met Gly Lys
            745                 750                 755

ggc ttt gtg gac caa tac ccc gcg tac tcc gtg ggt ctt ggc aac ctc   2419
Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val Gly Leu Gly Asn Leu
        760                 765                 770

cgc tcc ctg acc ggc aac aca tgt ggc ctt gcc tcc gac gcc atg ctg   2467
Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala Ser Asp Ala Met Leu
    775                 780                 785

gaa acc aac tcc aac gat tcc ttc ctc act cca gtg aac tcc aca ctt   2515
Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro Val Asn Ser Thr Leu
790                 795                 800                 805

ggc gag tcc ctg gaa tcc gaa gat att cgc ggc ttt agt gct gcc ggc   2563
Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly Phe Ser Ala Ala Gly
                810                 815                 820

atc cca cca tca atc agc cag gac caa gca gac ctg tct gct gtt ggt   2611
Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp Leu Ser Ala Val Gly
            825                 830                 835

gcc att gcc aac act gac gac tcc acc gaa acc ggc gga tcc gac gaa   2659
Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr Gly Gly Ser Asp Glu
        840                 845                 850

tca tcc gga caa tcc acc ggc aac acc ggc ggt gtc cga ggc tcc gaa   2707
Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly Val Arg Gly Ser Glu
    855                 860                 865
```

```
ggc atc aac ggc tcc aac gcc cgc ctg cca ttc aac ctg gac tac acc   2755
Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe Asn Leu Asp Tyr Thr
870                 875                 880                 885

caa gtt cca gtc gtc ggc tcc tgg tcc gct ggc acc caa aac cca gca   2803
Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly Thr Gln Asn Pro Ala
                890                 895                 900

aac atc acc acc gac tgg tac gaa atc cca gaa gcc acc gaa gaa gca   2851
Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu Ala Thr Glu Glu Ala
            905                 910                 915

ccc atc atc gtg gta tct gca gca ggt cgc atc gaa cac tac gac atc   2899
Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile Glu His Tyr Asp Ile
        920                 925                 930

aac ggc gtc cgc caa tcc gga caa tcc gtc atg ctc gaa tac ggt cgc   2947
Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met Leu Glu Tyr Gly Arg
    935                 940                 945

ctt cgc gat aac ggc gac gtt gaa gac ctc ggc gaa gcc atg atg tac   2995
Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly Glu Ala Met Met Tyr
950                 955                 960                 965

gac atc ggc ccc gag cca tcc tgg cgc aac ctc cgc tac cca ctt gac   3043
Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu Arg Tyr Pro Leu Asp
                970                 975                 980

caa ctc cca gaa gaa gcg gac gtc gtg cgc atc gtc gcc acc gac gtc   3091
Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile Val Ala Thr Asp Val
            985                 990                 995

aac ctc gac gaa gac caa tgg gta gca ctg acg cca cca cgc gta cct   3139
Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr Pro Pro Arg Val Pro
        1000                1005                1010

aac cta gat tct ctg aac aac gtc atc gga tcc gaa acc cca gga ctc   3187
Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser Glu Thr Pro Gly Leu
    1015                1020                1025

ctc gac tgg gca gtt ggc ctg caa ttc cca tgc caa cgc acc ttc gac   3235
Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys Gln Arg Thr Phe Asp
1030                1035                1040                1045

cac tac gcc gga gtc acc gag att cct gaa tac cga atc tcc cca gac   3283
His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp
                1050                1055                1060

cac ggc gga aaa tcc acc ctc tcc cca ttc caa gac tgg gca ggc ggc   3331
His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly
            1065                1070                1075

gga tcc atg ggc acg gcc gaa gca gta aac aac gcc tac gaa atc ccg   3379
Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro
        1080                1085                1090

tcc tac ctc cgc aac gac tgg ggc cgc gac tgg ggt tcc atc gaa cgc   3427
Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg
    1095                1100                1105

tac tcg ctg cgc acc aac tcc aac ggc gat gca cct aag gtt gca gac   3475
```

```
Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp
1110                1115                1120                1125

atc aac ctt gaa acc atc caa cgt tcc gga ctc tgg aat cca ggg cat   3523
Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His
               1130                1135                1140

atg aag gta gat gaa taagaccttc agtactggaa gtt                     3561
Met Lys Val Asp Glu
           1145
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<210> 476
<211> 1146
<212> PRT
<213> Corynebacterium glutamicum

<400> 476

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Met Arg Gln Val Gly Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn
  1               5                  10                  15

Val Ser Asp Val Val Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu
            20                  25                  30

Pro Pro Gln Val Ala Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser
        35                  40                  45

Gly Leu Leu Gly Leu Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val
    50                  55                  60

Asn Gln Val Gln Ser Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser
65                  70                  75                  80

Ser Val Asn Ala Pro Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala
                85                  90                  95

Ser Ile Pro Val Ser Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu
            100                 105                 110

Val Met Gly Thr Leu Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly
        115                 120                 125

Leu Phe Val Arg Thr Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly
    130                 135                 140

Glu Val Leu Leu Asp Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp
145                 150                 155                 160

Asp Ala Ile Leu Glu Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu
                165                 170                 175

Ile Thr Gly Thr Ala Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro
            180                 185                 190

Gln Val Thr Gly Val Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala
        195                 200                 205

Ser Ala Leu Ala Ser Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser
    210                 215                 220

Arg Phe Thr Ser Ser Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile
```

225 230 235 240

Gly Leu Ala Ser Val Leu Val Ser Leu Trp Thr Leu His Arg Met Asp
245 250 255

Ile Leu Asp Gly Arg Lys Ala His Arg Phe Leu Pro Ala Asn Trp Tyr
260 265 270

Lys Leu Lys Pro Leu Asp Gly Val Val Val Ala Ile Leu Val Phe Trp
275 280 285

His Phe Leu Gly Ala Asn Thr Ser Asp Asp Gly Phe Ile Met Thr Met
290 295 300

Ala Arg Val Ser Gln Asn Ala Asp Tyr Met Ala Asn Tyr Tyr Arg Trp
305 310 315 320

Phe Gly Val Pro Glu Ser Pro Phe Gly Ala Pro Tyr Tyr Asp Leu Leu
325 330 335

Ala Leu Met Ala Tyr Ile Ser Thr Ser Ser Ile Trp Leu Arg Leu Pro
340 345 350

Ala Leu Leu Ala Gly Leu Ile Met Trp Phe Val Ile Thr Arg Glu Val
355 360 365

Met Pro Arg Phe Gly Ser Leu Val Asn Gly Arg Arg Val Ala His Trp
370 375 380

Ser Ala Ala Met Val Phe Leu Ala Phe Trp Leu Pro Tyr Asn Asn Gly
385 390 395 400

Thr Arg Pro Glu Pro Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val
405 410 415

Ser Phe Glu Arg Ala Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile
420 425 430

Gly Val Ile Ile Ala Thr Ile Ser Leu Ala Ser Gly Pro Thr Gly Leu
435 440 445

Met Ala Val Ala Ala Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile
450 455 460

Leu Tyr Arg Arg Leu Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys
465 470 475 480

Ser Lys Val Phe Gly Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala
485 490 495

Ser Gly Thr Ala Ile Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser
500 505 510

Thr Val Met Glu Ser Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu
515 520 525

Thr Trp Tyr His Glu Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr
530 535 540

Val Asp Gly Ser Phe Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala
545 550 555 560

09209.00209

Cys Leu Ala Ile Val Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro
565 570 575

Gly Ala Ala Lys Gly Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly
580 585 590

Thr Met Phe Phe Met Met Phe Thr Pro Thr Lys Trp Thr His His Phe
595 600 605

Gly Val Tyr Ala Gly Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val
610 615 620

Gly Leu Ser Tyr Val Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser
625 630 635 640

Ile Gly Ala Phe Leu Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn
645 650 655

Gly Phe Trp Tyr Thr Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr
660 665 670

Ile Gln Ile Lys Gly Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala
675 680 685

Val Ile Val Leu Ile Ile Gly Val Ile Gln Ser Phe Val His Asp Val
690 695 700

Lys Thr Ala Gln Ala Glu Thr Asn His Ser Met Gly Glu Leu Val Ala
705 710 715 720

Glu Asp Glu Ala Lys Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala
725 730 735

Ala Ser Pro Ile Ala Gly Val Ser Ala Leu Val Val Leu Ile Thr Cys
740 745 750

Ala Ser Met Gly Lys Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val
755 760 765

Gly Leu Gly Asn Leu Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala
770 775 780

Ser Asp Ala Met Leu Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro
785 790 795 800

Val Asn Ser Thr Leu Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly
805 810 815

Phe Ser Ala Ala Gly Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp
820 825 830

Leu Ser Ala Val Gly Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr
835 840 845

Gly Gly Ser Asp Glu Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly
850 855 860

Val Arg Gly Ser Glu Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe
865 870 875 880

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Asn Leu Asp Tyr Thr Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly
                885                 890                 895

Thr Gln Asn Pro Ala Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu
            900                 905                 910

Ala Thr Glu Glu Ala Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile
        915                 920                 925

Glu His Tyr Asp Ile Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met
    930                 935                 940

Leu Glu Tyr Gly Arg Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly
945                 950                 955                 960

Glu Ala Met Met Tyr Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu
                965                 970                 975

Arg Tyr Pro Leu Asp Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile
            980                 985                 990

Val Ala Thr Asp Val Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr
        995                 1000                1005

Pro Pro Arg Val Pro Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser
    1010                1015                1020

Glu Thr Pro Gly Leu Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys
1025                1030                1035                1040

Gln Arg Thr Phe Asp His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr
                1045                1050                1055

Arg Ile Ser Pro Asp His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln
            1060                1065                1070

Asp Trp Ala Gly Gly Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn
        1075                1080                1085

Ala Tyr Glu Ile Pro Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp
    1090                1095                1100

Gly Ser Ile Glu Arg Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala
1105                1110                1115                1120

Pro Lys Val Ala Asp Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu
                1125                1130                1135

Trp Asn Pro Gly His Met Lys Val Asp Glu
            1140                1145


<210> 477
<211> 1509
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1486)
<223> RXN01175
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tcgcgtctct tagtcgatct gctcccattc cataggttgg gagaaaactt aactgttatt 60

ccattcctta aaacaccgat atcgtgctat gaataggggt gtg agt tgg aca gtt 115
Val Ser Trp Thr Val
1 5

gat atc cct aaa gaa gtt ctc cct gat ttg cca cca ttg cca gaa ggc 163
Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro Pro Leu Pro Glu Gly
10 15 20

atg cag cag cag ttc gag gac acc att tcc cgt gac gct aag cag caa 211
Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg Asp Ala Lys Gln Gln
25 30 35

cct acg tgg gat cgt gca cag gca gaa aac gtg cgc aag atc ctt gag 259
Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val Arg Lys Ile Leu Glu
40 45 50

tcg gtt cct cca atc gtt gtt gcc cct gag gta ctt gag ctg aag cag 307
Ser Val Pro Pro Ile Val Val Ala Pro Glu Val Leu Glu Leu Lys Gln
55 60 65

aag ctt gct gat gtt gcc aac ggt aag gcc ttc ctc ttg cag ggt ggt 355
Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe Leu Leu Gln Gly Gly
70 75 80 85

gac tgt gcg gaa act ttc gag tca aac act gag ccg cac att cgc gcc 403
Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu Pro His Ile Arg Ala
90 95 100

aac gta aag act ctg ctg cag atg gca gtt gtt ttg acc tac ggt gca 451
Asn Val Lys Thr Leu Leu Gln Met Ala Val Val Leu Thr Tyr Gly Ala
105 110 115

tcc act cct gtg atc aag atg gct cgt att gct ggt cag tac gca aag 499
Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala Gly Gln Tyr Ala Lys
120 125 130

cct cgc tct tct gat ctg gat gga aat ggt ctg cca aac tac cgt ggc 547
Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu Pro Asn Tyr Arg Gly
135 140 145

gat atc gtc aac ggt gtg gag gca acc cca gag gct cgt cgc cac gat 595
Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu Ala Arg Arg His Asp
150 155 160 165

cct gcc cgc atg atc cgt gct tac gct aac gct tct gct gcg atg aac 643
Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala Ser Ala Ala Met Asn
170 175 180

ttg gtg cgc gcg ctc acc agc tct ggc acc gct gat ctt tac cgt ctc 691
Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala Asp Leu Tyr Arg Leu
185 190 195

agc gag tgg aac cgc gag ttc gtt gcg aac tcc cca gct ggt gca cgc 739
Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser Pro Ala Gly Ala Arg
200 205 210

tac gag gct ctt gct cgt gag atc gac tcc ggt ctg cgc ttc atg gaa 787

```
Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly Leu Arg Phe Met Glu
    215                 220                 225

gca tgt ggc gtg tcc gat gag tcc ctg cgt gct gca gat atc tac tgc   835
Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala Ala Asp Ile Tyr Cys
230                 235                 240                 245

tcc cac gag gct ttg ctg gtg gat tac gag cgt tcc atg ctg cgt ctt   883
Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg Ser Met Leu Arg Leu
                250                 255                 260

gca acc gat gag gaa ggc aac gag gaa ctt tac gat ctt tca gct cac   931
Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr Asp Leu Ser Ala His
            265                 270                 275

cag ctg tgg atc ggc gag cgc acc cgt ggc atg gat gat ttc cat gtg   979
Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met Asp Asp Phe His Val
        280                 285                 290

aac ttc gca tcc atg atc tct aac cca atc ggc atc aag att ggt cct   1027
Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly Ile Lys Ile Gly Pro
    295                 300                 305

ggt atc acc cct gaa gag gct gtt gca tac gct gac aag ctc gat ccg   1075
Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala Asp Lys Leu Asp Pro
310                 315                 320                 325

aac ttc gag cct ggc cgt ttg acc atc gtt gct cgc atg ggc cac gac   1123
Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala Arg Met Gly His Asp
                330                 335                 340

aag gtt cgc tcc gta ctt cct ggt gtt atc cag gct gtt gag gca tcc   1171
Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln Ala Val Glu Ala Ser
            345                 350                 355

gga cac aag gtt att tgg cag tcc gat ccg atg cac ggc aac act ttc   1219
Gly His Lys Val Ile Trp Gln Ser Asp Pro Met His Gly Asn Thr Phe
        360                 365                 370

acc gca tcc aat ggc tac aag acc cgt cac ttc gac aag gtt atc gat   1267
Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe Asp Lys Val Ile Asp
    375                 380                 385

gag gtc cag ggc ttc ttc gag gtc cac cgc gca ttg ggc acc cac cca   1315
Glu Val Gln Gly Phe Phe Glu Val His Arg Ala Leu Gly Thr His Pro
390                 395                 400                 405

ggc gga atc cac att gag ttc act ggt gaa gat gtc acc gag tgc ctc   1363
Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp Val Thr Glu Cys Leu
                410                 415                 420

ggt ggc gct gaa gac atc acc gat gtt gat ctg cca ggc cgc tac gag   1411
Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu Pro Gly Arg Tyr Glu
            425                 430                 435

tcc gca tgc gat cct cgc ctg aac act cag cag tct ttg gag ttg gct   1459
Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln Ser Leu Glu Leu Ala
        440                 445                 450

ttc ctc gtt gca gaa atg ctg cgt aac taagctttta gaccaactct         1506
Phe Leu Val Ala Glu Met Leu Arg Asn
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455 460

aaa 1509

<210> 478
<211> 462
<212> PRT
<213> Corynebacterium glutamicum

<400> 478

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Val Ser Trp Thr Val Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro
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Pro Leu Pro Glu Gly Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg
            20                  25                  30

Asp Ala Lys Gln Gln Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val
        35                  40                  45

Arg Lys Ile Leu Glu Ser Val Pro Pro Ile Val Val Ala Pro Glu Val
    50                  55                  60

Leu Glu Leu Lys Gln Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe
65                  70                  75                  80

Leu Leu Gln Gly Gly Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu
                85                  90                  95

Pro His Ile Arg Ala Asn Val Lys Thr Leu Leu Gln Met Ala Val Val
            100                 105                 110

Leu Thr Tyr Gly Ala Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala
        115                 120                 125

Gly Gln Tyr Ala Lys Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu
    130                 135                 140

Pro Asn Tyr Arg Gly Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu
145                 150                 155                 160

Ala Arg Arg His Asp Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala
                165                 170                 175

Ser Ala Ala Met Asn Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala
            180                 185                 190

Asp Leu Tyr Arg Leu Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser
        195                 200                 205

Pro Ala Gly Ala Arg Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly
    210                 215                 220

Leu Arg Phe Met Glu Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala
225                 230                 235                 240

Ala Asp Ile Tyr Cys Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg
                245                 250                 255

Ser Met Leu Arg Leu Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr
            260                 265                 270
```

```
Asp Leu Ser Ala His Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met
        275                 280                 285

Asp Asp Phe His Val Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly
    290                 295                 300

Ile Lys Ile Gly Pro Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala
305                 310                 315                 320

Asp Lys Leu Asp Pro Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala
                325                 330                 335

Arg Met Gly His Asp Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln
            340                 345                 350

Ala Val Glu Ala Ser Gly His Lys Val Ile Trp Gln Ser Asp Pro Met
        355                 360                 365

His Gly Asn Thr Phe Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe
    370                 375                 380

Asp Lys Val Ile Asp Glu Val Gln Gly Phe Phe Glu Val His Arg Ala
385                 390                 395                 400

Leu Gly Thr His Pro Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp
                405                 410                 415

Val Thr Glu Cys Leu Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu
            420                 425                 430

Pro Gly Arg Tyr Glu Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln
        435                 440                 445

Ser Leu Glu Leu Ala Phe Leu Val Ala Glu Met Leu Arg Asn
    450                 455                 460


<210> 479
<211> 984
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(961)
<223> RXN01376

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cttcgtgagt actttgaaat cccccatcgc tgtgatcaca gtg acc tat tca cca   115
                                            Val Thr Tyr Ser Pro
                                              1               5

ggt aaa tac ttg gcg tcg ttc ctg gat tct ttg cct ggt gcg act tca   163
Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu Pro Gly Ala Thr Ser
                  10                  15                  20

cga gac acc cac gtt gtg atg gca gac aat ggt tct gtg gac ggt gtt   211
Arg Asp Thr His Val Val Met Ala Asp Asn Gly Ser Val Asp Gly Val
```

```
            25                  30                  35

cct gag cag gca gca gcc tca cgc agc aac gtg gag ttc ctc tca act   259
Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val Glu Phe Leu Ser Thr
        40                  45                  50

ggc ggc aac tta ggc tac gga acg gct att aat att gcc gcc cga tcg   307
Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn Ile Ala Ala Arg Ser
    55                  60                  65

ttg cgt gcg cgc cgg gag gca gga gag atc gat ggg gag ttc ttc ctc   355
Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp Gly Glu Phe Phe Leu
70                  75                  80                  85

gtc tca aac cct gat gtt gtt ttt gac gaa gac tct att gat caa ttg   403
Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp Ser Ile Asp Gln Leu
                90                  95                  100

ctt gaa tgt gcg aaa cgt cac cct gaa gca gga gcg gtt ggc ccg ttg   451
Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly Ala Val Gly Pro Leu
            105                 110                 115

atc cgt gag gcg gac ggt tcg gcg tat ccg tcg gct cgg gcg gta ccc   499
Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser Ala Arg Ala Val Pro
        120                 125                 130

act ttg gcg aat ggc att ggt cac gct ttg ttg ggt gct gtg tgg aaa   547
Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu Gly Ala Val Trp Lys
    135                 140                 145

tcc aat ccg tgg tcg gcg gct tac cgt gac gat gaa gat atg gac act   595
Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp Glu Asp Met Asp Thr
150                 155                 160                 165

gag cgc act gct ggc tgg ctg tcg gga tcg tgc ctg tta tta agg tgg   643
Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys Leu Leu Leu Arg Trp
                170                 175                 180

gat gcg ttt gat cga gtt ggt ggt ttt gat gag cgc tac ttc atg tac   691
Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu Arg Tyr Phe Met Tyr
            185                 190                 195

atg gaa gac gtt gac ctg gga gat cgg ctg gtt cgc gcc ggt ttc acc   739
Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val Arg Ala Gly Phe Thr
        200                 205                 210

aac gtc ttt tgc cca agt gcg cag atc atc cac gcg aaa ggt cat gtt   787
Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His Ala Lys Gly His Val
    215                 220                 225

gcg ggt aaa aac cca gag aac atg ttg ccc gca cac cac gag agc gcg   835
Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala His His Glu Ser Ala
230                 235                 240                 245

tat cgc ttc cag gct gat cgc ctc gcg aag ccg tgg caa gcc cca att   883
Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro Trp Gln Ala Pro Ile
                250                 255                 260

cgg ttg gct ctg cga att ggt ttg aaa tta cga gcc gga gtc gcg gtt   931
Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg Ala Gly Val Ala Val
            265                 270                 275
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ggt gtc tct aag atg aga acg aaa gcc tct tagaccgtcg acgaccaccg 981
Gly Val Ser Lys Met Arg Thr Lys Ala Ser
280 285

gac 984

<210> 480
<211> 287
<212> PRT
<213> Corynebacterium glutamicum

<400> 480
Val Thr Tyr Ser Pro Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu
1 5 10 15

Pro Gly Ala Thr Ser Arg Asp Thr His Val Val Met Ala Asp Asn Gly
20 25 30

Ser Val Asp Gly Val Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val
35 40 45

Glu Phe Leu Ser Thr Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn
50 55 60

Ile Ala Ala Arg Ser Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp
65 70 75 80

Gly Glu Phe Phe Leu Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp
85 90 95

Ser Ile Asp Gln Leu Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly
100 105 110

Ala Val Gly Pro Leu Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser
115 120 125

Ala Arg Ala Val Pro Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu
130 135 140

Gly Ala Val Trp Lys Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp
145 150 155 160

Glu Asp Met Asp Thr Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys
165 170 175

Leu Leu Leu Arg Trp Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu
180 185 190

Arg Tyr Phe Met Tyr Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val
195 200 205

Arg Ala Gly Phe Thr Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His
210 215 220

Ala Lys Gly His Val Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala
225 230 235 240

His His Glu Ser Ala Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro
245 250 255

```
Trp Gln Ala Pro Ile Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg
            260                 265                 270

Ala Gly Val Ala Val Gly Val Ser Lys Met Arg Thr Lys Ala Ser
        275                 280                 285


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<211> 1002
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(979)
<223> RXN01631

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caaccagggc atttccgtaa acatctaaga ggagcactcc atg aaa cca caa ctt   115
                                              Met Lys Pro Gln Leu
                                                1               5

att gca tct tgc tgg acc agc gcg gga gac gcc gca ccc gat cgt gac   163
Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala Ala Pro Asp Arg Asp
                10                  15                  20

gat ctc agc agc cca gta gca atc gat gag cgc atc gct cta gtc gct   211
Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg Ile Ala Leu Val Ala
            25                  30                  35

gaa acc ggt tgg gca ggc att ggg ctt gtt cac gcc gat ctc atc aaa   259
Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His Ala Asp Leu Ile Lys
        40                  45                  50

gca cgc gac acc att ggc tac gag gaa ttg cgc cga cgc atc cac gct   307
Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg Arg Arg Ile His Ala
    55                  60                  65

gca gga att gaa atc att gag gtg gag ttc ctc aat ggt tgg tgg gcg   355
Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu Asn Gly Trp Trp Ala
70                  75                  80                  85

act ggt gcg gaa cgc caa gag tcc gat gcc gtt cgt gcg gat ctg ttt   403
Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val Arg Ala Asp Leu Phe
                90                  95                  100

gct gcg gcg caa gct ctt ggt tcc cca cac att aag gtc gga gca gga   451
Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile Lys Val Gly Ala Gly
            105                 110                 115

gag ggc acc aat ggt gtg gtt ccc att gct cac atg gcc agt gcg ttt   499
Glu Gly Thr Asn Gly Val Val Pro Ile Ala His Met Ala Ser Ala Phe
        120                 125                 130

act gat ctc gct gcg gaa gct gaa gct cat ggc gtc aag ctc gcg ttg   547
Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly Val Lys Leu Ala Leu
    135                 140                 145
```

```
gaa gca act ccg ttt tct cac ctg aag acc atc tac gac gcg ctg gaa   595
Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile Tyr Asp Ala Leu Glu
150                 155                 160                 165

gtt gtc agc cat tcc gat agc cca tcg gct gga ctc atg gtt gat atc   643
Val Val Ser His Ser Asp Ser Pro Ser Ala Gly Leu Met Val Asp Ile
                170                 175                 180

tgg cac acc gcg aaa atc gga atc ccc aac gat gaa ctg tgg cgc aac   691
Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp Glu Leu Trp Arg Asn
            185                 190                 195

att cca ctg tcc aag gtc aac gca gtg gag gtt gat gat ggt ttc att   739
Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val Asp Asp Gly Phe Ile
        200                 205                 210

gac acc cca att gat ctt ttc gat gac tcc acc aac cgt cgc gcg tac   787
Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr Asn Arg Arg Ala Tyr
    215                 220                 225

tgc ggt gaa ggc gaa ttt gat ccc gca agc ttc atc cgt ggc gcc atc   835
Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe Ile Arg Gly Ala Ile
230                 235                 240                 245

gac gcc ggt tgg acg ggc gca tat ggt gtg gaa att att tcc gca gag   883
Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu Ile Ile Ser Ala Glu
                250                 255                 260

cac cga agc ctc ccg gtg aaa gaa ggg ctg caa cgt gct ttc gac acc   931
His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln Arg Ala Phe Asp Thr
            265                 270                 275

acc atc gca gcg ttt gaa caa gct gct cgt ctc gcc ccc tcc act aac   979
Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu Ala Pro Ser Thr Asn
        280                 285                 290

tgatctttga aaggctgaaa aaa                                        1002
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<210> 482
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 482

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Met Lys Pro Gln Leu Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala
  1               5                  10                  15

Ala Pro Asp Arg Asp Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg
             20                  25                  30

Ile Ala Leu Val Ala Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His
         35                  40                  45

Ala Asp Leu Ile Lys Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg
     50                  55                  60

Arg Arg Ile His Ala Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu
 65                  70                  75                  80

Asn Gly Trp Trp Ala Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val
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```
                85                  90                  95

Arg Ala Asp Leu Phe Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile
            100                 105                 110

Lys Val Gly Ala Gly Glu Gly Thr Asn Gly Val Val Pro Ile Ala His
        115                 120                 125

Met Ala Ser Ala Phe Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly
    130                 135                 140

Val Lys Leu Ala Leu Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile
145                 150                 155                 160

Tyr Asp Ala Leu Glu Val Val Ser His Ser Asp Ser Pro Ser Ala Gly
                165                 170                 175

Leu Met Val Asp Ile Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp
            180                 185                 190

Glu Leu Trp Arg Asn Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val
        195                 200                 205

Asp Asp Gly Phe Ile Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr
    210                 215                 220

Asn Arg Arg Ala Tyr Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe
225                 230                 235                 240

Ile Arg Gly Ala Ile Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu
                245                 250                 255

Ile Ile Ser Ala Glu His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln
            260                 265                 270

Arg Ala Phe Asp Thr Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu
        275                 280                 285

Ala Pro Ser Thr Asn
    290
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09253-0020US1

<210> 483
<211> 990
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(967)
<223> RXN01593

<400> 483
atatgacagc cttcttcttg atctagatgg aaccgtctac gagggcggcc gagccattga 60

gcacgtagtt tctgcgctct ctggcgccgg cctacccgtc atg tat gtc acc aat 115
                                          Met Tyr Val Thr Asn
                                           1   5

aat gcc tcc cgt gct ccg gag gtg gtg gct gcg caa ctc cgt gag att 163
Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala Gln Leu Arg Glu Ile

```
                  10                  15                  20

ggc ctt gcc gac acc act gcg gac aat gtg atg aca tct gct caa gct   211
Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met Thr Ser Ala Gln Ala
            25                  30                  35

gcc tgc aag atg gcg gcg gag aag att ccc gct gga tcc aag gtg tat   259
Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala Gly Ser Lys Val Tyr
        40                  45                  50

gtt ttg ggt tca gaa tcc ttc cgc gag cta gct act gaa gct ggt ttt   307
Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala Thr Glu Ala Gly Phe
    55                  60                  65

gtg gtg gtt gat tcg gct gat gat aaa cct gtg gct gtg ctt cac ggc   355
Val Val Val Asp Ser Ala Asp Asp Lys Pro Val Ala Val Leu His Gly
70                  75                  80                  85

cac aac cct gag acc ggt tgg gct cag ttg agc gag gct gcg ctg tca   403
His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser Glu Ala Ala Leu Ser
                90                  95                  100

att aat gct ggc gcg cag tat ttt gca tca aat ttg gat tcc acc ctt   451
Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn Leu Asp Ser Thr Leu
            105                 110                 115

ccc atg gaa cgc ggt cgt cac att ggc aac ggt tcc atg gtg gct gcc   499
Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly Ser Met Val Ala Ala
        120                 125                 130

gtg gtc aac gcg act ggc gta aag cct ctt tcc gca ggt aag cca ggc   547
Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser Ala Gly Lys Pro Gly
    135                 140                 145

ccc gcg atg ttc tat gcg ggg gct gaa act ctt aat tct tca aag cct   595
Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu Asn Ser Ser Lys Pro
150                 155                 160                 165

ttg gct gtc ggc gat cgt ctc gat acc gat atc gcc ggc gga aac gct   643
Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile Ala Gly Gly Asn Ala
                170                 175                 180

gca ggc atg gac aca ttc cag gtc ctg acc ggc gtc agc ggc tac tac   691
Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly Val Ser Gly Tyr Tyr
            185                 190                 195

gat ttg gtg cgc gcc att ccc aga gca gcg ccc cac cta tat cgc cac   739
Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro His Leu Tyr Arg His
        200                 205                 210

ctc gat gca gga tct cta cag cga tcc ggg cga gct caa gcc agg tgc   787
Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg Ala Gln Ala Arg Cys
    215                 220                 225

cca ggg cgg ttt ttc agc gct tat cga cgg cga cac cct ggt cat ttc   835
Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg His Pro Gly His Phe
230                 235                 240                 245

cgg cgg cga tgc cgg cgc aac tcc ggt tgc agc act ccg cac tgc gtt   883
Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser Thr Pro His Cys Val
                250                 255                 260
```

```
gga tgt ggc ctg ggc ggc cac aga gca gtc acc gag gta cgc gct gat   931
Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr Glu Val Arg Ala Asp
            265                 270                 275

tca gag gta gct gct act gca ttg cag agc tgg tgg taaacggtga       977
Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp Trp
        280                 285

attcaccaaa gcc                                                   990
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<210> 484
<211> 289
<212> PRT
<213> Corynebacterium glutamicum

<400> 484

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Met Tyr Val Thr Asn Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala
  1               5                  10                  15

Gln Leu Arg Glu Ile Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met
            20                  25                  30

Thr Ser Ala Gln Ala Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala
        35                  40                  45

Gly Ser Lys Val Tyr Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala
    50                  55                  60

Thr Glu Ala Gly Phe Val Val Val Asp Ser Ala Asp Asp Lys Pro Val
65                  70                  75                  80

Ala Val Leu His Gly His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser
                85                  90                  95

Glu Ala Ala Leu Ser Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn
            100                 105                 110

Leu Asp Ser Thr Leu Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly
        115                 120                 125

Ser Met Val Ala Ala Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser
    130                 135                 140

Ala Gly Lys Pro Gly Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu
145                 150                 155                 160

Asn Ser Ser Lys Pro Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile
                165                 170                 175

Ala Gly Gly Asn Ala Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly
            180                 185                 190

Val Ser Gly Tyr Tyr Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro
        195                 200                 205

His Leu Tyr Arg His Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg
    210                 215                 220

Ala Gln Ala Arg Cys Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg
```

```
225                 230                 235                 240

His Pro Gly His Phe Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser
                245                 250                 255

Thr Pro His Cys Val Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr
            260                 265                 270

Glu Val Arg Ala Asp Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp
        275                 280                 285

Trp
```

<210> 485
<211> 1173
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1150)
<223> RXN00337

<400> 485

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ggacgcttat tggtgagcat tcggattacg ccggtggtgt ggtgctggcg gctaatgcga 60

attgccggac tgcggctgcc gtcaataaag aaccgcgacg atg ttg tta acg tat   115
                                            Met Leu Leu Thr Tyr
                                              1               5

gcg ttt gtg gat gtg gag gga ggc gtc gaa aag cat tct tta agc act   163
Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr
                  10                  15                  20

gcg gac att gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt   211
Ala Asp Ile Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val
              25                  30                  35

ttg ggg cgg cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc   259
Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala
          40                  45                  50

cgg ttg ggc ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg   307
Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser
      55                  60                  65

cgt gac aca aaa ggc ctg gat atc acc gtg ttg agc acc att cct gag   355
Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu
  70                  75                  80                  85

ggg gtg ggg ctg ggt gaa aat tcc gcc atg gat gtg gcg ctc gca ttg   403
Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu
                  90                  95                 100

gcg ctg tat cgg gaa aat att gag gaa gcc ccc acg aag gcg cgc att   451
Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile
              105                 110                 115

gcg gag att tgt tcg cag tcc gca ttc atg ttc agt gag act tca gtg   499
```

```
Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val
        120                 125                 130

ttg cgt gcg cgg cac acc gtg gcg ttg cgg ggt gaa act gga cag att   547
Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly Glu Thr Gly Gln Ile
    135                 140                 145

tcg gtg gtt gat tac gcc gat ggt tcg gtc act cag gcg cca cat ccg   595
Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr Gln Ala Pro His Pro
150                 155                 160                 165

gtg agt cgt tcc gct ggt ttg tcg gca ttt gtt gtt gct gcg caa act   643
Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val Val Ala Ala Gln Thr
                170                 175                 180

gaa act gat ccg agc att tac cgc gag atc tat gct cga cat gcg ttt   691
Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr Ala Arg His Ala Phe
            185                 190                 195

atc gat gaa gct gcg cgc gct ttc agt gtg gaa tct ttg cgg ttg ctt   739
Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu Ser Leu Arg Leu Leu
        200                 205                 210

ccc gac gct tcc act cgt gtt gtg gat tgg ttg cag gcc gtg att gag   787
Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu Gln Ala Val Ile Glu
    215                 220                 225

gtg act ggt cga gag gat ctg ccc tcg att gaa caa gcc cag cgc tgg   835
Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu Gln Ala Gln Arg Trp
230                 235                 240                 245

ttg aat ctg tgg gaa aac gaa acc cgg cgc gct cag agg aca gcc aat   883
Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala Gln Arg Thr Ala Asn
                250                 255                 260

gcc ctg cgt tcg aga agg ctg agt gag ttt tct gag ctg ctg atg gaa   931
Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser Glu Leu Leu Met Glu
            265                 270                 275

tcc caa gat gat ttg agc gac acc ttc gat ttc ccc cct gct gat ttg   979
Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe Pro Pro Ala Asp Leu
        280                 285                 290

gcg ctt gct cgt ttg tgc gtc gag cgg ggt gcc aca gct gct cgg tcc   1027
Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala Thr Ala Ala Arg Ser
    295                 300                 305

acg tca gcg cgc ggt gtg att gcg ttg gtt gat gcc cat cat gcg cac   1075
Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp Ala His His Ala His
310                 315                 320                 325

aat ttt gct gcg gat ctc agc gag gat ggc ttg ttg gtg gtt cct ctc   1123
Asn Phe Ala Ala Asp Leu Ser Glu Asp Gly Leu Leu Val Val Pro Leu
                330                 335                 340

ggg cac ggg gac gtc gcg gaa cag ggc tagcacgcct acttaaccag         1170
Gly His Gly Asp Val Ala Glu Gln Gly
            345                 350

cct                                                              1173
```

<210> 486
<211> 350
<212> PRT
<213> Corynebacterium glutamicum

<400> 486
Met Leu Leu Thr Tyr Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys
1 5 10 15

His Ser Leu Ser Thr Ala Asp Ile Ala Ala Arg Ala His Ala His Met
20 25 30

Lys Ser His Asp Val Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu
35 40 45

Gly Gly Val Ala Ala Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His
50 55 60

Lys Gln Met Leu Ser Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu
65 70 75 80

Ser Thr Ile Pro Glu Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp
85 90 95

Val Ala Leu Ala Leu Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro
100 105 110

Thr Lys Ala Arg Ile Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe
115 120 125

Ser Glu Thr Ser Val Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly
130 135 140

Glu Thr Gly Gln Ile Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr
145 150 155 160

Gln Ala Pro His Pro Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val
165 170 175

Val Ala Ala Gln Thr Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr
180 185 190

Ala Arg His Ala Phe Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu
195 200 205

Ser Leu Arg Leu Leu Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu
210 215 220

Gln Ala Val Ile Glu Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu
225 230 235 240

Gln Ala Gln Arg Trp Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala
245 250 255

Gln Arg Thr Ala Asn Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser
260 265 270

Glu Leu Leu Met Glu Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe
275 280 285

```
Pro Pro Ala Asp Leu Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala
    290                 295                 300

Thr Ala Ala Arg Ser Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp
305                 310                 315                 320

Ala His His Ala His Asn Phe Ala Ala Asp Leu Ser Glu Asp Gly Leu
                325                 330                 335

Leu Val Val Pro Leu Gly His Gly Asp Val Ala Glu Gln Gly
            340                 345                 350


<210> 487
<211> 1248
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1225)
<223> RXS00584

<400> 487
tagttgtgcc acctaaaacg cgaacagaac cggagtcgag cagcacctcc ccgcaagggt 60

agaggggctg ctttttttgtt tcctaaattc accccatccc atg cat agc cct gaa   115
                                              Met His Ser Pro Glu
                                                1               5

agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca   163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser
                10                  15                  20

acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca   211
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr
            25                  30                  35

gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg   259
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val
        40                  45                  50

gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac   307
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp
    55                  60                  65

cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca   355
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala
70                  75                  80                  85

gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat   403
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp
                90                  95                  100

cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc   451
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr
            105                 110                 115

atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc   499
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr
        120                 125                 130
```

```
tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac   547
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp
    135                 140                 145

gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac   595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn
150                 155                 160                 165

agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct   643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala
                170                 175                 180

cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct   691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser
            185                 190                 195

atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca   739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala
        200                 205                 210

gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc   787
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr
    215                 220                 225

tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac   835
Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn
230                 235                 240                 245

tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca   883
Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala
                250                 255                 260

gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc   931
Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu
            265                 270                 275

atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag   979
Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln
        280                 285                 290

gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa   1027
Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu
    295                 300                 305

gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag   1075
Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln
310                 315                 320                 325

aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg   1123
Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val
                330                 335                 340

tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc   1171
Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile
            345                 350                 355

gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca   1219
Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala
        360                 365                 370
```

gcc aag taattaaggg cgctagactg tta 1248
Ala Lys
375

<210> 488
<211> 375
<212> PRT
<213> Corynebacterium glutamicum

<400> 488
Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu
1 5 10 15

Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu
20 25 30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys
35 40 45

Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe
50 55 60

Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val
65 70 75 80

His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu
85 90 95

Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe
100 105 110

Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro
115 120 125

His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg
130 135 140

Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu
145 150 155 160

Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp
165 170 175

Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu
180 185 190

Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly
195 200 205

Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His
210 215 220

Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr
225 230 235 240

Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly
245 250 255

Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly
260 265 270

```
Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys
        275                 280                 285

Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile
    290                 295                 300

Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu
305                 310                 315                 320

Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly
                325                 330                 335

Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp
            340                 345                 350

Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg
        355                 360                 365

Glu Arg Arg Ala Ala Ala Lys
    370                 375


<210> 489
<211> 1131
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1108)
<223> RXS02574

<400> 489
tgtgctcctt gcgggctgcg cagaagagcc ggaacagcaa aaagcaataa gccgcttatc 60

gacgtccccc tccacccctc ccgcaccgac cgcggaggat ttg gcg cgc gcg caa   115
                                              Leu Ala Arg Ala Gln
                                                1               5

atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga   163
Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly
                10                  15                  20

gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt   211
Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly
            25                  30                  35

ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct   259
Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro
        40                  45                  50

ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc   307
Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser
    55                  60                  65

gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att   355
Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile
70                  75                  80                  85

ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg   403
```

```
Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala Gln Thr Met Thr Pro
                 90                  95                 100

gaa caa gta gaa gat ctc gca gaa atc cta ggc act ggt tta gct gca   451
Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly Thr Gly Leu Ala Ala
            105                 110                 115

cat ggt gtg aca gtt aac ttt gca cct gtt gta gat gta gat gct tgg   499
His Gly Val Thr Val Asn Phe Ala Pro Val Val Asp Val Asp Ala Trp
        120                 125                 130

ggt ctc ccc gtc gtt ggc gat cgt tcc ttt tcc aac gac cca gcc gta   547
Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser Asn Asp Pro Ala Val
    135                 140                 145

gca gct act tat gcc aca gct ttt gca aag ggc tta agc aaa gta gga   595
Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly Leu Ser Lys Val Gly
150                 155                 160                 165

att acc cca gta ttc aaa cat ttc cca ggt cac ggt cgt gca agt ggc   643
Ile Thr Pro Val Phe Lys His Phe Pro Gly His Gly Arg Ala Ser Gly
                170                 175                 180

gat tcg cac acc caa gat gtg gtg acc ccc gca ctt gat gag ctt aaa   691
Asp Ser His Thr Gln Asp Val Val Thr Pro Ala Leu Asp Glu Leu Lys
            185                 190                 195

act tac gac ctc atc cct tat ggt caa gca ctt tct gaa act gac gga   739
Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu Ser Glu Thr Asp Gly
        200                 205                 210

gcc gtc atg gtg ggc cac atg att gtt cca ggt ctt ggc acc gac gga   787
Ala Val Met Val Gly His Met Ile Val Pro Gly Leu Gly Thr Asp Gly
    215                 220                 225

gtt cca tcc tct atc gac ccc gcc acc tat caa ctg ctc cgc agt ggc   835
Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln Leu Leu Arg Ser Gly
230                 235                 240                 245

gat tac cca ggt ggc gtg cct ttc gat ggc gtg atc tac acc gac gat   883
Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val Ile Tyr Thr Asp Asp
                250                 255                 260

ctc tct gga atg agt gcc att tcc gcc acc cat tca ccc gca gaa gca   931
Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His Ser Pro Ala Glu Ala
            265                 270                 275

gtg ctt gcc tcc ctc aaa gca ggc gca gac caa gca cta tgg atc gac   979
Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln Ala Leu Trp Ile Asp
        280                 285                 290

tat ggg tcg ttg ggc tcc gcg att gat cgc gtt gat gct gcc gtt agc   1027
Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val Asp Ala Ala Val Ser
    295                 300                 305

agc ggt gaa tac cct caa gaa caa atg ctg gca tct gcg tta aga gtc   1075
Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala Ser Ala Leu Arg Val
310                 315                 320                 325

caa ttg ctc tac atc aca cgt ctc gaa caa aag tgaagttacc agtccgtaac 1128
Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys
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09629149.060502

330 335

ccc 1131

<210> 490
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 490

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Leu Ala Arg Ala Gln Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser
  1               5                  10                  15

Leu Met Met Val Gly Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu
             20                  25                  30

Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn
         35                  40                  45

Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val
     50                  55                  60

Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln
 65                  70                  75                  80

Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala
                 85                  90                  95

Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly
            100                 105                 110

Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val
        115                 120                 125

Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser
    130                 135                 140

Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly
145                 150                 155                 160

Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His
                165                 170                 175

Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala
            180                 185                 190

Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu
        195                 200                 205

Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly
    210                 215                 220

Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln
225                 230                 235                 240

Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val
                245                 250                 255

Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His
            260                 265                 270
```

```
Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln
        275                 280                 285

Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val
    290                 295                 300

Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala
305                 310                 315                 320

Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys
                325                 330                 335
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<210> 491
<211> 1038
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1008)
<223> RXS03215

<400> 491

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atc gat gtt gtc agc gtc gtg gtg gct aac ttc ctg cac cgc gaa atc   48
Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
  1               5                  10                  15

gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca   96
Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
             20                  25                  30

ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc   144
Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
         35                  40                  45

cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc   192
Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
     50                  55                  60

cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag   240
Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
 65                  70                  75                  80

ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga   288
Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
                 85                  90                  95

tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc   336
Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
            100                 105                 110

tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa   384
Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
        115                 120                 125

ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc   432
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```
Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
    130                 135                 140

acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac   480
Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
145                 150                 155                 160

gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac   528
Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
                165                 170                 175

att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc   576
Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
            180                 185                 190

cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa   624
Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
        195                 200                 205

gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc   672
Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
    210                 215                 220

gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa   720
Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
225                 230                 235                 240

gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc   768
Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
                245                 250                 255

ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa   816
Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
            260                 265                 270

ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc   864
Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
        275                 280                 285

tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta   912
Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
    290                 295                 300

cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt   960
His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
305                 310                 315                 320

ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac  1008
Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
                325                 330                 335

tagaaactat tcagaaagca tcaccatgaa                                1038


<210> 492
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 492
Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
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1 5 10 15

Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
20 25 30

Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
35 40 45

Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
50 55 60

Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
65 70 75 80

Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
85 90 95

Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
100 105 110

Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
115 120 125

Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
130 135 140

Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
145 150 155 160

Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
165 170 175

Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
180 185 190

Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
195 200 205

Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
210 215 220

Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
225 230 235 240

Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
245 250 255

Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
260 265 270

Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
275 280 285

Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
290 295 300

His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
305 310 315 320

Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
325 330 335

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<210> 493
<211> 1031
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1008)
<223> FRXA01915

<400> 493

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atc gat gtt gtc agc gtc gtg gtg gct aac ttc ctg cac cgc gaa atc   48
Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
  1               5                  10                  15

gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca   96
Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
            20                  25                  30

ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc   144
Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
        35                  40                  45

cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc   192
Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
    50                  55                  60

cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag   240
Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
65                  70                  75                  80

ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga   288
Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
                85                  90                  95

tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc   336
Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
            100                 105                 110

tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa   384
Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
        115                 120                 125

ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc   432
Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
    130                 135                 140

acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac   480
Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
145                 150                 155                 160

gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac   528
Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
                165                 170                 175

att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc   576
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Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
            180                 185                 190

cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa   624
Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
        195                 200                 205

gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc   672
Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
    210                 215                 220

gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa   720
Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
225                 230                 235                 240

gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc   768
Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
                245                 250                 255

ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa   816
Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
            260                 265                 270

ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc   864
Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
        275                 280                 285

tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta   912
Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
    290                 295                 300

cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt   960
His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
305                 310                 315                 320

ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac  1008
Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
                325                 330                 335

tagaaactat tcagaaagca tca                                       1031


<210> 494
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 494
Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
  1               5                  10                  15

Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
             20                  25                  30

Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
         35                  40                  45

Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
     50                  55                  60

Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
```

65 70 75 80

Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
85 90 95

Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
100 105 110

Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
115 120 125

Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
130 135 140

Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
145 150 155 160

Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
165 170 175

Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
180 185 190

Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
195 200 205

Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
210 215 220

Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
225 230 235 240

Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
245 250 255

Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
260 265 270

Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
275 280 285

Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
290 295 300

His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
305 310 315 320

Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
325 330 335

<210> 495
<211> 1288
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1258)
<223> RXS03224

<400> 495
acgattgtgc tgtcgtttgc gttggtgaat agttctggac cgggtatttt gcggcgcaca 60

tggaactcat tgaacgccgc gcccggctaa ggtgggaggc atg agt ttt gct gaa 115
Met Ser Phe Ala Glu
1 5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
10 15 20

atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
25 30 35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
40 45 50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
55 60 65

ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
70 75 80 85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly
90 95 100

gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc 451
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr
105 110 115

ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg 499
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr
120 125 130

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc 547
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu
135 140 145

gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc 595
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala
150 155 160 165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca 643
Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro
170 175 180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac 691
His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr
185 190 195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa 739
Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys
200 205 210

Sequence Listing

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gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg   787
Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp
    215                 220                 225

act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca   835
Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr
230                 235                 240                 245

ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa   883
Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln
                250                 255                 260

tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc   931
Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr
            265                 270                 275

cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag   979
Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu
        280                 285                 290

gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag   1027
Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu
    295                 300                 305

ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc   1075
Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile
310                 315                 320                 325

gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc   1123
Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val
                330                 335                 340

ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga   1171
Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly
            345                 350                 355

ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg   1219
Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg
        360                 365                 370

atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg   1268
Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala
    375                 380                 385

ttcaagggta ggggaacaaa                                           1288


<210> 496
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 496
Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly
  1               5                  10                  15

Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His
            20                  25                  30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
```

```
         35                  40                  45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
     50                  55                  60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
 65                  70                  75                  80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
                 85                  90                  95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
            100                 105                 110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
        115                 120                 125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
    130                 135                 140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
145                 150                 155                 160

Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
                165                 170                 175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
            180                 185                 190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
        195                 200                 205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
    210                 215                 220

Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
225                 230                 235                 240

Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
                245                 250                 255

Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
            260                 265                 270

Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
        275                 280                 285

Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
    290                 295                 300

Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile
305                 310                 315                 320

Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln
                325                 330                 335

Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys
            340                 345                 350

Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu
        355                 360                 365
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09623410.060305

```
Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr
    370                 375                 380

Ser Ala
385
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<210> 497
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> FRXA00038

<400> 497

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acgattgtgc tgtcgtttgc gttggtgaat agttctggac cgggtatttt gcggcgcaca 60

tggaactcat tgaacgccgc gcccggctaa ggtgggaggc atg agt ttt gct gaa   115
                                            Met Ser Phe Ala Glu
                                              1               5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc   163
His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
                 10                  15                  20

atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta   211
Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
             25                  30                  35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg   259
Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
         40                  45                  50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat   307
Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
     55                  60                  65

ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg   355
Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
 70                  75                  80                  85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc   403
Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly
                 90                  95                 100

gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc   451
Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr
            105                 110                 115

ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg   499
Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr
        120                 125                 130

aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc   547
Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu
    135                 140                 145
```

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gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc   595
Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala
150                 155                 160                 165

cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca   643
Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro
                170                 175                 180

cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac   691
His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr
            185                 190                 195

gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa   739
Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys
        200                 205                 210

gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg   787
Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp
    215                 220                 225

act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca   835
Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr
230                 235                 240                 245

ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa   883
Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln
                250                 255                 260

tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc   931
Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr
            265                 270                 275

cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag   979
Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu
        280                 285                 290

gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag   1027
Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu
    295                 300                 305

ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc   1075
Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile
310                 315                 320                 325

gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc   1123
Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val
                330                 335                 340

ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga   1171
Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly
            345                 350                 355

ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg   1219
Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg
        360                 365                 370

atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg   1268
Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala
    375                 380                 385

ttcaagggta ggg                                                  1281
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US 09/902,000

<210> 498
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 498
Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly
1 5 10 15

Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His
20 25 30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
35 40 45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
50 55 60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
65 70 75 80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
85 90 95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
100 105 110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
115 120 125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
130 135 140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
145 150 155 160

Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
165 170 175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
180 185 190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
195 200 205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
210 215 220

Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
225 230 235 240

Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
245 250 255

Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
260 265 270

Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
275 280 285

```
Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
    290                 295                 300

Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile
305                 310                 315                 320

Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln
                325                 330                 335

Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys
            340                 345                 350

Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu
        355                 360                 365

Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr
    370                 375                 380

Ser Ala
385
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09609260.090502

<210> 499
<211> 517
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(517)
<223> RXC00233

<400> 499
cgcctccagc agttgaggga gaagttccaa cacttgcacc aactgaggaa gcaactgtgc 60

aatagcgctt tagacacaga ctcatgacag aatagaagac atg agt gtg aat gaa 115
                                        Met Ser Val Asn Glu
                                          1   5

gca gat ctg aac gct gtc gaa gag caa ttg gga agg gcc cca cga ggt 163
Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly
                  10   15   20

gtc ctc gat att tct tac cgc agc cct gat gga gta ccc ggt gtg gtg 211
Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val
              25   30   35

atg acc gca cca aaa ctg gat gac gga acc cca ttc cca acc ctg tac 259
Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr
          40   45   50

tac ttg aca gat cca cgc ctg acc acc gag gca tcc cgc ctc gag gtc 307
Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val
      55   60   65

gca ttg gta atg aag tgg atg act gat cgc ctt tcc acc gac gaa gag 355
Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu
  70   75   80   85

ctt cgt gcc gac tac cag cgc gcc cac gag cac ttc ctg gca aag cgc 403
```
```

```
Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg
                 90                  95                 100

aac gca att gaa gat ctc ggc acg gat ttt tcc ggc ggt ggc atg cct   451
Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro
            105                 110                 115

gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa   499
Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu
        120                 125                 130

ggc cca cac cat ttc ctt                                          517
Gly Pro His His Phe Leu
    135
```

<210> 500
<211> 139
<212> PRT
<213> Corynebacterium glutamicum

<400> 500

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Met Ser Val Asn Glu Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly
  1               5                  10                  15

Arg Ala Pro Arg Gly Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly
            20                  25                  30

Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro
        35                  40                  45

Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala
    50                  55                  60

Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu
65                  70                  75                  80

Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His
                85                  90                  95

Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser
            100                 105                 110

Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp
        115                 120                 125

Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu
    130                 135
```

<210> 501
<211> 849
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> RXC00236

<400> 501

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aatgcgagag ttctaaaacg agccggtaac atcgaccccc atgagttcag gggttagaaa 60

agcaatggga tttggatgcg gttcggtttt ggccgtcatc atg gtg atc tca ttt   115
                                            Met Val Ile Ser Phe
                                              1               5

gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa   163
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln
                 10                  15                  20

ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt   211
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val
             25                  30                  35

ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt   259
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg
         40                  45                  50

ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg   307
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala
     55                  60                  65

att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct   355
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro
 70                  75                  80                  85

ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa   403
Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu
                 90                  95                 100

acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg   451
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu
            105                 110                 115

gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat   499
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp
        120                 125                 130

ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta   547
Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu
    135                 140                 145

gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att   595
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile
150                 155                 160                 165

ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta   643
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val
                170                 175                 180

gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg   691
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu
            185                 190                 195

ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca   739
Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala
        200                 205                 210

gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga   787
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg
    215                 220                 225
```

```
gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa     836
Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro Ala Ile
230                 235                 240

caagcgcaac ccc                                                    849
```

<210> 502
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 502

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Met Val Ile Ser Phe Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr
  1               5                  10                  15

Ala Pro Ile Arg Gln Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala
            20                  25                  30

Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr
        35                  40                  45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
    50                  55                  60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
65                  70                  75                  80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
                85                  90                  95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
            100                 105                 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
        115                 120                 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
    130                 135                 140

Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
145                 150                 155                 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
                165                 170                 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
            180                 185                 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
        195                 200                 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr
    210                 215                 220

Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro
225                 230                 235                 240

Ala Ile
```

<210> 503
<211> 1113
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1090)
<223> RXC00271

<400> 503
tagtttaaat catgagacat ttcacatatg gttctttatc cgagacatgt gttgacgctg 60

tctgcccctt tttgaaaata acactttaag gagatgtgcc atg ttt tct tcc cgt 115
Met Phe Ser Ser Arg
1 5

tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct 163
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
10 15 20

tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca 211
Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
25 30 35

ggt ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct 259
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
40 45 50

gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca 307
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala
55 60 65

ggc gtt gac gtc acc ttt gat gag caa aac gct aac ggc gag cag ggc 355
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
70 75 80 85

act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc 403
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
90 95 100

gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc 451
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
105 110 115

act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca 499
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
120 125 130

gag ctg gtg gat tct aat gaa gca cct ggc gga aac gtc acc ggt act 547
Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr
135 140 145

tct gat atc gca ccg att gag cag cag ttg gag ctt ttg cag cag ctg 595
Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu Leu Leu Gln Gln Leu
150 155 160 165

gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc 643
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val

```
                170                 175                 180

aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg   691
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu
            185                 190                 195

ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag   739
Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln
        200                 205                 210

cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act   787
Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr
    215                 220                 225

gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag   835
Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu
230                 235                 240                 245

cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt   883
Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly
                250                 255                 260

ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag   931
Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln
            265                 270                 275

act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca   979
Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala
        280                 285                 290

acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa   1027
Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu
    295                 300                 305

gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat   1075
Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp
310                 315                 320                 325

aag gcc gaa cgc gta tgatcggcgc ttttgagttc gga                    1113
Lys Ala Glu Arg Val
                330
```

<210> 504
<211> 330
<212> PRT
<213> Corynebacterium glutamicum

<400> 504

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Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly
  1               5                  10                  15

Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr
             20                  25                  30

Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln
         35                  40                  45

Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu
     50                  55                  60
```

```
Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala
 65                  70                  75                  80

Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser
                85                  90                  95

Asp Asn Leu Asp Leu Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala
            100                 105                 110

Thr Ala Gln Asn Ile Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr
        115                 120                 125

Asp Ala Val Ser Ala Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly
    130                 135                 140

Asn Val Thr Gly Thr Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu
145                 150                 155                 160

Leu Leu Gln Gln Leu Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr
                165                 170                 175

Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys
            180                 185                 190

Ala Ala Glu Pro Leu Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr
        195                 200                 205

Val Asn Glu Ile Gln Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val
    210                 215                 220

Ile Tyr Val Pro Thr Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu
225                 230                 235                 240

Val Gln Val Ala Glu Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser
                245                 250                 255

Gly Thr Val Glu Gly Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr
            260                 265                 270

Glu Leu Gly Arg Gln Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp
        275                 280                 285

Gly Glu Asp Pro Ala Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr
    290                 295                 300

Tyr Val Ile Asn Glu Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro
305                 310                 315                 320

Gln Glu Ile Leu Asp Lys Ala Glu Arg Val
                325                 330
```

<210> 505
<211> 1263
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1240)
<223> RXC00338

09252005.09252005.0

<400> 505
tcttagaagg cgtagtcaca ccattaacct tgccagaatt tttcaaggct tggctagact 60

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tgggaaacga acatgcggta ccaaccaggg gagttaatgc gtg agt gat gta acc   115
                                            Val Ser Asp Val Thr
                                              1               5

gtt ggc gat att cgc cgc att ttg gat gag gct tat ccg ccg gcg ttg   163
Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala Tyr Pro Pro Ala Leu
                 10                  15                  20

gcg gaa agc tgg gac aaa gtg ggg ctg atc tgc ggt gat cca aca gag   211
Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys Gly Asp Pro Thr Glu
             25                  30                  35

tcg gtg aag cgt gtc ggt tta gca ctc gat tgc acc cag gca gtg gcc   259
Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys Thr Gln Ala Val Ala
         40                  45                  50

gac aag gct gtg gac atg ggt ttg gac atg ctg atc att cac cac cca   307
Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu Ile Ile His His Pro
     55                  60                  65

ttg ctg ctg cgt ggg gtg acg tct gtt gct gcg gat gag cca aaa ggc   355
Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala Asp Glu Pro Lys Gly
 70                  75                  80                  85

aag gtc att cac acc cta att cgc ggc ggg gtg gca ctg ttt tcc gcg   403
Lys Val Ile His Thr Leu Ile Arg Gly Gly Val Ala Leu Phe Ser Ala
                 90                  95                 100

cac act aat gcg gat tcc gcg cgc cca ggt gtc aac gat aaa ctc gcc   451
His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val Asn Asp Lys Leu Ala
            105                 110                 115

gag ctc gtc ggc atc acg gcc ggg cga ccc atc gcg aca cgg ctt tta   499
Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu
        120                 125                 130

ggc ggc atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg   547
Gly Gly Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala
    135                 140                 145

tac cta aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac   595
Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp
150                 155                 160                 165

tac cga gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc   643
Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro
                170                 175                 180

gtg gag ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa   691
Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys
            185                 190                 195

tcc ctt gag ctg cgc atc gag ttt gtt gca ccg cgc aac ctg cgc gcc   739
Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala
        200                 205                 210

cgg ctc acg tcg gtg ctg cgg gag gct cat ccg tat gag gag cct gcc   787
```

US 2009/0156409 A1

```
Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala
    215                 220                 225

ttc gat att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc   835
Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr
230                 235                 240                 245

gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat   883
Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp
                250                 255                 260

ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg   931
Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val
            265                 270                 275

cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca   979
Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser
        280                 285                 290

tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg   1027
Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val
    295                 300                 305

gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat   1075
Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr
310                 315                 320                 325

ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc   1123
Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser
                330                 335                 340

gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc   1171
Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala
            345                 350                 355

cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc   1219
Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr
        360                 365                 370

atg tct gcg cga gca gtg aac taaattcttg agaactaaaa aag            1263
Met Ser Ala Arg Ala Val Asn
    375                 380


<210> 506
<211> 380
<212> PRT
<213> Corynebacterium glutamicum

<400> 506
Val Ser Asp Val Thr Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala
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Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys
             20                  25                  30

Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
         35                  40                  45

Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
     50                  55                  60
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```
Ile Ile His His Pro Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala
 65                  70                  75                  80

Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val
                 85                  90                  95

Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val
            100                 105                 110

Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile
        115                 120                 125

Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu
    130                 135                 140

Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala
145                 150                 155                 160

Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr
                165                 170                 175

Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val
            180                 185                 190

Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro
        195                 200                 205

Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro
    210                 215                 220

Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser
225                 230                 235                 240

Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro
                245                 250                 255

Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val
            260                 265                 270

Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser
        275                 280                 285

Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val
    290                 295                 300

Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His
305                 310                 315                 320

Pro Val Asp Glu Tyr Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr
                325                 330                 335

Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile
            340                 345                 350

Leu Gln Asp Lys Ala Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg
        355                 360                 365

Thr Asp Pro Trp Thr Met Ser Ala Arg Ala Val Asn
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09050450.030303

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<211> 1470
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1447)
<223> RXC00362

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aacatgctac ggtttttttcg gtcacttaaa ggaggcgctt atg gga atc att gct 115
Met Gly Ile Ile Ala
1 5

ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa 163
Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys
10 15 20

cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt 211
Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu
25 30 35

gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat 259
Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
40 45 50

gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg 307
Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met Ala Phe Val Phe Met
55 60 65

ggc atc gtt gtg caa tca act gga ttg att gat cga tta atc gca atc 355
Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp Arg Leu Ile Ala Ile
70 75 80 85

ctt aac tcg att ttt ggt cgg ctt cga ggt ggc gca ggt tat gtt tcc 403
Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser
90 95 100

act ctt gga tct gcg ctc att gga ctc atc gct gga tca acg gct gga 451
Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala Gly Ser Thr Ala Gly
105 110 115

aac tcc gcg acg gtt ggc tca gtg acg atc cct tgg atg aaa aag acg 499
Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr
120 125 130

gga tgg act gct gaa agg tcc gca acg tta gtc gcg ggc aac tct ggc 547
Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly
135 140 145

ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc atc att ttg gca 595
Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala
150 155 160 165

ttg cca gct gca gca gct tct tcg gcc tct cag gtg tac att gct ttg 643
Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val Tyr Ile Ala Leu
170 175 180

```
gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta gcg gtc gtc ttt   691
Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Val Phe
            185                 190                 195

tac tgg aca cgt aaa gat aaa att cct gcc acc cct gat gat caa cgg   739
Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro Asp Asp Gln Arg
        200                 205                 210

gtg tca ttc ggt gag gca atg aag act gga tgg cgt tca ccg ttg atc   787
Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg Ser Pro Leu Ile
    215                 220                 225

ttc ctt gga att ttg atc ccc gta atc ctc aca atc ggc cca ttg tct   835
Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile Gly Pro Leu Ser
230                 235                 240                 245

gaa tgg tta aag aca cat gga gtt ggg gag tct ggt gtt aaa tcg atg   883
Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly Val Lys Ser Met
                250                 255                 260

tcg atc atc gtg tgg gtg cca att ctg att acg gca att gct ctg att   931
Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile
            265                 270                 275

gaa ggg cgt aaa cga att gct aac aac atg gca cac ttt agg gtt cag   979
Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His Phe Arg Val Gln
        280                 285                 290

atc tcc aag gac ttg cca caa ttt gcc acc gta gga att tcg ttg ttt   1027
Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly Ile Ser Leu Phe
    295                 300                 305

tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg ggt gtt ggc ccg   1075
Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro
310                 315                 320                 325

cag ttg tct aac tgg ctt gat tcc atg gac cta cct aag tct gtc atg   1123
Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met
                330                 335                 340

gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tcg   1171
Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser
            345                 350                 355

tca aca gca acc gcg gct gcg att ggt gct ccc gct gtc gct gcg ttg   1219
Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu
        360                 365                 370

gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg   1267
Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu
    375                 380                 385

tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc gcg ccg att tac   1315
Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr
390                 395                 400                 405

ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca   1363
Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro
                410                 415                 420
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```
ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt   1411
Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val
            425                 430                 435

gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta        1457
Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
        440                 445

aaaatgaact caa                                                   1470
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<210> 508
<211> 449
<212> PRT
<213> Corynebacterium glutamicum

<400> 508

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Met Gly Ile Ile Ala Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu
  1               5                  10                  15

Asn Val Phe Leu Lys Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu
             20                  25                  30

Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile
         35                  40                  45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met
     50                  55                  60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp
 65                  70                  75                  80

Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly
                 85                  90                  95

Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala
            100                 105                 110

Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro
        115                 120                 125

Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val
    130                 135                 140

Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met
145                 150                 155                 160

Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln
                165                 170                 175

Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg
            180                 185                 190

Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr
        195                 200                 205

Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp
    210                 215                 220

Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr
225                 230                 235                 240
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US 2009/0298150 A1

Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser
245 250 255

Gly Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr
260 265 270

Ala Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala
275 280 285

His Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val
290 295 300

Gly Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu
305 310 315 320

Leu Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu
325 330 335

Pro Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val
340 345 350

Ala Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro
355 360 365

Ala Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile
370 375 380

Val Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val
385 390 395 400

Gly Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr
405 410 415

Lys Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu
420 425 430

Leu Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr
435 440 445

Gly

<210> 509
<211> 1203
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1180)
<223> RXC00412

<400> 509
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cttttgtccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115
Val Ser His Thr Ala
1 5

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tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag   163
Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln
                 10                  15                  20

ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat   211
Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn
             25                  30                  35

aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa   259
Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu
         40                  45                  50

ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc   307
Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser
     55                  60                  65

act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg   355
Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser
 70                  75                  80                  85

ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg   403
Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu
                 90                  95                 100

cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg   451
Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu
             105                 110                 115

ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt   499
Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val
         120                 125                 130

gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc   547
Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu
     135                 140                 145

gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg   595
Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu
150                 155                 160                 165

tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc   643
Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr
                 170                 175                 180

aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca   691
Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro
             185                 190                 195

gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa   739
Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu
         200                 205                 210

ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt   787
Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg
     215                 220                 225

tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa   835
Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu
230                 235                 240                 245

tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct   883
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US 2005/0260609 A1

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Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala
                250                 255                 260

caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa   931
Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu
            265                 270                 275

tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg   979
Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu
        280                 285                 290

act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa   1027
Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln
    295                 300                 305

ggt gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc   1075
Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg
310                 315                 320                 325

caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg   1123
Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala
                330                 335                 340

att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag   1171
Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu
            345                 350                 355

atc acc cga tgaacgagat gatcctcgca gct                            1203
Ile Thr Arg
        360
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09625260.SEQ

<210> 510
<211> 360
<212> PRT
<213> Corynebacterium glutamicum

<400> 510

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Val Ser His Thr Ala Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln
  1               5                  10                  15

Gln Pro Ser Thr Gln Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys
            20                  25                  30

Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val
        35                  40                  45

Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser
    50                  55                  60

Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser
65                  70                  75                  80

Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met
                85                  90                  95

Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe
            100                 105                 110

Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu
        115                 120                 125
```

```
Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg
    130                 135                 140

Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn
145                 150                 155                 160

Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala
                165                 170                 175

Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr
            180                 185                 190

Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg
        195                 200                 205

Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu
    210                 215                 220

Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser
225                 230                 235                 240

Gly Lys Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro
                245                 250                 255

Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr
            260                 265                 270

Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu
        275                 280                 285

Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala
    290                 295                 300

Arg Ala Ala Glu Gln Gly Ala Phe Val Asn Ile Val His Gly Gly Val
305                 310                 315                 320

Thr Thr Leu Gln Arg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr
                325                 330                 335

Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr
            340                 345                 350

Thr Thr Ile Lys Glu Ile Thr Arg
        355                 360
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<210> 511
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXC00526

<400> 511
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cgtttctgcc aagcaaaccg tgggccaggt gatttagcct atg agc ctc atc gaa 115

```
                                                    Met Ser Leu Ile Glu
                                                      1               5

atg cga aat att gtc aag acc tac aac att gga tct gaa ggt gaa ctc   163
Met Arg Asn Ile Val Lys Thr Tyr Asn Ile Gly Ser Glu Gly Glu Leu
                  10                  15                  20

acc gtg ttg cac ggt gtg gat ttc cat gtg gac cgt ggc gaa ttc gtg   211
Thr Val Leu His Gly Val Asp Phe His Val Asp Arg Gly Glu Phe Val
             25                  30                  35

tcg gtt gtg ggt acg tcc ggc tca ggt aaa tca acg atg atg aac atc   259
Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser Thr Met Met Asn Ile
         40                  45                  50

att ggg ttg ttg gat aag cca act gat ggc acg tac acc ttg gat ggc   307
Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr Tyr Thr Leu Asp Gly
     55                  60                  65

gtg gat gtg ttg gat atc agc gat gat gct ttg gcg agc cac cgc gct   355
Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu Ala Ser His Arg Ala
 70                  75                  80                  85

aaa tcg att ggt ttt gtg ttt cag aac ttc aat ctg att ggc cgg atc   403
Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn Leu Ile Gly Arg Ile
                 90                  95                 100

gat gcg ttg aag aat gtg gaa atg ccc atg atg tat gcg ggc att ccg   451
Asp Ala Leu Lys Asn Val Glu Met Pro Met Met Tyr Ala Gly Ile Pro
            105                 110                 115

gct aag cag cgg aga agt cgt gcg gtt gaa tta ttg gaa atg gtc ggg   499
Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu Leu Glu Met Val Gly
        120                 125                 130

atg ggt gag cgt ctc aac cat gag ccc aat gag ctt tcg ggt ggt cag   547
Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu Leu Ser Gly Gly Gln
    135                 140                 145

aag cag cgc gtg gcc att gct cgc gcg ttg gcg aac gat cct gag atc   595
Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala Asn Asp Pro Glu Ile
150                 155                 160                 165

att ctt gct gat gaa cca act ggt gcg ttg gat tct gca acg ggc cgg   643
Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp Ser Ala Thr Gly Arg
                170                 175                 180

atg gtg atg gat att ttc cac cag ctc aac aag gag cag ggc aaa acc   691
Met Val Met Asp Ile Phe His Gln Leu Asn Lys Glu Gln Gly Lys Thr
            185                 190                 195

atc gtg ttt att act cac aac cct gag ctt gct gat gaa tct gat cgg   739
Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala Asp Glu Ser Asp Arg
        200                 205                 210

gtg gtc acc atg gtt gac ggg cgc atc att ggg tct gag gtg aaa cac   787
Val Val Thr Met Val Asp Gly Arg Ile Ile Gly Ser Glu Val Lys His
    215                 220                 225

tca tgagccttgc agaatcaatt ctt                                    813
Ser
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230

<210> 512
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 512
Met Ser Leu Ile Glu Met Arg Asn Ile Val Lys Thr Tyr Asn Ile Gly
1 5 10 15

Ser Glu Gly Glu Leu Thr Val Leu His Gly Val Asp Phe His Val Asp
20 25 30

Arg Gly Glu Phe Val Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser
35 40 45

Thr Met Met Asn Ile Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr
50 55 60

Tyr Thr Leu Asp Gly Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu
65 70 75 80

Ala Ser His Arg Ala Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn
85 90 95

Leu Ile Gly Arg Ile Asp Ala Leu Lys Asn Val Glu Met Pro Met Met
100 105 110

Tyr Ala Gly Ile Pro Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu
115 120 125

Leu Glu Met Val Gly Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu
130 135 140

Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala
145 150 155 160

Asn Asp Pro Glu Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp
165 170 175

Ser Ala Thr Gly Arg Met Val Met Asp Ile Phe His Gln Leu Asn Lys
180 185 190

Glu Gln Gly Lys Thr Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala
195 200 205

Asp Glu Ser Asp Arg Val Val Thr Met Val Asp Gly Arg Ile Ile Gly
210 215 220

Ser Glu Val Lys His Ser
225 230

<210> 513
<211> 1185
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1162)
<223> RXC01004

<400> 513
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tcacccccat cacccatgaa gaagcaaagg agtacgaaaa gtg agt att tgg gca 115
Val Ser Ile Trp Ala
1 5

act gtc ctt cta att atc gtc ctt ctt tcc gcc aac gcc ttc ttc gtg 163
Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val
10 15 20

gcc gcg gag ttc gca ctg att tcc tcg cgc cgg gac cgc ctg gat tcc 211
Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser
25 30 35

ctg gta tcc cag ggt aaa aag gga gct gaa aag gtt ctc tac gca acc 259
Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr
40 45 50

gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc 307
Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val
55 60 65

tgt tct ctg att ctg ggt aaa gtc gca gaa cct gcg atc gcc cac ttc 355
Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe
70 75 80 85

att gag gtg cct ttc acc tcc tgg ggt gtt cca aat gat ttg atc cac 403
Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro Asn Asp Leu Ile His
90 95 100

cca att tcc ttc gtc atc gca ctg gcg atc atc acc tgg ttg cac att 451
Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile Thr Trp Leu His Ile
105 110 115

ctc ttt ggt gaa atg gtg cca aag aac atc gct att gct ggc cct gaa 499
Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala Ile Ala Gly Pro Glu
120 125 130

acc tta ggc atg tgg ctt gct cca gtg ctc att gcg ttt gtg aag att 547
Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile Ala Phe Val Lys Ile
135 140 145

acc cgc ccg ttg atc gag ttc atg aac tgg atc gcc cgt ctg acc ctt 595
Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile Ala Arg Leu Thr Leu
150 155 160 165

cgc gcc ttt ggt gtg gag caa aaa aac gag ctg gat tcc acc gtg gac 643
Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu Asp Ser Thr Val Asp
170 175 180

cca gag cag ctg gca tca atg att tcc gag tcc cgt tcc gaa ggc ctc 691
Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser Arg Ser Glu Gly Leu
185 190 195

ctt gat gct gaa gag cac gcc cgc ctg tcc aag gcg ctg cgc tct gag 739
Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys Ala Leu Arg Ser Glu

```
        200                 205                 210

cag cgt tcc atc aag gaa ctg gtg att aag gat gag gac gtg cgc acg   787
Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr
    215                 220                 225

ctg gcg ttc ggt aaa tct ggc ccg acc ttg cac cag ttg gag gaa gca   835
Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala
230                 235                 240                 245

gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc ggc cgc gat gga   883
Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly
                250                 255                 260

tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct   931
Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala
            265                 270                 275

gat cct gag atg gat ccc tcc gag acc att ccg cgt tct gca ctg cgc   979
Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg
        280                 285                 290

cct ttg agc aat gtg gat gcc gac ggc ctc atg gat gac gtc ttg gat   1027
Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp
    295                 300                 305

ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt   1075
Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly
310                 315                 320                 325

gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg   1123
Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val
                330                 335                 340

ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt    1172
Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp
            345                 350

aactgtgttg gac                                                   1185


<210> 514
<211> 354
<212> PRT
<213> Corynebacterium glutamicum

<400> 514
Val Ser Ile Trp Ala Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala
  1               5                  10                  15

Asn Ala Phe Phe Val Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg
             20                  25                  30

Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys
         35                  40                  45

Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln
     50                  55                  60

Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro
 65                  70                  75                  80
```

```
Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro
                85                  90                  95

Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile
            100                 105                 110

Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala
        115                 120                 125

Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile
    130                 135                 140

Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile
145                 150                 155                 160

Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu
                165                 170                 175

Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser
            180                 185                 190

Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys
        195                 200                 205

Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp
    210                 215                 220

Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His
225                 230                 235                 240

Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val
                245                 250                 255

Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile
            260                 265                 270

Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro
        275                 280                 285

Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met
    290                 295                 300

Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln
305                 310                 315                 320

Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu
                325                 330                 335

Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser
            340                 345                 350

Asp Asp
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<210> 515
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXC01017

<400> 515
gaaatttgag ggggcgctac ccttagaagg tgcgcaatga caccacgata gttcgcgcct 60

agtgtggatt gctagaaaac tttaagaaag aggaaataat atg gct caa aaa gta 115
Met Ala Gln Lys Val
1 5

acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc 163
Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg
10 15 20

tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt 211
Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val
25 30 35

cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat 259
Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp
40 45 50

tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca 307
Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala
55 60 65

gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca 355
Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala
70 75 80 85

atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc 403
Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser
90 95 100

ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct 451
Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala
105 110 115

gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc 499
Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg
120 125 130

gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc 547
Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr
135 140 145

cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc 595
Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr
150 155 160 165

cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc 643
Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe
170 175 180

aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act 691
Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr
185 190 195

gag aac cca cag ttc gac taattaacgc tgtctctgct tat 732

Glu Asn Pro Gln Phe Asp
200

<210> 516
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 516
Met Ala Gln Lys Val Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys
1 5 10 15

Trp Val Thr Ser Arg Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile
20 25 30

Glu Ile Gln Trp Val Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg
35 40 45

Asp Leu Pro Glu Asp Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro
50 55 60

Ala Arg Val Phe Ala Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly
65 70 75 80

Asp Leu Tyr Thr Ala Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly
85 90 95

Pro Ile Glu Gly Ser Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu
100 105 110

Val Gly Leu Asp Ala Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp
115 120 125

Asp Asp Ala Leu Arg Ala Phe His Gln Thr Ala Met Asp Glu Val Gly
130 135 140

Asn Asp Val Gly Thr Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe
145 150 155 160

Gly Pro Val Leu Thr Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile
165 170 175

Phe Asp Ala Ser Phe Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile
180 185 190

Lys Arg Ser Arg Thr Glu Asn Pro Gln Phe Asp
195 200

<210> 517
<211> 622
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(622)
<223> RXC01021

<400> 517

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cgagaggctt ttttggctct aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa   115
                                        Met Ser Ser Ser Glu
                                          1               5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa   163
Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu
                 10                  15                  20

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct   211
Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala
             25                  30                  35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct   259
Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala
         40                  45                  50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc   307
Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val
     55                  60                  65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg   355
Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met
 70                  75                  80                  85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc   403
Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val
                 90                  95                 100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga   451
Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg
            105                 110                 115

gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag   499
Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln
        120                 125                 130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta   547
Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu
    135                 140                 145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag   595
Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu
150                 155                 160                 165

ggc act gtt gtc act gtg ttg cgt tct                              622
Gly Thr Val Val Thr Val Leu Arg Ser
                170
```

<210> 518
<211> 174
<212> PRT
<213> Corynebacterium glutamicum

<400> 518

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Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro
  1               5                  10                  15

Ser Val Gln Pro Glu Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala
```

```
            20                  25                  30

Ala Ser Lys Glu Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu
         35                  40                  45

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile
     50                  55                  60

Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn
 65                  70                  75                  80

Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly
                 85                  90                  95

Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser
            100                 105                 110

Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu
        115                 120                 125

Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr
    130                 135                 140

Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile
145                 150                 155                 160

Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser
                165                 170
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<210> 519
<211> 1047
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1024)
<223> RXC01212

<400> 519

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tttagaagcc acatgacata tgtcatgaaa attatgtgca aagtgcagta atactcctga 60

catatggctc taccagcgcc aatgcgaagt aggaagaatt atg cct atg aca acg   115
                                              Met Pro Met Thr Thr
                                                1               5

aca cca gca atc gac gta aca gac ctc gtg aga acc tac ggc gac tac   163
Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg Thr Tyr Gly Asp Tyr
            10                  15                  20

acc gca gtc aag ggc ctg aat ttc cat gta cag cgc ggt gaa gta ttt   211
Thr Ala Val Lys Gly Leu Asn Phe His Val Gln Arg Gly Glu Val Phe
        25                  30                  35

ggt ctg ctc ggc acc aac ggg gcc ggc aaa acc tcc acc ttg gaa gtc   259
Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val
    40                  45                  50

atc gaa gga ctt tcc gca ccc agc tcc ggc acc gtg cgc atc tcc ggg   307
Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly
```

```
     55                  60                  65

ctt gac ccc gtt gcc gac cgc gcg atc ctg cgc ccc gag ctc ggc atc   355
Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile
 70                  75                  80                  85

atg ctg caa tca ggc ggc ctg cca tca cag ctc acc gtc gcc gaa acc   403
Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr
                 90                  95                 100

atg gac atg tgg cac ggc acc tgc acg tat ccg cgc gcc att aaa gat   451
Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp
            105                 110                 115

gtg ctt gcc gac gtc gac ctc cta cac cgc gaa aac gtc aag gtc ggc   499
Val Leu Ala Asp Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly
        120                 125                 130

gcg ctt tcc gga ggc gaa caa cga cgc ctt gat ttg gcc tgc gca ctg   547
Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu
    135                 140                 145

ctt ggc gac ccc tca att ttg ttc ctc gac gaa ccc acc acc ggc ctc   595
Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu
150                 155                 160                 165

gac cca gaa tct agg cgc cac acc tgg caa ctc ctg ctg gac ctg aaa   643
Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu Leu Leu Asp Leu Lys
                170                 175                 180

cag cgc ggc gtc acc atg atg ctg acc acc cac tac ctg gag gaa gcc   691
Gln Arg Gly Val Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala
            185                 190                 195

gaa ttc ctc tgc gac cgg att gcc atc atg aac gcc ggt gag atc gca   739
Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala
        200                 205                 210

gtg gaa ggc acc ttg gat gaa ctg gtg gcc cgc gag aag tcg atc atc   787
Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile
    215                 220                 225

agt ttc gtg ctg cgt ggc ggg cag gtg gag ttg ccg gtc ttg agt ggg   835
Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu Pro Val Leu Ser Gly
230                 235                 240                 245

gct gaa atc atc cgc gac aac aac cac gtc cgc atc gcc acc acc acc   883
Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr Thr
                250                 255                 260

ctg cag cag cac acc tta gaa ata ctt acc tgg gct gca gag acc ggg   931
Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly
            265                 270                 275

atc gcg ctg gaa ggc ttc gct gca aaa ccc gcc acc ttg gaa tcc gta   979
Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val
        280                 285                 290

ttc atg gac atc gcc tca ctc gag aac acc tcg ctg caa acc gcc       1024
Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser Leu Gln Thr Ala
    295                 300                 305
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US 2006/0134709 A1

tagaatcttt aaggagacca caa 1047

<210> 520
<211> 308
<212> PRT
<213> Corynebacterium glutamicum

<400> 520
Met Pro Met Thr Thr Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg
1 5 10 15

Thr Tyr Gly Asp Tyr Thr Ala Val Lys Gly Leu Asn Phe His Val Gln
20 25 30

Arg Gly Glu Val Phe Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr
35 40 45

Ser Thr Leu Glu Val Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr
50 55 60

Val Arg Ile Ser Gly Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg
65 70 75 80

Pro Glu Leu Gly Ile Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu
85 90 95

Thr Val Ala Glu Thr Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro
100 105 110

Arg Ala Ile Lys Asp Val Leu Ala Asp Val Asp Leu Leu His Arg Glu
115 120 125

Asn Val Lys Val Gly Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp
130 135 140

Leu Ala Cys Ala Leu Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu
145 150 155 160

Pro Thr Thr Gly Leu Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu
165 170 175

Leu Leu Asp Leu Lys Gln Arg Gly Val Thr Met Met Leu Thr Thr His
180 185 190

Tyr Leu Glu Glu Ala Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn
195 200 205

Ala Gly Glu Ile Ala Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg
210 215 220

Glu Lys Ser Ile Ile Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu
225 230 235 240

Pro Val Leu Ser Gly Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg
245 250 255

Ile Ala Thr Thr Thr Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp
260 265 270

```
Ala Ala Glu Thr Gly Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala
        275                 280                 285

Thr Leu Glu Ser Val Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser
    290                 295                 300

Leu Gln Thr Ala
305
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<210> 521
<211> 1131
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1108)
<223> RXC01306

<400> 521

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tgttttagag gtagagcgaa acgtgcctgt aaaactggcg ctcgctgtgc tcgaagacca 60

cccagacaat caccccgctc cgaaggagaa tcgctaagcc atg act gaa tgg tat   115
                                            Met Thr Glu Trp Tyr
                                              1               5

gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc   163
Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala Leu Ser Ala Phe Phe
                10                  15                  20

gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag   211
Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg Arg Asn Arg Leu Glu
            25                  30                  35

gag act gtg gaa acc tcg cgg tct tcc cgc gct gcg ttg cga agc ctc   259
Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala Ala Leu Arg Ser Leu
        40                  45                  50

aat gaa ctt act ctc atg ctc gcg ggc gcg cag ttg gga atc acc atg   307
Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln Leu Gly Ile Thr Met
    55                  60                  65

gtg act ttc gcg ttg ggt gct atc acg aag ccg tgg gtt cat tat gct   355
Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro Trp Val His Tyr Ala
70                  75                  80                  85

ttg atg ccg ctc ttc gaa tgg gcg cgt ata ccg ctg gtt atg gca gat   403
Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro Leu Val Met Ala Asp
                90                  95                  100

gtc att gcg ttt att ttg tcg ctg ttt atc gta acg ttt ctg cac ttg   451
Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val Thr Phe Leu His Leu
            105                 110                 115

gtc atc ggc gaa atg gct ccg aaa tcc tgg gca atc gcg cat ccg gag   499
Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala Ile Ala His Pro Glu
        120                 125                 130

acg gca ctt cga act atc gcg att ccc gca cgg ggc ttc att aac ctg   547
Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg Gly Phe Ile Asn Leu
```

```
    135                 140                 145

ttt cgt cca ttg ctg cag tgg atc aac aaa atg gcg aac gat ttg gtc   595
Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met Ala Asn Asp Leu Val
150                 155                 160                 165

cgc aaa gtt ggt gaa act ccc gtt gat cga gct gca gct ggt ggc tat   643
Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala Ala Ala Gly Gly Tyr
                170                 175                 180

gac acc gat acc ctc cat gcc ctc att gag cat tcc cga gaa act ggc   691
Asp Thr Asp Thr Leu His Ala Leu Ile Glu His Ser Arg Glu Thr Gly
            185                 190                 195

gct ctg gat cag caa tcc gcc gcc caa atc agc gga att atc aag ctg   739
Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser Gly Ile Ile Lys Leu
        200                 205                 210

gat aaa atc acg gtc ggt caa acc ctg acc gca tct cca ttt acg cac   787
Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala Ser Pro Phe Thr His
    215                 220                 225

agc gcc agc gcc acg gtt gct gag gtg caa gcc gca gct cag cgc agt   835
Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala Ala Ala Gln Arg Ser
230                 235                 240                 245

ggc agc ttg cgt gtg ctt atc gac gcc ccc tcc cac ctt ttc cca cac   883
Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser His Leu Phe Pro His
                250                 255                 260

gtc att cat gtg cga gac acc ctt ggt gcc tcg cca gac gag aag gct   931
Val Ile His Val Arg Asp Thr Leu Gly Ala Ser Pro Asp Glu Lys Ala
            265                 270                 275

tcg aag tgg tct cgc cca atc ctc acc gtt gct gag acc gac acg tta   979
Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala Glu Thr Asp Thr Leu
        280                 285                 290

cac caa gcg ctg gaa tac atg cgg gag cat aac gag cag atc agt gcg   1027
His Gln Ala Leu Glu Tyr Met Arg Glu His Asn Glu Gln Ile Ser Ala
    295                 300                 305

gtg ctt tcc gct gat ggg aaa acg gtg ctt ggt gta ata act tgg gat   1075
Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly Val Ile Thr Trp Asp
310                 315                 320                 325

cac atc ttg aaa tac ctg tgg cct gca tcg gtg tagctaattt gaggtgcgct 1128
His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
                330                 335

gaa                                                               1131
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<210> 522
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 522

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Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala
  1               5                  10                  15
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Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg
20 25 30

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
35 40 45

Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
50 55 60

Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
65 70 75 80

Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
85 90 95

Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
100 105 110

Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
115 120 125

Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
130 135 140

Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
145 150 155 160

Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
165 170 175

Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His
180 185 190

Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser
195 200 205

Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala
210 215 220

Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala
225 230 235 240

Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser
245 250 255

His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser
260 265 270

Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala
275 280 285

Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn
290 295 300

Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly
305 310 315 320

Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
325 330 335

Doc No. 6695

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<211> 513
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(490)
<223> RXC01366

<400> 523
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gactgtccaa acctaaacca aaggtctaaa ctttggcttc gtg agt cag ttt cgt 115
Val Ser Gln Phe Arg
1 5

cgt tgt tcc cgc cct ggt tgt ggc aag cct gcc gtc gca acc ctc acc 163
Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala Val Ala Thr Leu Thr
10 15 20

tac gca tat tcg gat tcc act gcg gtg gtt ggt cct ttg gcg cct gca 211
Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly Pro Leu Ala Pro Ala
25 30 35

gca gag ccc cat agt tgg gat ctg tgt gag cat cat gcc gag cgt att 259
Ala Glu Pro His Ser Trp Asp Leu Cys Glu His His Ala Glu Arg Ile
40 45 50

act gcg ccc ctt ggt tgg gag atg ctg cgg gtg aac gac atc aaa gtc 307
Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val Asn Asp Ile Lys Val
55 60 65

gat gac gat gag gat ctg acg gct ctt gct cag gct gtt cgt gag gct 355
Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln Ala Val Arg Glu Ala
70 75 80 85

gga cgc act gtg agt ggt ctg gtt cct gaa gac gaa gtg ggc ggc aac 403
Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp Glu Val Gly Gly Asn
90 95 100

cat ccg gtg aac cgg agt gcg cgg atc gcg gaa cag aag gtt cac cgc 451
His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu Gln Lys Val His Arg
105 110 115

agg ggt cat ctc tat gtt gtg cct gat cag gac gaa tca taaggtttgc 500
Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp Glu Ser
120 125 130

tattcggatt gga 513

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<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 524
Val Ser Gln Phe Arg Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala
1 5 10 15

Val Ala Thr Leu Thr Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly
20 25 30

Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His
35 40 45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val
50 55 60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln
65 70 75 80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp
85 90 95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu
100 105 110

Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp
115 120 125

Glu Ser
130

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<211> 614
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<223> RXC01372

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Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser
1 5 10 15

cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa 96
Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
20 25 30

gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc 144
Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
35 40 45

att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc 192
Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
50 55 60

aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg 240
Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
65 70 75 80

cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc 288

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His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
                 85                  90                  95

cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc   336
Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
            100                 105                 110

gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc   384
Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
        115                 120                 125

gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta   432
Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
    130                 135                 140

ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat   480
Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
145                 150                 155                 160

gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa   528
Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
                165                 170                 175

gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att   576
Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
            180                 185                 190

gaa gaa aag gac ttg taaatggagc tattggaagg ctc                    614
Glu Glu Lys Asp Leu
        195
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<210> 526
<211> 197
<212> PRT
<213> Corynebacterium glutamicum

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<400> 526
Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser
  1               5                  10                  15

Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu
             20                  25                  30

Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys
         35                  40                  45

Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val
     50                  55                  60

Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val
 65                  70                  75                  80

His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala
                 85                  90                  95

Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro
            100                 105                 110

Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr
        115                 120                 125
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```
Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val
    130                 135                 140

Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp
145                 150                 155                 160

Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln
                165                 170                 175

Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile
            180                 185                 190

Glu Glu Lys Asp Leu
        195
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<210> 527
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXC01659

<400> 527

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tcgagattga taccgtctct ggattccgcc tgctcagtac gtg gcg ggg gtt gcg   115
                                               Val Ala Gly Val Ala
                                                 1               5

cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca   163
Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro
                  10                  15                  20

gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa   211
Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu
              25                  30                  35

acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg   259
Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro
          40                  45                  50

ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg   307
Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr
      55                  60                  65

cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag   355
Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys
  70                  75                  80                  85

ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa   403
Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu
                  90                  95                 100

gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg   451
Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met
            105                 110                 115
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```
ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca   499
Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser
        120                 125                 130

ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag cgt   547
Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg
    135                 140                 145

ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt cag   595
Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln
150                 155                 160                 165

tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag   643
Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys Lys
                170                 175                 180

tgg tagaaaactg gtgtttttcg gcc                                    669
Trp
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US20070269869A1

<210> 528
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 528

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Val Ala Gly Val Ala Gln Arg Phe Val Asp Glu Arg Ile His Val Gly
  1               5                  10                  15

Leu Asp Ser Met Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp
            20                  25                  30

Trp Val Leu Ala Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu
        35                  40                  45

Glu Ile Leu Arg Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu
    50                  55                  60

Pro Pro Arg Ser Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu
65                  70                  75                  80

Pro Ser Arg Leu Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro
                85                  90                  95

Asn Ala Ser Glu Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu
            100                 105                 110

Glu Pro Leu Gln Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val
        115                 120                 125

Val Glu Pro Arg Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu
    130                 135                 140

Gly Asp Pro Glu Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg
145                 150                 155                 160

Asp Leu Asn Gly Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp
                165                 170                 175
```

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Glu Pro Pro Lys Lys Trp
            180


<210> 529
<211> 981
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(958)
<223> RXC01663

<400> 529
tattttgctg gttggtcaca gtggagcgct aaccccgaga atcctatcga ggcctaaaat 60

cgtggcttga gtacgcactg ccagtaaggt gtgtgatgtg atg gaa ata agt gtc   115
                                        Met Glu Ile Ser Val
                                          1               5

ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc   163
Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
                 10                  15                  20

gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc   211
Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
             25                  30                  35

tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag   259
Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
         40                  45                  50

ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag   307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu
     55                  60                  65

ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag   355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu
 70                  75                  80                  85

ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat   403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp
                 90                  95                 100

gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac   451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr
             105                 110                 115

ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg   499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala
         120                 125                 130

gag gta gct gcg gac gag gag caa cgg ggc gtc gat aag cat tcg ttt   547
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp Lys His Ser Phe
     135                 140                 145

ttg agc tct ttg cct ggt tcg cag cgc cgg gag cgc cga aac tgg gcg   595
Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu Arg Arg Asn Trp Ala
150                 155                 160                 165
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gcg aag cac cac ttc gat ttc atc aag gaa gat gcc ttt ttg acc gat   643
Ala Lys His His Phe Asp Phe Ile Lys Glu Asp Ala Phe Leu Thr Asp
                170                 175                 180

gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg   691
Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val
            185                 190                 195

gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg   739
Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala
        200                 205                 210

ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc   787
Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val
    215                 220                 225

att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa   835
Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu
230                 235                 240                 245

tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc   883
Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu
                250                 255                 260

agt acg tgg cgg ggg ttg cgc agc gtt ttg tcg acg agc gca ttc acg   931
Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr
            265                 270                 275

tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa        978
Ser Val Trp Ile Pro Cys Gln Lys Leu
        280                 285

tct                                                              981


<210> 530
<211> 286
<212> PRT
<213> Corynebacterium glutamicum

<400> 530
Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly
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Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala
            20                  25                  30

Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu
        35                  40                  45

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala
    50                  55                  60

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro
65                  70                  75                  80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp
                85                  90                  95

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr
            100                 105                 110
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Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln
        115                 120                 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val
    130                 135                 140

Asp Lys His Ser Phe Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu
145                 150                 155                 160

Arg Arg Asn Trp Ala Ala Lys His His Phe Asp Phe Ile Lys Glu Asp
                165                 170                 175

Ala Phe Leu Thr Asp Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala
            180                 185                 190

Val Ala Arg Asp Val Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His
        195                 200                 205

Leu Val Asp Leu Ala Gly Val Pro Val Met Ala Met Arg Arg Gly Ile
    210                 215                 220

Thr Ser Asp Val Val Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp
225                 230                 235                 240

Pro Glu Arg Glu Glu Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser
                245                 250                 255

Gly Phe Arg Leu Leu Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser
            260                 265                 270

Thr Ser Ala Phe Thr Ser Val Trp Ile Pro Cys Gln Lys Leu
        275                 280                 285


<210> 531
<211> 1545
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1522)
<223> RXC01693

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gtcccaacaa ttgccagaac ccgaacacta ggcttgaacc atg aat act gca cct   115
                                            Met Asn Thr Ala Pro
                                              1               5

ttc aaa ctc gaa gct gac ttc gca tca gcc ctg ccc acc atg gca gcc   163
Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu Pro Thr Met Ala Ala
                10                  15                  20

ccc tgg caa ggt gag gaa gcc ccc aac cct gag ctc gtg att tta aat   211
Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu Leu Val Ile Leu Asn
            25                  30                  35

gac gac ctc gcc tac agc ctc ggg ctt gat ccg aca tgg ctt cgc aca   259
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Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro Thr Trp Leu Arg Thr
         40                  45                  50

cct gag ggc gtt caa ttt ctt ctc gga ctc aac ccc gag ccc tta aca   307
Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn Pro Glu Pro Leu Thr
     55                  60                  65

aaa gca gtt gcg cag gcc tat tcc ggc cac caa ttc gga cag ttt gtg   355
Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln Phe Gly Gln Phe Val
 70                  75                  80                  85

gca agc ctt ggt gat ggc cga gcg ctt ctt ctc ggc gaa gcc cgc tca   403
Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu Gly Glu Ala Arg Ser
                 90                  95                 100

gct gac ggc gta ctg cat gat atc cac ctc aaa gga tct gga cga acc   451
Ala Asp Gly Val Leu His Asp Ile His Leu Lys Gly Ser Gly Arg Thr
            105                 110                 115

caa ttc tcc cga gga gcc gat gga cgc gcc gtc ctt ggc ccc gtc tta   499
Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val Leu Gly Pro Val Leu
        120                 125                 130

cgc gaa tac atc atc tcc gaa gcg atg cat gca ctt ggt gtt ccc acc   547
Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala Leu Gly Val Pro Thr
    135                 140                 145

acc agg tca ctt gca gta att agc acc ggt agg aaa atc caa cga gga   595
Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg Lys Ile Gln Arg Gly
150                 155                 160                 165

agc gta gcc cca ggc gca gtc ctt gtt cga gta gca acc agc ctc att   643
Ser Val Ala Pro Gly Ala Val Leu Val Arg Val Ala Thr Ser Leu Ile
                170                 175                 180

cga gtc gga tcc ttc caa tac tcc aac atc tct ggt ggc atc gaa cta   691
Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser Gly Gly Ile Glu Leu
            185                 190                 195

tct caa cac ctg gcg aac tat acg atc acc agg cat ttc cct tcg ttg   739
Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg His Phe Pro Ser Leu
        200                 205                 210

gta gct gaa cta tcc gca cca acc ccc gca act tat gta tca ctg ttt   787
Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr Tyr Val Ser Leu Phe
    215                 220                 225

aaa gcg att ctt cag cgc caa gca gac acc gtt gga aaa tgg acc agg   835
Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val Gly Lys Trp Thr Arg
230                 235                 240                 245

ctg ggt ttc gtt cac gga gcc ctc aac aca gac aac acg ttg ata tcc   883
Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp Asn Thr Leu Ile Ser
                250                 255                 260

gga gaa act gtt gac tac ggc cca tgc gct ttc atg gag cgc tac cgt   931
Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe Met Glu Arg Tyr Arg
            265                 270                 275

ggc gac gcg aaa ttt agc tcc atc gac act tat ggt cgc tac aaa ttt   979
Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr Gly Arg Tyr Lys Phe
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Sequence Listing

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        280                 285                 290

gaa aac caa cct atg atc ctc gga tgg aac atg gcc cgc ctc gta gaa   1027
Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met Ala Arg Leu Val Glu
    295                 300                 305

acc ctc ctc cca ctc ctg ggc gcc aca cca gac gaa ggc atg aca gca   1075
Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp Glu Gly Met Thr Ala
310                 315                 320                 325

gcc caa gaa gct ctc gta gaa ttc gat gac ctc tgc gaa caa gca atc   1123
Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu Cys Glu Gln Ala Ile
                330                 335                 340

cga aaa gaa ttc gcc act gca ctg ggc ctt gac gag tca gac acc ggc   1171
Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp Glu Ser Asp Thr Gly
            345                 350                 355

acg gta gag cag ttc cgt gaa ctg ctc tac ctc cat aac ccc gac atc   1219
Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu His Asn Pro Asp Ile
        360                 365                 370

acc acg ctg ctg cgc gca ctc acc gac aac acc gca cca ccg agt ggc   1267
Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr Ala Pro Pro Ser Gly
    375                 380                 385

ttt gaa gca ttc gtt cac gac tgg aaa acc caa gac cca gat atc gaa   1315
Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln Asp Pro Asp Ile Glu
390                 395                 400                 405

gca atg cga gca gta aat cca ctt ttc att cca cgc aat cac ctc gtg   1363
Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro Arg Asn His Leu Val
                410                 415                 420

gaa gct gct ctc gca gac gca gtt gaa ggg aat cta gaa aag ttc cac   1411
Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn Leu Glu Lys Phe His
            425                 430                 435

gaa ctc ctc gct gct gtc acc aat cct ttt gat cca act gcg ggc ccc   1459
Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp Pro Thr Ala Gly Pro
        440                 445                 450

gat gaa cta cgc ctg cca agc gaa gaa gga ttt gaa gaa gac tac atg   1507
Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe Glu Glu Asp Tyr Met
    455                 460                 465

acc ttc tgc ggt acc taggacagat ggtggggcag acg                    1545
Thr Phe Cys Gly Thr
470
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<210> 532
<211> 474
<212> PRT
<213> Corynebacterium glutamicum

<400> 532

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Met Asn Thr Ala Pro Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu
  1               5                  10                  15

Pro Thr Met Ala Ala Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu
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            20                  25                  30

Leu Val Ile Leu Asn Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro
         35                  40                  45

Thr Trp Leu Arg Thr Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn
     50                  55                  60

Pro Glu Pro Leu Thr Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln
 65                  70                  75                  80

Phe Gly Gln Phe Val Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu
                 85                  90                  95

Gly Glu Ala Arg Ser Ala Asp Gly Val Leu His Asp Ile His Leu Lys
            100                 105                 110

Gly Ser Gly Arg Thr Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val
        115                 120                 125

Leu Gly Pro Val Leu Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala
    130                 135                 140

Leu Gly Val Pro Thr Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg
145                 150                 155                 160

Lys Ile Gln Arg Gly Ser Val Ala Pro Gly Ala Val Leu Val Arg Val
                165                 170                 175

Ala Thr Ser Leu Ile Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser
            180                 185                 190

Gly Gly Ile Glu Leu Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg
        195                 200                 205

His Phe Pro Ser Leu Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr
    210                 215                 220

Tyr Val Ser Leu Phe Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val
225                 230                 235                 240

Gly Lys Trp Thr Arg Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp
                245                 250                 255

Asn Thr Leu Ile Ser Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe
            260                 265                 270

Met Glu Arg Tyr Arg Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr
        275                 280                 285

Gly Arg Tyr Lys Phe Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met
    290                 295                 300

Ala Arg Leu Val Glu Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp
305                 310                 315                 320

Glu Gly Met Thr Ala Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu
                325                 330                 335

Cys Glu Gln Ala Ile Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp
            340                 345                 350
```

Sequence - Copyright

```
Glu Ser Asp Thr Gly Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu
        355                 360                 365

His Asn Pro Asp Ile Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr
    370                 375                 380

Ala Pro Pro Ser Gly Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln
385                 390                 395                 400

Asp Pro Asp Ile Glu Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro
                405                 410                 415

Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn
            420                 425                 430

Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp
        435                 440                 445

Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe
    450                 455                 460

Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr
465                 470
```

<210> 533
<211> 1236
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1213)
<223> RXC01703

<400> 533

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gttagacaaa tgggtaaaca gagctgacct agcggaatcc gccatcaacg aaaggcattc 60

cgcgagggtt tggggtctgc ctcgaacaaa tcttgggttt gtg gca tgg cca tcc   115
                                              Val Ala Trp Pro Ser
                                                1               5

aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg   163
Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala
            10                  15                  20

cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag   211
His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg Arg Arg Thr Thr Lys
        25                  30                  35

gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tcg gtg cgc   259
Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg
    40                  45                  50

aat gtg ggc aag ctg acc tcg aat cgt tat tac gac gac aaa gct tgg   307
Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp
55                  60                  65

ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca   355
Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr
```

```
 70                  75                  80                  85

cca aaa tca ttg ccc tcg ttg gaa caa aac atc gtc gat ggc att gat   403
Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp
                 90                  95                 100

tcc ctt act ggt gtg ctg ccg tgg cgt tcc ggc gaa acc ttc tac aac   451
Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly Glu Thr Phe Tyr Asn
            105                 110                 115

gtt ccc tcc aac ggt cct gct gcg atc atg atg gcc cgc acc gac cgt   499
Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met Ala Arg Thr Asp Arg
        120                 125                 130

ttg gac gag gct atg aaa atc acc gat tgg att ttt gac aac ctg atc   547
Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile Phe Asp Asn Leu Ile
    135                 140                 145

gat ggc gac ggc ctt gtg atg gac gga ttg cgc atg cgc atg cac gga   595
Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg Met Arg Met His Gly
150                 155                 160                 165

cct gag ctt gtc cgt tcc atc cac ccg tat tgc caa ggt gtc gcc att   643
Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys Gln Gly Val Ala Ile
                170                 175                 180

ggt gcg tgt ttg gaa att gct ctc aaa ctg cgt gag cgc gca ggc ttg   691
Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg Glu Arg Ala Gly Leu
            185                 190                 195

acc act act gtg gtg gat cac tgg tcg gat gcc gat aag gca gaa gac   739
Thr Thr Thr Val Val Asp His Trp Ser Asp Ala Asp Lys Ala Glu Asp
        200                 205                 210

tcc ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tcg   787
Ser Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser
    215                 220                 225

cgg aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac   835
Arg Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp
230                 235                 240                 245

ggc gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat   883
Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp
                250                 255                 260

gtg gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa   931
Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys
            265                 270                 275

aag att gca gca cgc ctg gta ctg gaa tcg gcg gaa agc gta tgg aac   979
Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn
        280                 285                 290

cac cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca  1027
His Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr
    295                 300                 305

acg gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg  1075
Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu
310                 315                 320                 325
```

```
agc gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg   1123
Ser Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val
                330                 335                 340

caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa   1171
Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu
            345                 350                 355

gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga           1213
Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
        360                 365                 370

tagccccgat agtgtatgtg ctg                                        1236
```

<210> 534
<211> 371
<212> PRT
<213> Corynebacterium glutamicum

<400> 534

```
Val Ala Trp Pro Ser Asn Ala Lys Glu Lys Leu Phe Ile His Trp His
  1               5                  10                  15

Tyr Trp Trp Gln Ala His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg
             20                  25                  30

Arg Arg Thr Thr Lys Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg
         35                  40                  45

Gly Ile Ser Val Arg Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr
     50                  55                  60

Asp Asp Lys Ala Trp Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val
 65                  70                  75                  80

Arg Lys Val Arg Thr Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile
                 85                  90                  95

Val Asp Gly Ile Asp Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly
            100                 105                 110

Glu Thr Phe Tyr Asn Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met
        115                 120                 125

Ala Arg Thr Asp Arg Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile
    130                 135                 140

Phe Asp Asn Leu Ile Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg
145                 150                 155                 160

Met Arg Met His Gly Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys
                165                 170                 175

Gln Gly Val Ala Ile Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg
            180                 185                 190

Glu Arg Ala Gly Leu Thr Thr Thr Val Val Asp His Trp Ser Asp Ala
        195                 200                 205
```

Sequence Listing

```
Asp Lys Ala Glu Asp Ser Leu Lys Tyr Phe Ala His Ile His Ala Val
    210                 215                 220

Val Gln Ala Val Ser Arg Lys Met Thr Asn Phe His Gly Val Ile Asp
225                 230                 235                 240

Trp Asp Thr Gly Asp Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val
                245                 250                 255

Arg Tyr Leu Ala Asp Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr
            260                 265                 270

Asn Arg Glu Thr Lys Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala
        275                 280                 285

Glu Ser Val Trp Asn His Arg Leu Glu Val Asp Gly Leu Pro Val Phe
    290                 295                 300

Ala Thr Asp Trp Thr Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu
305                 310                 315                 320

Ser Ser Ser Ser Leu Ser Asp Leu Val Ser Val Val Arg Val Asp Glu
                325                 330                 335

Arg Asp Leu Ser Val Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala
            340                 345                 350

Ala Lys Val Ala Glu Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly
        355                 360                 365

Arg Ser Arg
    370


<210> 535
<211> 800
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(777)
<223> RXC02254

<400> 535
atc gcc gtt gcc gaa gaa ggc gga ttg tgg gaa aac ctc ctg cag cac   48
Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His
  1               5                  10                  15

cgc ttc ggt gga cat ggt gcg cta gct ggt cac gcc ttg gga aac ctc   96
Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
             20                  25                  30

gtg atc gcg gcg ttg acc gac att ttg ggc acc tcc cag cat gcg ctt   144
Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
         35                  40                  45

gat caa atc gct caa ctc gct gga gcc aaa gga cgc atc atc ccg gta   192
Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
     50                  55                  60
```

```
tgt gct gaa cct ttg gat ctt gaa gcg gaa gta tca ggt cta gac tct   240
Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
 65                  70                  75                  80

gat gct cga gtc atg cgt caa gtt cgt ggt caa gtg gcg gta gct gca   288
Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
                85                  90                  95

acc ccc ggg cag gtg cga cgc gtt cga atc att ccg gac aat cca gaa   336
Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
            100                 105                 110

ccg aac ccc gct gcc atc gag gcc att ctc gat gca gat ttg gtc acc   384
Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
        115                 120                 125

ctt ggc cca ggt tcc tgg ttc tcc tct gtg att cca cac att ttg gtc   432
Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
    130                 135                 140

cca ggg atc gtt gat gcc ttg gcg cag aca aaa gca acc aaa acc gtg   480
Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
145                 150                 155                 160

gtg tta aac ctg acg tcc gag cca ggg gag acc gcg gga ttc tct gca   528
Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
                165                 170                 175

gaa cga cac atc cat gtg ctc cgc cag cat gct cga aac ctt cag gtt   576
Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
            180                 185                 190

gac caa gtc att gtc gat gcc aag aca ctg tcc tca caa acc gaa cgc   624
Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
        195                 200                 205

aat cat gta gaa cga gct gct cgc acc ctt ggt gca gaa gtc tcc ttc   672
Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
    210                 215                 220

cat gat gtc cag gct gaa gat ggc cgt ggt cga ttc acc agt att cac   720
His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
225                 230                 235                 240

gat cca gca aag ctg tgt gca gcg ttg ctg gca agt ttt gct gga gca   768
Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
                245                 250                 255

cga aag cgt taaggagtag gcgtgtcact gac                            800
Arg Lys Arg
```

<210> 536
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 536

```
Ile Ala Val Ala Glu Glu Gly Gly Leu Trp Glu Asn Leu Leu Gln His
  1               5                  10                  15
```

Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
20 25 30

Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
35 40 45

Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
50 55 60

Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
65 70 75 80

Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
85 90 95

Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
100 105 110

Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
115 120 125

Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
130 135 140

Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
145 150 155 160

Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
165 170 175

Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
180 185 190

Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
195 200 205

Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
210 215 220

His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
225 230 235 240

Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
245 250 255

Arg Lys Arg

<210> 537
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXC02255

<400> 537

09609260.030502

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gtgtgcagcg ttgctggcaa gttttgctgg agcacgaaag cgttaaggag taggcgtgtc 60

actgacgagt gatatcaaac aagaattggc gcaggtccat gtg gcc aaa aac agt   115
                                            Val Ala Lys Asn Ser
                                              1               5

gtt cgt gct gcg gaa gtg tct gca att tta agg ttt gct ggt gag atg   163
Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg Phe Ala Gly Glu Met
                 10                  15                  20

caa gct gtc ggc ggc aag ctg gtc atc gaa gca aat ttg gac agc atg   211
Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala Asn Leu Asp Ser Met
             25                  30                  35

caa gtc ggt atg agg ctt cag gag ttt atc caa ggt ttg tac aac tct   259
Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln Gly Leu Tyr Asn Ser
         40                  45                  50

cga gtc gat gtg cac acc gtg aac ccg act gtg agc agg aaa acg cca   307
Arg Val Asp Val His Thr Val Asn Pro Thr Val Ser Arg Lys Thr Pro
     55                  60                  65

cgg tat ttg gtg cgc atc att gac aat gcc gat gaa att gcg cga cgc   355
Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp Glu Ile Ala Arg Arg
 70                  75                  80                  85

acc gga ctg gtc acc agg tct gga cat gtg gtt aaa ggt cta gcg cct   403
Thr Gly Leu Val Thr Arg Ser Gly His Val Val Lys Gly Leu Ala Pro
                 90                  95                 100

tct gtg gtc agc gga aca atc agt gac gct gaa gct gca tgg cgc ggt   451
Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu Ala Ala Trp Arg Gly
            105                 110                 115

gcg ttt cta gcc aat gga tct tta agt gat cca ggt cgt tcc tct tcg   499
Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro Gly Arg Ser Ser Ser
        120                 125                 130

ttg gag gtg ttg tgt cct ggt caa gaa tca gca ttg gca ctg gtt gga   547
Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala Leu Ala Leu Val Gly
    135                 140                 145

tgt gcg cga aga att ggg atc gcg gcg aaa acg aaa gat tct cga gga   595
Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr Lys Asp Ser Arg Gly
150                 155                 160                 165

ttt gat cgc gtc aat gtt cgt gat gcg gaa gca att ggg gca ctg ctc   643
Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala Ile Gly Ala Leu Leu
                170                 175                 180

act cga atg ggt gcc cag aaa act cgc atg ttg tgg gaa gaa aaa cgc   691
Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu Trp Glu Glu Lys Arg
            185                 190                 195

atc aag cgg gaa agt cga act ccg caa acc ggg ttg gcc aac ttc gac   739
Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly Leu Ala Asn Phe Asp
        200                 205                 210

gat gcc aat ctg cgc agg tca gcc cga gca gca gtt gcc gct gca gcg   787
Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala Val Ala Ala Ala Ala
    215                 220                 225
```

```
agg gta gaa cgc gcc atg aag att ctt ggt gat gat gtt cct gag cat   835
Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp Asp Val Pro Glu His
230                 235                 240                 245

ttg gct gag gct gga cag ctg cgt gtg cag cac cgt cag gca tcg ttg   883
Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His Arg Gln Ala Ser Leu
                250                 255                 260

gag gag ttg ggc cgg ttg gct gat cct caa atg acc aag gat gct gtg   931
Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met Thr Lys Asp Ala Val
            265                 270                 275

gcc ggt cgt att cgt cgt ctt ttg acg atg gca gat aag cgc gcc gaa   979
Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala Asp Lys Arg Ala Glu
        280                 285                 290

gat ctg aag att cct gat aca aat tct gtt gtg acg gaa gat ttg ttg   1027
Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val Thr Glu Asp Leu Leu
    295                 300                 305

gaa gaa att tagatgattg aagcctaaaa acg                            1059
Glu Glu Ile
310
```

<210> 538
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 538

```
Val Ala Lys Asn Ser Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg
  1               5                  10                  15

Phe Ala Gly Glu Met Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala
             20                  25                  30

Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln
         35                  40                  45

Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val
     50                  55                  60

Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp
 65                  70                  75                  80

Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val
                 85                  90                  95

Lys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu
            100                 105                 110

Ala Ala Trp Arg Gly Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro
        115                 120                 125

Gly Arg Ser Ser Ser Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala
    130                 135                 140

Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr
145                 150                 155                 160
```

```
Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala
                165                 170                 175

Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu
            180                 185                 190

Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly
        195                 200                 205

Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala
    210                 215                 220

Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp
225                 230                 235                 240

Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His
                245                 250                 255

Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met
            260                 265                 270

Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala
        275                 280                 285

Asp Lys Arg Ala Glu Asp Leu Lys Ile Pro Asp Thr Asn Ser Val Val
    290                 295                 300

Thr Glu Asp Leu Leu Glu Glu Ile
305                 310
```

<210> 539
<211> 681
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(658)
<223> RXC02435

<400> 539
tcatgaatgt agaacggatt tatcgacaag cgccagcaag tacgttgatc tctttagcca 60

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tcatcgctgt gtacgcagtg cggccattca atcgagatca gtg aca gac aac ctg   115
                                               Val Thr Asp Asn Leu
                                                 1               5

ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg   163
Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met
                10                  15                  20

gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg   211
Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu
            25                  30                  35

cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg   259
His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu
        40                  45                  50
```

```
ctg gga aga gaa att gaa cga gac ttc ggt tct gcg ctt ttc act gcg   307
Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser Ala Leu Phe Thr Ala
     55                  60                  65

atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg   355
Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met
 70                  75                  80                  85

gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg   403
Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met
                 90                  95                 100

atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga   451
Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg Ser Ala Asp Ile Arg
            105                 110                 115

gca ccc ttg atc ctt atc gcc atc aac atc gcc tat acc ttg atg tcc   499
Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala Tyr Thr Leu Met Ser
        120                 125                 130

acc aat gtt tct ctg tgg gga cac ctt gga ggt ttg atc act gga gct   547
Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly Leu Ile Thr Gly Ala
    135                 140                 145

tta att act tgg cca atg gtt aaa gcg aaa act caa aga aca cgg tgg   595
Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr Gln Arg Thr Arg Trp
150                 155                 160                 165

att atc gtg ctc att ggt ttt gct gta gtt gtg gct gct gtc att cta   643
Ile Ile Val Leu Ile Gly Phe Ala Val Val Val Ala Ala Val Ile Leu
                170                 175                 180

gga att gac cgg gtg tagacacatt ccgcccattg ccc                    681
Gly Ile Asp Arg Val
            185
```

<210> 540
<211> 186
<212> PRT
<213> Corynebacterium glutamicum

<400> 540

```
Val Thr Asp Asn Leu Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu
  1               5                  10                  15

Tyr Ala Pro Leu Met Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile
             20                  25                  30

Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu
         35                  40                  45

Val Leu Leu Trp Leu Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser
     50                  55                  60

Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala
 65                  70                  75                  80

Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly
                 85                  90                  95
```

```
Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg
            100                 105                 110

Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala
        115                 120                 125

Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly
    130                 135                 140

Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr
145                 150                 155                 160

Gln Arg Thr Arg Trp Ile Ile Val Leu Ile Gly Phe Ala Val Val Val
                165                 170                 175

Ala Ala Val Ile Leu Gly Ile Asp Arg Val
            180                 185


<210> 541
<211> 681
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(658)
<223> FRXA02435

<400> 541
tcatgaatgt agaacggatt tatcgacaag cgccagcaag tacgttgatc tctttagcca 60

tcatcgctgt gtacgcagtg cggccattca atcgagatca gtg aca gac aac ctg   115
                                            Val Thr Asp Asn Leu
                                              1               5

ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg   163
Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met
                  10                  15                  20

gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg   211
Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu
              25                  30                  35

cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg   259
His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu
          40                  45                  50

ctg gga aga gaa att gaa cga gac ttc ggt tct gcg ctt ttc act gcg   307
Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser Ala Leu Phe Thr Ala
      55                  60                  65

atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg   355
Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met
  70                  75                  80                  85

gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg   403
Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met
                  90                  95                 100

atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga   451
```

```
Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg Ser Ala Asp Ile Arg
            105                 110                 115

gca ccc ttg atc ctt atc gcc atc aac atc gcc tat acc ttg atg tcc   499
Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala Tyr Thr Leu Met Ser
        120                 125                 130

acc aat gtt tct ctg tgg gga cac ctt gga ggt ttg atc act gga gct   547
Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly Leu Ile Thr Gly Ala
    135                 140                 145

tta att act tgg cca atg gtt aaa gcg aaa act caa aga aca cgg tgg   595
Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr Gln Arg Thr Arg Trp
150                 155                 160                 165

att atc gtg ctc att ggt ttt gct gta gtt gtg gct gct gtc att cta   643
Ile Ile Val Leu Ile Gly Phe Ala Val Val Val Ala Ala Val Ile Leu
                170                 175                 180

gga att gac cgg gtg tagacacatt ccgcccattg ccc                    681
Gly Ile Asp Arg Val
            185
```

Sequence Listing

<210> 542
<211> 186
<212> PRT
<213> Corynebacterium glutamicum

<400> 542

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Val Thr Asp Asn Leu Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu
  1               5                  10                  15

Tyr Ala Pro Leu Met Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile
             20                  25                  30

Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu
         35                  40                  45

Val Leu Leu Trp Leu Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser
     50                  55                  60

Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala
 65                  70                  75                  80

Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly
                 85                  90                  95

Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg
            100                 105                 110

Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala
        115                 120                 125

Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly
    130                 135                 140

Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr
145                 150                 155                 160

Gln Arg Thr Arg Trp Ile Ile Val Leu Ile Gly Phe Ala Val Val Val
```

```
                165                 170                 175

Ala Ala Val Ile Leu Gly Ile Asp Arg Val
            180                 185


<210> 543
<211> 1141
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1111)
<223> RXC03216

<400> 543
gctgtatcac agtcagctgc agcaggtggc gaaaccgttg cggtcccagc ggctgctctg 60

atccctgcaa acaactagaa actattcaga aagcatcacc atg aaa ctc ggt ctc   115
                                            Met Lys Leu Gly Leu
                                              1               5

tac aac gcg atc ttc cac gac cgc acc ctg cca gaa gcg ctc gca gcc   163
Tyr Asn Ala Ile Phe His Asp Arg Thr Leu Pro Glu Ala Leu Ala Ala
                 10                  15                  20

atc aaa gct gca ggt ctc acc gga att gaa ctc aac acc ggc gga ttt   211
Ile Lys Ala Ala Gly Leu Thr Gly Ile Glu Leu Asn Thr Gly Gly Phe
             25                  30                  35

ttg cct gca acc cac atc ccg acc atc gat gac atc ctg gtc agc gat   259
Leu Pro Ala Thr His Ile Pro Thr Ile Asp Asp Ile Leu Val Ser Asp
         40                  45                  50

gat gcc cgc gat gaa ttc ctc ggg att ttc gaa ggc acc ggc gtc gac   307
Asp Ala Arg Asp Glu Phe Leu Gly Ile Phe Glu Gly Thr Gly Val Asp
     55                  60                  65

atc tac ggc ctt aac tgc aac ggc aac ccg ctt cac ccc aac aag gcg   355
Ile Tyr Gly Leu Asn Cys Asn Gly Asn Pro Leu His Pro Asn Lys Ala
 70                  75                  80                  85

atc ggg gac aag cat gcc gaa gac att cga cgt tcc atc cgc ctc gca   403
Ile Gly Asp Lys His Ala Glu Asp Ile Arg Arg Ser Ile Arg Leu Ala
                 90                  95                 100

gag cgc ctc ggc caa aac cgt gtg gtc acc atg tct ggt ctt cct ggt   451
Glu Arg Leu Gly Gln Asn Arg Val Val Thr Met Ser Gly Leu Pro Gly
            105                 110                 115

ggc gaa cca ggc gcg aag tac acc aac tgg gtt gtc aac gcg tgg aac   499
Gly Glu Pro Gly Ala Lys Tyr Thr Asn Trp Val Val Asn Ala Trp Asn
        120                 125                 130

tcc gca gcc ttg gat gtc ctt gat tac caa tgg gat atc gca gct gaa   547
Ser Ala Ala Leu Asp Val Leu Asp Tyr Gln Trp Asp Ile Ala Ala Glu
    135                 140                 145

ttc tgg cgc gag acc gac cgc ttc gcc gca gat cac ggc gtg aaa gtg   595
Phe Trp Arg Glu Thr Asp Arg Phe Ala Ala Asp His Gly Val Lys Val
```

```
150                 155                 160                 165

gct ctt gag ctg cac cca cag aac atc gtg ttc aac tcc gct gac gtg   643
Ala Leu Glu Leu His Pro Gln Asn Ile Val Phe Asn Ser Ala Asp Val
                170                 175                 180

cat aag ctc atc gat ctc acc ggc gcc acc cac gtg ggc gtc gaa ctg   691
His Lys Leu Ile Asp Leu Thr Gly Ala Thr His Val Gly Val Glu Leu
            185                 190                 195

gat gca tca cac ctg ttc tgg cag cag atg gac cca atc gct gtg att   739
Asp Ala Ser His Leu Phe Trp Gln Gln Met Asp Pro Ile Ala Val Ile
        200                 205                 210

gat cac ctc ggc gag ctc atc ttc cac gcc gcc gcc aaa gac gtg cga   787
Asp His Leu Gly Glu Leu Ile Phe His Ala Ala Ala Lys Asp Val Arg
    215                 220                 225

gtt aat aag gaa tgg gct cag ctc aac ggt gtg ctg gac aac agc ttc   835
Val Asn Lys Glu Trp Ala Gln Leu Asn Gly Val Leu Asp Asn Ser Phe
230                 235                 240                 245

cga cgc ctt gac cca tcc gaa aac cgc acc aac ttg ggc ggc gac gag   883
Arg Arg Leu Asp Pro Ser Glu Asn Arg Thr Asn Leu Gly Gly Asp Glu
                250                 255                 260

tgg gcg aat gaa tgg cca aag aac tct gct tgg gat ttc gtt gct ctg   931
Trp Ala Asn Glu Trp Pro Lys Asn Ser Ala Trp Asp Phe Val Ala Leu
            265                 270                 275

ggc cgc ggt cat gac gtt gct tac tgg acc gaa ttc ctc cgc gca ctt   979
Gly Arg Gly His Asp Val Ala Tyr Trp Thr Glu Phe Leu Arg Ala Leu
        280                 285                 290

cac cgc gtc gat cca aac atg ctg gtc aac atc gaa cac gag gat gtt   1027
His Arg Val Asp Pro Asn Met Leu Val Asn Ile Glu His Glu Asp Val
    295                 300                 305

tca ctc ggt cgc gaa gaa ggc gtc aac gaa gcc gct aag gtg ctg atc   1075
Ser Leu Gly Arg Glu Glu Gly Val Asn Glu Ala Ala Lys Val Leu Ile
310                 315                 320                 325

gag gcc aac aag gca ctc gaa gag tcc ctg gtt tct taaaaaaact        1121
Glu Ala Asn Lys Ala Leu Glu Glu Ser Leu Val Ser
                330                 335

acgcctgccc cgcaacgctt                                            1141
```

09355-0020

<210> 544
<211> 337
<212> PRT
<213> Corynebacterium glutamicum

<400> 544

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Met Lys Leu Gly Leu Tyr Asn Ala Ile Phe His Asp Arg Thr Leu Pro
  1               5                  10                  15

Glu Ala Leu Ala Ala Ile Lys Ala Ala Gly Leu Thr Gly Ile Glu Leu
            20                  25                  30
```

```
Asn Thr Gly Gly Phe Leu Pro Ala Thr His Ile Pro Thr Ile Asp Asp
          35                  40                  45

Ile Leu Val Ser Asp Asp Ala Arg Asp Glu Phe Leu Gly Ile Phe Glu
      50                  55                  60

Gly Thr Gly Val Asp Ile Tyr Gly Leu Asn Cys Asn Gly Asn Pro Leu
 65                  70                  75                  80

His Pro Asn Lys Ala Ile Gly Asp Lys His Ala Glu Asp Ile Arg Arg
                 85                  90                  95

Ser Ile Arg Leu Ala Glu Arg Leu Gly Gln Asn Arg Val Val Thr Met
            100                 105                 110

Ser Gly Leu Pro Gly Gly Glu Pro Gly Ala Lys Tyr Thr Asn Trp Val
        115                 120                 125

Val Asn Ala Trp Asn Ser Ala Ala Leu Asp Val Leu Asp Tyr Gln Trp
    130                 135                 140

Asp Ile Ala Ala Glu Phe Trp Arg Glu Thr Asp Arg Phe Ala Ala Asp
145                 150                 155                 160

His Gly Val Lys Val Ala Leu Glu Leu His Pro Gln Asn Ile Val Phe
                165                 170                 175

Asn Ser Ala Asp Val His Lys Leu Ile Asp Leu Thr Gly Ala Thr His
            180                 185                 190

Val Gly Val Glu Leu Asp Ala Ser His Leu Phe Trp Gln Gln Met Asp
        195                 200                 205

Pro Ile Ala Val Ile Asp His Leu Gly Glu Leu Ile Phe His Ala Ala
    210                 215                 220

Ala Lys Asp Val Arg Val Asn Lys Glu Trp Ala Gln Leu Asn Gly Val
225                 230                 235                 240

Leu Asp Asn Ser Phe Arg Arg Leu Asp Pro Ser Glu Asn Arg Thr Asn
                245                 250                 255

Leu Gly Gly Asp Glu Trp Ala Asn Glu Trp Pro Lys Asn Ser Ala Trp
            260                 265                 270

Asp Phe Val Ala Leu Gly Arg Gly His Asp Val Ala Tyr Trp Thr Glu
        275                 280                 285

Phe Leu Arg Ala Leu His Arg Val Asp Pro Asn Met Leu Val Asn Ile
    290                 295                 300

Glu His Glu Asp Val Ser Leu Gly Arg Glu Glu Gly Val Asn Glu Ala
305                 310                 315                 320

Ala Lys Val Leu Ile Glu Ala Asn Lys Ala Leu Glu Glu Ser Leu Val
                325                 330                 335

Ser
```

Replacement Sheet

<210> 545
<211> 1416
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1393)
<223> RXA02175

<400> 545
tgacatgcgc ttggcgcatc ccagttggta agaataaacg ggactacttc cgtaatccgg 60

aagagttttt ttccgaacaa atatgtttga aagggatatc gtg gct act gat aac 115
Val Ala Thr Asp Asn
1 5

aac aag gct gtc ctg cac tac ccc ggt ggc gag ttc gaa atg gac atc 163
Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile
10 15 20

atc gag gct tct gag ggt aac aac ggt gtt gtc ctg ggc aag atg ctg 211
Ile Glu Ala Ser Glu Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu
25 30 35

tct gag act gga ctg atc act ttt gac cca ggt tat gtg agc act ggc 259
Ser Glu Thr Gly Leu Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly
40 45 50

tcc acc gag tcg aag atc acc tac atc gat ggc gat gcg gga atc ctg 307
Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu
55 60 65

cgt tac cgc ggc tat gac atc gct gat ctg gct gag aat gcc acc ttc 355
Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe
70 75 80 85

aac gag gtt tct tac cta ctt atc aac ggt gag cta cca acc cca gat 403
Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp
90 95 100

gag ctt cac aag ttt aac gac gag att cgc cac cac acc ctt ctg gac 451
Glu Leu His Lys Phe Asn Asp Glu Ile Arg His His Thr Leu Leu Asp
105 110 115

gag gac ttc aag tcc cag ttc aac gtg ttc cca cgc gac gct cac cca 499
Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro
120 125 130

atg gca acc ttg gct tcc tcg gtt aac att ttg tct acc tac tac cag 547
Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln
135 140 145

gac cag ctg aac cca ctc gat gag gca cag ctt gat aag gca acc gtt 595
Asp Gln Leu Asn Pro Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val
150 155 160 165

cgc ctc atg gca aag gtt cca atg ctg gct gcg tac gca cac cgc gca 643
Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala
170 175 180

```
cgc aag ggt gct cct tac atg tac cca gac aac tcc ctc aat gcg cgt   691
Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg
            185                 190                 195

gag aac ttc ctg cgc atg atg ttc ggt tac cca acc gag cca tac gag   739
Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu
        200                 205                 210

atc gac cca atc atg gtc aag gct ctg gac aag ctg ctc atc ctg cac   787
Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His
    215                 220                 225

gct gac cac gag cag aac tgc tcc acc tcc acc gtt cgt atg atc ggt   835
Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly
230                 235                 240                 245

tcc gca cag gcc aac atg ttt gtc tcc atc gct ggt ggc atc aac gct   883
Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala
                250                 255                 260

ctg tcc ggc cca ctg cac ggt ggc gca aac cag gct gtt ctg gag atg   931
Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln Ala Val Leu Glu Met
            265                 270                 275

ctc gaa gac atc aag agc aac cac ggt ggc gac gca acc gag ttc atg   979
Leu Glu Asp Ile Lys Ser Asn His Gly Gly Asp Ala Thr Glu Phe Met
        280                 285                 290

aac aag gtc aag aac aag gaa gac ggc gtc cgc ctc atg ggc ttc gga   1027
Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly
    295                 300                 305

cac cgc gtt tac aag aac tac gat cca cgt gca gca atc gtc aag gag   1075
His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu
310                 315                 320                 325

acc gca cac gag atc ctc gag cac ctc ggt ggc gac gat ctt ctg gat   1123
Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp
                330                 335                 340

ctg gca atc aag ctg gaa gaa att gca ctg gct gat gat tac ttc atc   1171
Leu Ala Ile Lys Leu Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile
            345                 350                 355

tcc cgc aag ctc tac ccg aac gta gac ttc tac acc ggc ctg atc tac   1219
Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr
        360                 365                 370

cgc gca atg ggc ttc cca act gac ttc ttc acc gta ttg ttc gca atc   1267
Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile
    375                 380                 385

ggt cgt ctg cca gga tgg atc gct cac tac cgc gag cag ctc ggt gca   1315
Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala
390                 395                 400                 405

gca ggc aac aag atc aac cgc cca cgc cag gtc tac acc ggc aac gaa   1363
Ala Gly Asn Lys Ile Asn Arg Pro Arg Gln Val Tyr Thr Gly Asn Glu
                410                 415                 420

tcc cgc aag ttg gtt cct cgc gag gag cgc taaatttagc ggatgattct     1413
```

```
Ser Arg Lys Leu Val Pro Arg Glu Glu Arg
            425                 430

cgt                                                                  1416


<210> 546
<211> 431
<212> PRT
<213> Corynebacterium glutamicum

<400> 546
Val Ala Thr Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu
  1               5                  10                  15

Phe Glu Met Asp Ile Ile Glu Ala Ser Glu Gly Asn Asn Gly Val Val
             20                  25                  30

Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Ile Thr Phe Asp Pro Gly
         35                  40                  45

Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly
     50                  55                  60

Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala
 65                  70                  75                  80

Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu
                 85                  90                  95

Leu Pro Thr Pro Asp Glu Leu His Lys Phe Asn Asp Glu Ile Arg His
            100                 105                 110

His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro
        115                 120                 125

Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu
    130                 135                 140

Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro Leu Asp Glu Ala Gln Leu
145                 150                 155                 160

Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala
                165                 170                 175

Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn
            180                 185                 190

Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro
        195                 200                 205

Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys
    210                 215                 220

Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr
225                 230                 235                 240

Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala
                245                 250                 255

Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln
```

```
            260                 265                 270

Ala Val Leu Glu Met Leu Glu Asp Ile Lys Ser Asn His Gly Gly Asp
        275                 280                 285

Ala Thr Glu Phe Met Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg
    290                 295                 300

Leu Met Gly Phe Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala
305                 310                 315                 320

Ala Ile Val Lys Glu Thr Ala His Glu Ile Leu Glu His Leu Gly Gly
                325                 330                 335

Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu Glu Glu Ile Ala Leu Ala
            340                 345                 350

Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr
        355                 360                 365

Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr
    370                 375                 380

Val Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg
385                 390                 395                 400

Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile Asn Arg Pro Arg Gln Val
                405                 410                 415

Tyr Thr Gly Asn Glu Ser Arg Lys Leu Val Pro Arg Glu Glu Arg
            420                 425                 430
```

<210> 547
<211> 942
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(919)
<223> RXA02621

<400> 547
atgtacctga ctggtgcgcg acacttcgct cactaaagtt tttaaagatt tcgcttgaag 60

gcagaccata aggtctgcct tttcgcgtat taatgagtac atg tct gaa ctt att 115
                                        Met Ser Glu Leu Ile
                                          1   5

tgt gga cca gct att ctc ttc gca cca gct gga cgt gct gag atc att 163
Cys Gly Pro Ala Ile Leu Phe Ala Pro Ala Gly Arg Ala Glu Ile Ile
                 10   15   20

cca aaa gca gca tcg aag gcc gat atg gtc atc att gat ttg gaa gat 211
Pro Lys Ala Ala Ser Lys Ala Asp Met Val Ile Ile Asp Leu Glu Asp
             25   30   35

ggg gca ggg gag gta gac cgt gag gtc gcc tac agg aac att aga gaa 259
Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr Arg Asn Ile Arg Glu
         40   45   50
```
```

```
tcg ggg ttg gat cct aaa cga acc att gtg aga acc gta ggg ccg agc   307
Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg Thr Val Gly Pro Ser
     55                  60                  65

gat cca cac ttt ttg gct gac gtg gag atg gtg aag tcc acg gat ttc   355
Asp Pro His Phe Leu Ala Asp Val Glu Met Val Lys Ser Thr Asp Phe
 70                  75                  80                  85

aca ctt gtt atg gtt cct aaa ctt ctt ggc agc gtg cct gag gaa tta   403
Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser Val Pro Glu Glu Leu
                 90                  95                 100

gat ggc ctc aac att atc gcc atg att gaa acc cct cag gct gca acc   451
Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr Pro Gln Ala Ala Thr
            105                 110                 115

agc att cct cag att gct gcg gac cct aaa gtc gtt gga atg ttc tgg   499
Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val Val Gly Met Phe Trp
        120                 125                 130

ggc gcg gag gat ctc aca cac ctc ttg gga ggc act cat tct agg ttc   547
Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly Thr His Ser Arg Phe
    135                 140                 145

ttg ggt gat gag tcc aat gaa ggc tcc tac cga gac acc atg agg ctt   595
Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg Asp Thr Met Arg Leu
150                 155                 160                 165

aca cgc gcc ctg atg cac ctc cac gcg gcg gcg aat ggg aag ttc acc   643
Thr Arg Ala Leu Met His Leu His Ala Ala Ala Asn Gly Lys Phe Thr
                170                 175                 180

att gat gcc atc cat gcg gat ttc cac gat gaa gag ggc ctc tat tta   691
Ile Asp Ala Ile His Ala Asp Phe His Asp Glu Glu Gly Leu Tyr Leu
            185                 190                 195

gaa gcg gtc gat gct gcg cgg act ggt ttc gct ggc acc gca tgc att   739
Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala Gly Thr Ala Cys Ile
        200                 205                 210

cac ccc aag cag atc gag att gtt cgg aga gcc tat cgg cca gag gct   787
His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala Tyr Arg Pro Glu Ala
    215                 220                 225

aac cag ttg gag tgg gcg aag aaa gtg gtg gag gaa gca gaa aac cat   835
Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu Glu Ala Glu Asn His
230                 235                 240                 245

cca ggt gcg ttc aaa ctg gat ggt cag atg att gat gct ccg ttg att   883
Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile Asp Ala Pro Leu Ile
                250                 255                 260

tcg cag gcg cgg atg gtt att tcg cgt cag cct gct tgattagttc        929
Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro Ala
            265                 270

aagcgttttt tcg                                                   942
```

<210> 548

<211> 273
<212> PRT
<213> Corynebacterium glutamicum

<400> 548

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Met Ser Glu Leu Ile Cys Gly Pro Ala Ile Leu Phe Ala Pro Ala Gly
  1               5                  10                  15

Arg Ala Glu Ile Ile Pro Lys Ala Ala Ser Lys Ala Asp Met Val Ile
            20                  25                  30

Ile Asp Leu Glu Asp Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr
        35                  40                  45

Arg Asn Ile Arg Glu Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg
    50                  55                  60

Thr Val Gly Pro Ser Asp Pro His Phe Leu Ala Asp Val Glu Met Val
65                  70                  75                  80

Lys Ser Thr Asp Phe Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser
                85                  90                  95

Val Pro Glu Glu Leu Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr
            100                 105                 110

Pro Gln Ala Ala Thr Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val
        115                 120                 125

Val Gly Met Phe Trp Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly
    130                 135                 140

Thr His Ser Arg Phe Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg
145                 150                 155                 160

Asp Thr Met Arg Leu Thr Arg Ala Leu Met His Leu His Ala Ala Ala
                165                 170                 175

Asn Gly Lys Phe Thr Ile Asp Ala Ile His Ala Asp Phe His Asp Glu
            180                 185                 190

Glu Gly Leu Tyr Leu Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala
        195                 200                 205

Gly Thr Ala Cys Ile His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala
    210                 215                 220

Tyr Arg Pro Glu Ala Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu
225                 230                 235                 240

Glu Ala Glu Asn His Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile
                245                 250                 255

Asp Ala Pro Leu Ile Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro
            260                 265                 270

Ala
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<210> 549

<211> 2337
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2314)
<223> RXN00519

<400> 549
tttccatgcg gggctgaaac tgccaccata ggcgccagca attagtagaa cactgtattc 60

taggtagctg aacaaaagag cccatcaacc aaggagactc atg gct aag atc atc 115
Met Ala Lys Ile Ile
1 5

tgg acc cgc acc gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag 163
Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys
10 15 20

ccg gtc gtc gag gca ttt gct gct acc gcg ggc att gag gtc gag acc 211
Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr
25 30 35

cgg gac att tca ctc gct gga cgc atc ctc gcc cag ttc cca gag cgc 259
Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala Gln Phe Pro Glu Arg
40 45 50

ctc acc gaa gat cag aag gta ggc aac gca ctc gca gaa ctc ggc gag 307
Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu Ala Glu Leu Gly Glu
55 60 65

ctt gct aag act cct gaa gca aac atc att aag ctt cca aac atc tcc 355
Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser
70 75 80 85

gct tct gtt cca cag ctc aag gct gct att aag gaa ctg cag gac cag 403
Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys Glu Leu Gln Asp Gln
90 95 100

ggc tac gac atc cca gaa ctg cct gat aac gcc acc acc gac gag gaa 451
Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala Thr Thr Asp Glu Glu
105 110 115

aaa gac atc ctc gca cgc tac aac gct gtt aag ggt tcc gct gtg aac 499
Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys Gly Ser Ala Val Asn
120 125 130

cca gtg ctg cgt gaa ggc aac tct gac cgc cgc gca cca atc gct gtc 547
Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro Ile Ala Val
135 140 145

aag aac ttt gtt aag aag ttc cca cac cgc atg ggc gag tgg tct gca 595
Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala
150 155 160 165

gat tcc aag acc aac gtt gca acc atg gat gca aac gac ttc cgc cac 643
Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala Asn Asp Phe Arg His
170 175 180

aac gag aag tcc atc atc ctc gac gct gct gat gaa gtt cag atc aag 691

```
Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp Glu Val Gln Ile Lys
            185                 190                 195

cac atc gca gct gac ggc acc gag acc atc ctc aag gac agc ctc aag   739
His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys
        200                 205                 210

ctt ctt gaa ggc gaa gtt cta gac gga acc gtt ctg tcc gca aag gca   787
Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val Leu Ser Ala Lys Ala
    215                 220                 225

ctg gac gca ttc ctt ctc gag cag gtc gct cgc gca aag gca gaa ggt   835
Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg Ala Lys Ala Glu Gly
230                 235                 240                 245

atc ctc ttc tcc gca cac ctg aag gcc acc atg atg aag gtc tcc gac   883
Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met Met Lys Val Ser Asp
                250                 255                 260

cca atc atc ttc ggc cac gtt gtg cgc gct tac ttc gca gac gtt ttc   931
Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr Phe Ala Asp Val Phe
            265                 270                 275

gca cag tac ggt gag cag ctg ctc gca gct ggc ctc aac ggc gaa aac   979
Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn
        280                 285                 290

ggc ctc gct gca atc ctc tcc ggc ttg gag tcc ctg gac aac ggc gaa   1027
Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu
    295                 300                 305

gaa atc aag gct gca ttc gag aag ggc ttg gaa gac ggc cca gac ctg   1075
Glu Ile Lys Ala Ala Phe Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu
310                 315                 320                 325

gcc atg gtt aac tcc gct cgc ggc atc acc aac ctg cat gtc cct tcc   1123
Ala Met Val Asn Ser Ala Arg Gly Ile Thr Asn Leu His Val Pro Ser
                330                 335                 340

gat gtc atc gtg gac gct tcc atg cca gca atg att cgt acc tcc ggc   1171
Asp Val Ile Val Asp Ala Ser Met Pro Ala Met Ile Arg Thr Ser Gly
            345                 350                 355

cac atg tgg aac aaa gac gac cag gag cag gac acc ctg gca atc atc   1219
His Met Trp Asn Lys Asp Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile
        360                 365                 370

cca gac tcc tcc tac gct ggc gtc tac cag acc gtt atc gaa gac tgc   1267
Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr Val Ile Glu Asp Cys
    375                 380                 385

cgc aag aac ggc gca ttc gat cca acc acc atg ggt acc gtc cct aac   1315
Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met Gly Thr Val Pro Asn
390                 395                 400                 405

gtt ggt ctg atg gct cag aag gct gaa gag tac ggc tcc cat gac aag   1363
Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr Gly Ser His Asp Lys
                410                 415                 420

acc ttc cgc atc gaa gca gac ggt gtg gtt cag gtt gtt tcc tcc aac   1411
Thr Phe Arg Ile Glu Ala Asp Gly Val Val Gln Val Val Ser Ser Asn
```

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            425                 430                 435

ggc gac gtt ctc atc gag cac gac gtt gag gca aat gac atc tgg cgt   1459
Gly Asp Val Leu Ile Glu His Asp Val Glu Ala Asn Asp Ile Trp Arg
        440                 445                 450

gca tgc cag gtc aag gat gcc cca atc cag gat tgg gta aag ctt gct   1507
Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala
    455                 460                 465

gtc acc cgc tcc cgt ctc tcc gga atg cct gca gtg ttc tgg ttg gat   1555
Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp
470                 475                 480                 485

cca gag cgc gca cac gac cgc aac ctg gct tcc ctc gtt gag aag tac   1603
Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr
                490                 495                 500

ctg gct gac cac gac acc gag ggc ctg gac atc cag atc ctc tcc cct   1651
Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro
            505                 510                 515

gtt gag gca acc cag ctc tcc atc gac cgc atc cgc cgt ggc gag gac   1699
Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp
        520                 525                 530

acc atc tct gtc acc ggt aac gtt ctg cgt gac tac aac acc gac ctc   1747
Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu
    535                 540                 545

ttc cca atc ctg gag ctg ggc acc tct gca aag atg ctg tct gtc gtt   1795
Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val
550                 555                 560                 565

cct ttg atg gct ggc ggc gga ctg ttc gag acc ggt gct ggt gga tct   1843
Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser
                570                 575                 580

gct cct aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg   1891
Ala Pro Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp
            585                 590                 595

gat tcc ctc ggt gag ttc ctc gca ctg gct gag tcc ttc cgc cac gag   1939
Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu
        600                 605                 610

ctc aac aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg   1987
Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu
    615                 620                 625

gac aag gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc   2035
Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg
630                 635                 640                 645

aag gtt ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag   2083
Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys
                650                 655                 660

ttc tgg gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct   2131
Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala
            665                 670                 675
```

```
gct acc ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac   2179
Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp
        680                 685                 690

atc gat gct gca ctg ctc gca gtt cag ggt gga gca act gac ctt ggt   2227
Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly
    695                 700                 705

ggc tac tac tcc cct aac gag gag aag ctc acc aac atc atg cgc cca   2275
Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro
710                 715                 720                 725

gtc gca cag ttc aac gag atc gtt gac gca ctg aag aag taaagtctct   2324
Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys
                730                 735

tcacaaaaag cgc                                                  2337
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<210> 550
<211> 738
<212> PRT
<213> Corynebacterium glutamicum

<400> 550

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Met Ala Lys Ile Ile Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala
  1               5                  10                  15

Thr Tyr Ser Leu Lys Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly
            20                  25                  30

Ile Glu Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala
        35                  40                  45

Gln Phe Pro Glu Arg Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu
    50                  55                  60

Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
65                  70                  75                  80

Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys
                85                  90                  95

Glu Leu Gln Asp Gln Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala
            100                 105                 110

Thr Thr Asp Glu Glu Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys
        115                 120                 125

Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg
    130                 135                 140

Ala Pro Ile Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met
145                 150                 155                 160

Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala
                165                 170                 175

Asn Asp Phe Arg His Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp
            180                 185                 190
```

```
Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu
        195                 200                 205

Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val
    210                 215                 220

Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg
225                 230                 235                 240

Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met
                245                 250                 255

Met Lys Val Ser Asp Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr
            260                 265                 270

Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly
        275                 280                 285

Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser
    290                 295                 300

Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe Glu Lys Gly Leu Glu
305                 310                 315                 320

Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala Arg Gly Ile Thr Asn
                325                 330                 335

Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met
            340                 345                 350

Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp Asp Gln Glu Gln Asp
        355                 360                 365

Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr
    370                 375                 380

Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met
385                 390                 395                 400

Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr
                405                 410                 415

Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Val Val Gln
            420                 425                 430

Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Ala
        435                 440                 445

Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp
    450                 455                 460

Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala
465                 470                 475                 480

Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser
                485                 490                 495

Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile
            500                 505                 510
```

```
Gln Ile Leu Ser Pro Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile
        515                 520                 525

Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp
    530                 535                 540

Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys
545                 550                 555                 560

Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr
                565                 570                 575

Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Gln Glu Glu
            580                 585                 590

Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu
        595                 600                 605

Ser Phe Arg His Glu Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val
    610                 615                 620

Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu
625                 630                 635                 640

Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His
                645                 650                 655

Phe Trp Leu Thr Lys Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu
            660                 665                 670

Asp Ala Asp Leu Ala Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn
        675                 680                 685

Thr Gly Ala Ala Asp Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly
    690                 695                 700

Ala Thr Asp Leu Gly Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr
705                 710                 715                 720

Asn Ile Met Arg Pro Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu
                725                 730                 735

Lys Lys
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09/09/2004 15:09:09

<210> 551
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1059)
<223> FRXA00521

<400> 551

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ctc gac gct gct gat gaa gtt cag atc aag cac atc gca gct gac ggc   48
Leu Asp Ala Ala Asp Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly
  1               5                  10                  15
```

```
acc gag acc atc ctc aag gac agc ctc aag ctt ctt gaa ggc gaa gtt   96
Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val
            20                  25                  30

cta gac gga acc gtt ctg tcc gca aag gca ctg gac gca ttc ctt ctc  144
Leu Asp Gly Thr Val Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu
        35                  40                  45

gag cag gtc gct cgc gca aag gca gaa ggt atc ctc ttc tcc gca cac  192
Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His
    50                  55                  60

ctg aag gcc acc atg atg aag gtc tcc gac cca atc atc ttc ggc cac  240
Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His
65                  70                  75                  80

gtt gtg cgc gct tac ttc gca gac gtt ttc gca cag tac ggt gag cag  288
Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln
                85                  90                  95

ctg ctc gca gct ggc ctc aac ggc gaa aac ggc ctc gct gca atc ctc  336
Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu
            100                 105                 110

tcc ggc ttg gag tcc ctg gac aac ggc gaa gaa atc aag gct gca ttc  384
Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe
        115                 120                 125

gag aag ggc ttg gaa gac ggc cca gac ctg gcc atg gtt aac tcc gct  432
Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala
    130                 135                 140

cgc ggc atc acc aac ctg cat gtc cct tcc gat gtc atc gtg gac gct  480
Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala
145                 150                 155                 160

tcc atg cca gca atg att cgt acc tcc ggc cac atg tgg aac aaa gac  528
Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp
                165                 170                 175

gac cag gag cag gac acc ctg gca atc atc cca gac tcc tcc tac gct  576
Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala
            180                 185                 190

ggc gtc tac cag acc gtt atc gaa gac tgc cgc aag aac ggc gca ttc  624
Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe
        195                 200                 205

gat cca acc acc atg ggt acc gtc cct aac gtt ggt ctg atg gct cag  672
Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln
    210                 215                 220

aag gct gaa gag tac ggc tcc cat gac aag acc ttc cgc atc gaa gca  720
Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala
225                 230                 235                 240

gac ggt gtg gtt cag gtt gtt tcc tcc aac ggc gac gtt ctc atc gag  768
Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu
                245                 250                 255

cac gac gtt gag gca aat gac atc tgg cgt gca tgc cag gtc aag gat  816
```

```
His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp
            260                 265                 270

gcc cca atc cag gat tgg gta aag ctt gct gtc acc cgc tcc cgt ctc   864
Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu
        275                 280                 285

tcc gga atg cct gca gtg ttc tgg ttg gat cca gag cgc gca cac gac   912
Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp
    290                 295                 300

cgc aac ctg gct tcc ctc gtt gag aag tac ctg gct gac cac gac acc   960
Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr
305                 310                 315                 320

gag ggc ctg gac atc cag atc ctc tac cct gtt gag gca acc cag ctc  1008
Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu
                325                 330                 335

tcc atc gac cgc atc cgc cgt ggc gag gac acc atc tct gtc acc ggt  1056
Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly
            340                 345                 350

aac                                                             1059
Asn
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<210> 552
<211> 353
<212> PRT
<213> Corynebacterium glutamicum

<400> 552

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Leu Asp Ala Ala Asp Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly
  1               5                  10                  15

Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val
             20                  25                  30

Leu Asp Gly Thr Val Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu
         35                  40                  45

Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His
     50                  55                  60

Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His
 65                  70                  75                  80

Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln
                 85                  90                  95

Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu
            100                 105                 110

Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe
        115                 120                 125

Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala
    130                 135                 140
```

```
Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala
145                 150                 155                 160

Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp
                165                 170                 175

Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala
            180                 185                 190

Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe
        195                 200                 205

Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln
    210                 215                 220

Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala
225                 230                 235                 240

Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu
                245                 250                 255

His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp
            260                 265                 270

Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu
        275                 280                 285

Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp
    290                 295                 300

Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr
305                 310                 315                 320

Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu
                325                 330                 335

Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly
            340                 345                 350

Asn
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<210> 553
<211> 1694
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1671)
<223> RXN02209

<400> 553

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acc gag tcc acc gtt gtt cct tcc atc gct ggc cct aag cgc cca cag   48
Thr Glu Ser Thr Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln
  1               5                  10                  15

gac cgc atc ctt ctc tcc gag gca aag gag cag ttc cgt aag gat ctg   96
Asp Arg Ile Leu Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu
             20                  25                  30
```

```
cca acc tac acc gac gac gct gtt tcc gta gac acc tcc atc cct gca   144
Pro Thr Tyr Thr Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala
         35                  40                  45

acc cgc atg gtt aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa   192
Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu
     50                  55                  60

gct gac aac tac aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct   240
Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala
 65                  70                  75                  80

act ggc gca gaa gga cgt cct tcc aag cca gtc acc gtt gca tcc cca   288
Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro
                 85                  90                  95

cag ggt ggc gag tac acc atc gac cac ggc atg gtt gca att gca tcc   336
Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser
            100                 105                 110

atc acc tct tgc acc aac acc tct aac cca tcc gtg atg atc ggc gct   384
Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala
        115                 120                 125

ggc ctg atc gca cgt aag gca gca gaa aag ggc ctc aag tcc aag cct   432
Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro
    130                 135                 140

tgg gtt aag acc atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac   480
Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr
145                 150                 155                 160

tac cag cgc gca gac ctc tgg aag gac ctt gag gcc atg ggc ttc tac   528
Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr
                165                 170                 175

ctc tcc ggc ttc ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg   576
Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu
            180                 185                 190

cca gag gaa atc tcc gct gcg atc aac gag cac gac ctg acc gca acc   624
Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr
        195                 200                 205

gca gtt ttg tcc ggt aac cgt aac ttc gag gga cgt atc tcc cct gac   672
Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp
    210                 215                 220

gtt aag atg aac tac ctg gca tcc cca atc atg gtc att gct tac gca   720
Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala
225                 230                 235                 240

atc gct ggc acc atg gac ttc gac ttc gag aac gaa gct ctt gga cag   768
Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln
                245                 250                 255

gac cag gac ggc aac gac gtc ttc ctg aag gac atc tgg cct tcc acc   816
Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr
            260                 265                 270
```

```
gag gaa atc gaa gac acc atc cag cag gca atc tcc cgt gag ctt tac   864
Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr
        275                 280                 285

gaa gct gac tac gca gat gtc ttc aag ggt gac aag cag tgg cag gaa   912
Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu
    290                 295                 300

ctc gat gtt cct acc ggt gac acc ttc gag tgg gac gag aac tcc acc   960
Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr
305                 310                 315                 320

tac atc cgc aag gca cct tac ttc gac ggc atg cct gtc gag cca gtg   1008
Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val
                325                 330                 335

gca gtc acc gac atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac   1056
Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp
            340                 345                 350

tct gtc acc acc gac cac atc tcc cct gct tcc tcc att aag cca ggt   1104
Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly
        355                 360                 365

acc cct gca gct cag tac ttg gat gag cac ggt gtg gaa cgc cac gac   1152
Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp
    370                 375                 380

tac aac tcc ctg ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc   1200
Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg
385                 390                 395                 400

ggc acc ttc gcc aac atc cgc ctc cag aac cag ctg gtt gac atc gca   1248
Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala
                405                 410                 415

ggt ggc tac acc cgc gac ttc acc cag gag ggt gct cca cag gcg ttc   1296
Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe
            420                 425                 430

atc tac gac gct tcc gtc aac tac aag gct gct ggc att ccg ctg gtc   1344
Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val
        435                 440                 445

gtc ttg ggc ggc aag gag tac ggc acc ggt tct tcc cgt gac tgg gca   1392
Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala
    450                 455                 460

gct aag ggc act aac ctg ctc gga att cgc gca gtt atc acc gag tcc   1440
Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser
465                 470                 475                 480

ttc gag cgt att cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca   1488
Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro
                485                 490                 495

ctg cag ttc cct gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc   1536
Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly
            500                 505                 510

acc gag acc ttc gac atc acc gga ctg acc gca ctt aac gag ggc gag   1584
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Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu
        515                 520                 525

act cct aag act gtc aag gtc acc gca acc aag gag aac ggc gac gtc   1632
Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val
    530                 535                 540

gtc gag ttc gac gca att tgt ccg cat cga cac ccc agg tgaggctgac   1681
Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg
545                 550                 555

tactaccgcc acg                                                  1694


<210> 554
<211> 557
<212> PRT
<213> Corynebacterium glutamicum

<400> 554
Thr Glu Ser Thr Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln
  1               5                  10                  15

Asp Arg Ile Leu Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu
            20                  25                  30

Pro Thr Tyr Thr Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala
        35                  40                  45

Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu
    50                  55                  60

Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala
65                  70                  75                  80

Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro
                85                  90                  95

Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser
            100                 105                 110

Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala
        115                 120                 125

Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro
    130                 135                 140

Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr
145                 150                 155                 160

Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr
                165                 170                 175

Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu
            180                 185                 190

Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr
        195                 200                 205

Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp
    210                 215                 220
```

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Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala
225                 230                 235                 240

Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln
                245                 250                 255

Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr
            260                 265                 270

Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr
        275                 280                 285

Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu
    290                 295                 300

Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr
305                 310                 315                 320

Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val
                325                 330                 335

Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp
            340                 345                 350

Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly
        355                 360                 365

Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp
    370                 375                 380

Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg
385                 390                 395                 400

Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala
                405                 410                 415

Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe
            420                 425                 430

Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val
        435                 440                 445

Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala
    450                 455                 460

Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser
465                 470                 475                 480

Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro
                485                 490                 495

Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly
            500                 505                 510

Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu
        515                 520                 525

Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val
    530                 535                 540
```

Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg
545 550 555

<210> 555
<211> 1682
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1659)
<223> FRXA02209

<400> 555
gtt gtt cct tcc atc gct ggc cct aag cgc cca cag gac cgc atc ctt 48
Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu
1 5 10 15

ctc tcc gag gca aag gag cag ttc cgt aag gat ctg cca acc tac acc 96
Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr
20 25 30

gac gac gct gtt tcc gta gac acc tcc atc cct gca acc cgc atg gtt 144
Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val
35 40 45

aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa gct gac aac tac 192
Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
50 55 60

aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct act ggc gca gaa 240
Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu
65 70 75 80

gga cgt cct tcc aag cca gtc acc gtt gca tcc cca cag ggt ggc gag 288
Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu
85 90 95

tac acc atc gac cac ggc atg gtt gca att gca tcc atc acc tct tgc 336
Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys
100 105 110

acc aac acc tct aac cca tcc gtg atg atc ggc gct ggc ctg atc gca 384
Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala
115 120 125

cgt aag gca gca gaa aag ggc ctc aag tcc aag cct tgg gtt aag acc 432
Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr
130 135 140

atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac tac cag cgc gca 480
Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala
145 150 155 160

gac ctc tgg aag gac ctt gag gcc atg ggc ttc tac ctc tcc ggc ttc 528
Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe
165 170 175

ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg cca gag gaa atc 576
Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile

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            180                 185                 190

tcc gct gcg atc aac gag cac gac ctg acc gca acc gca gtt ttg tcc   624
Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser
        195                 200                 205

ggt aac cgt aac ttc gag gga cgt atc tcc cct gac gtt aag atg aac   672
Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn
    210                 215                 220

tac ctg gca tcc cca atc atg gtc att gct tac gca atc gct ggc acc   720
Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr
225                 230                 235                 240

atg gac ttc gac ttc gag aac gaa gct ctt gga cag gac cag gac ggc   768
Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly
                245                 250                 255

aac gac gtc ttc ctg aag gac atc tgg cct tcc acc gag gaa atc gaa   816
Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu
            260                 265                 270

gac acc atc cag cag gca atc tcc cgt gag ctt tac gaa gct gac tac   864
Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr
        275                 280                 285

gca gat gtc ttc aag ggt gac aag cag tgg cag gaa ctc gat gtt cct   912
Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro
    290                 295                 300

acc ggt gac acc ttc gag tgg gac gag aac tcc acc tac atc cgc aag   960
Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys
305                 310                 315                 320

gca cct tac ttc gac ggc atg cct gtc gag cca gtg gca gtc acc gac   1008
Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp
                325                 330                 335

atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac tct gtc acc acc   1056
Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr
            340                 345                 350

gac cac atc tcc cct gct tcc tcc att aag cca ggt acc cct gca gct   1104
Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala
        355                 360                 365

cag tac ttg gat gag cac ggt gtg gaa cgc cac gac tac aac tcc ctg   1152
Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu
    370                 375                 380

ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc ggc acc ttc gcc   1200
Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala
385                 390                 395                 400

aac atc cgc ctc cag aac cag ctg gtt gac atc gca ggt ggc tac acc   1248
Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr
                405                 410                 415

cgc gac ttc acc cag gag ggt gct cca cag gcg ttc atc tac gac gct   1296
Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala
            420                 425                 430
```

```
tcc gtc aac tac aag gct gct ggc att ccg ctg gtc gtc ttg ggc ggc   1344
Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly
        435                 440                 445

aag gag tac ggc acc ggt tct tcc cgt gac tgg gca gct aag ggc act   1392
Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr
    450                 455                 460

aac ctg ctc gga att cgc gca gtt atc acc gag tcc ttc gag cgt att   1440
Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile
465                 470                 475                 480

cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca ctg cag ttc cct   1488
His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro
                485                 490                 495

gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc acc gag acc ttc   1536
Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe
            500                 505                 510

gac atc acc gga ctg acc gca ctt aac gag ggc gag act cct aag act   1584
Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr
        515                 520                 525

gtc aag gtc acc gca acc aag gag aac ggc gac gtc gtc gag ttc gac   1632
Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp
    530                 535                 540

gca att tgt ccg cat cga cac ccc agg tgaggctgac tactaccgcc         1679
Ala Ile Cys Pro His Arg His Pro Arg
545                 550

acg                                                               1682
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<210> 556
<211> 553
<212> PRT
<213> Corynebacterium glutamicum

<400> 556

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Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu
  1               5                  10                  15

Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr
             20                  25                  30

Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val
         35                  40                  45

Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
     50                  55                  60

Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu
 65                  70                  75                  80

Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu
                 85                  90                  95

Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys
```

```
            100                 105                 110

Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala
        115                 120                 125

Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr
    130                 135                 140

Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala
145                 150                 155                 160

Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe
                165                 170                 175

Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile
            180                 185                 190

Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser
        195                 200                 205

Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn
    210                 215                 220

Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr
225                 230                 235                 240

Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly
                245                 250                 255

Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu
            260                 265                 270

Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr
        275                 280                 285

Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro
    290                 295                 300

Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys
305                 310                 315                 320

Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp
                325                 330                 335

Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr
            340                 345                 350

Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala
        355                 360                 365

Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu
    370                 375                 380

Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala
385                 390                 395                 400

Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr
                405                 410                 415

Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala
            420                 425                 430
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```
Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly
        435                 440                 445

Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr
    450                 455                 460

Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile
465                 470                 475                 480

His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro
                485                 490                 495

Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe
            500                 505                 510

Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr
        515                 520                 525

Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp
    530                 535                 540

Ala Ile Cys Pro His Arg His Pro Arg
545                 550


<210> 557
<211> 874
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXN02213

<400> 557
ttctgtggaa tgagaatccg atgtttttct cacgccggct cagccgaagc agacgccgtc 60

gcgaaatctc accctaaaaa agttagaatt ggagctcact gtg act gaa agc aag   115
                                          Val Thr Glu Ser Lys
                                            1               5

aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat   163
Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr
                10                  15                  20

gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac   211
Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr
            25                  30                  35

tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca   259
Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala
        40                  45                  50

aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct   307
Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser
    55                  60                  65

tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg   355
Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met
```

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70                  75                  80                  85

cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt   403
Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg
                90                  95                  100

gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg   451
Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu
            105                 110                 115

aac cca gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc   499
Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe
        120                 125                 130

ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc   547
Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg
    135                 140                 145

aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc   595
Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser
150                 155                 160                 165

aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac   643
Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn
                170                 175                 180

att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac   691
Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr
            185                 190                 195

cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc   739
Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly
        200                 205                 210

ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca   787
Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala
    215                 220                 225

atg ctc ggc cag cca gtg tcc atg ctg atc cct cgc gtt gtt ggc ttc   835
Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro Arg Val Val Gly Phe
230                 235                 240                 245

aag ttg acc ggc gag atc cca gta ggc gtt acc gca act               874
Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr Ala Thr
                250                 255
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<210> 558
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 558

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Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val
  1               5                  10                  15

Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met
             20                  25                  30

Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
         35                  40                  45
```

```
Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala
     50                  55                  60

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro
 65                  70                  75                  80

Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp
                 85                  90                  95

Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn
            100                 105                 110

Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
        115                 120                 125

Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu
    130                 135                 140

Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
145                 150                 155                 160

Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
                165                 170                 175

Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn
            180                 185                 190

Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
        195                 200                 205

Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
    210                 215                 220

Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro
225                 230                 235                 240

Arg Val Val Gly Phe Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr
                245                 250                 255

Ala Thr
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<210> 559
<211> 817
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> FRXA02213

<400> 559
ttctgtggaa tgagaatccg atgtttttct cacgccggct cagccgaagc agacgccgtc 60

gcgaaatctc accctaaaaa agttagaatt ggagctcact gtg act gaa agc aag 115
                                    Val Thr Glu Ser Lys
                                      1   5

```
aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat   163
Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr
                10                  15                  20

gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac   211
Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr
            25                  30                  35

tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca   259
Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala
        40                  45                  50

aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct   307
Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser
    55                  60                  65

tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg   355
Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met
70                  75                  80                  85

cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt   403
Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg
                90                  95                  100

gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg   451
Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu
            105                 110                 115

aac cca gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc   499
Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe
        120                 125                 130

ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc   547
Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg
    135                 140                 145

aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc   595
Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser
150                 155                 160                 165

aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac   643
Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn
                170                 175                 180

att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac   691
Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr
            185                 190                 195

cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc   739
Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly
        200                 205                 210

ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca   787
Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala
    215                 220                 225

atg ctc ggc cag cca gtg tcc atg ctg atc                          817
Met Leu Gly Gln Pro Val Ser Met Leu Ile
230                 235
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<210> 560
<211> 239
<212> PRT
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Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
35 40 45

Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala
50 55 60

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro
65 70 75 80

Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp
85 90 95

Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn
100 105 110

Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
115 120 125

Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu
130 135 140

Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
145 150 155 160

Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
165 170 175

Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn
180 185 190

Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
195 200 205

Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
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Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile
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gtc ggt tcc atg gat tac cca gca gag ttc cag ggc gct tca gaa gac   96
Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp
            20                  25                  30

cgc ctt gca gag ctc ggc gtt ggc aaa ctt gtc acc atc acc tcc acc   144
Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr
        35                  40                  45

tac gat cac cgc gtg atc cag ggt gct gtg tcc ggt gaa ttc ctg cgc   192
Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg
    50                  55                  60

acc atg tct cgc ctg ctc acc gat gat tcc ttc tgg gat gag atc ttc   240
Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe
65                  70                  75                  80

gac gca atg aac gtt cct tac acc cca atg cgt tgg gca cag gac gtt   288
Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val
                85                  90                  95

cca aac acc ggt gtt gat aag aac acc cgc gtc atg cag ctc att gag   336
Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu
            100                 105                 110

gca tac cgc tcc cgt gga cac ctc atc gct gac acc aac cca ctt tca   384
Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser
        115                 120                 125

tgg gtt cag cct ggc atg cca gtt cca gac cac cgc gac ctc gac atc   432
Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile
    130                 135                 140

gag acc cac aac ctg acc atc tgg gat ctg gac cgt acc ttc aac gtc   480
Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val
145                 150                 155                 160

ggt ggc ttc ggc ggc aag gag acc atg acc ctg cgc gag gta ctg tcc   528
Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser
                165                 170                 175

cgc ctc cgc gct gcg tac acc ctc aag gtc ggc tcc gaa tac acc cac   576
Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His
            180                 185                 190

atc ctg gac cgc gac gag cgc acc tgg ctg cag gac cgc ctc gag gcc   624
Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala
        195                 200                 205

gga atg cca aag cca acc cag gca gag cag aag tac atc ctg cag aag   672
Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys
    210                 215                 220

ctg aac gcc gcg gag gct ttc gag aac ttc ctg cag acc aag tac gtc   720
Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val
225                 230                 235                 240
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09/29/2006 15:09:29

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ggc cag aag cgc ttc tcc ctc gaa ggt gca gaa gca ctt atc cca ctg   768
Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu
                245                 250                 255

atg gac tcc gcc atc gac acc gcc gca ggc caa ggc ctc gac gaa gtt   816
Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val
            260                 265                 270

gtc atc ggt atg cca cac cgt ggt cgc ctc aac gtg ctg ttc aac atc   864
Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile
        275                 280                 285

gtg ggc aag cca ctg gca tcc atc ttc aac gag ttt gaa ggc caa atg   912
Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met
    290                 295                 300

gag cag ggc cag atc ggt ggc tcc ggt gac gtg aag tac cac ctc ggt   960
Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly
305                 310                 315                 320

tcc gaa ggc cag cac ctg cag atg ttc ggc gac ggc gag atc aag gtc   1008
Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val
                325                 330                 335

tcc ctg act gct aac ccg tcc cac ctg gaa gct gtt aac cca gcg atg   1056
Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met
            340                 345                 350

gaa ggt att gtc cgc gca aag cag gac tac ctg gac aag ggc gta gac   1104
Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp
        355                 360                 365

ggc aag act gtt gtg cca ctg ctg ctc cac ggt gac gct gca ttc gca   1152
Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala
    370                 375                 380

ggc ctg ggc atc gtg cca gaa acc atc aac ctg gct aag ctg cgt ggc   1200
Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly
385                 390                 395                 400

tac gac gtc ggc ggc acc atc cac atc gtg gtg aac aac cag atc ggc   1248
Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly
                405                 410                 415

ttc acc acc acc cca gac tcc agc cgc tcc atg cac tac gca acc gac   1296
Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp
            420                 425                 430

tac gcc aag gca ttc ggc tgc cca gtc ttc cac gtc aac ggc gac gac   1344
Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp
        435                 440                 445

cca gag gca gtt gtc tgg gtt ggc cag ctg gcc acc gag tac cgt cgt   1392
Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg
    450                 455                 460

cgc ttc ggc aag gac gtc ttc atc gac ctc gtc tgc tac cgc ctc cgc   1440
Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg
465                 470                 475                 480
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ggc cac aac gaa gct gat gat cct tcc atg acc cag cca aag atg tat   1488
Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr
                485                 490                 495

gag ctc atc acc ggc cgc gag acc gtt cgt gct cag tac acc gaa gac   1536
Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp
            500                 505                 510

ctg ctc gga cgt gga gac ctc tcc aac gaa gat gca gaa gca gtc gtc   1584
Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val
        515                 520                 525

cgc gac ttc cac gac cag atg gaa tct gtg ttc aac gaa gtc aag gaa   1632
Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu
    530                 535                 540

ggc ggc aag aag cag gct gag gca cag acc ggc atc acc ggc tcc cag   1680
Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln
545                 550                 555                 560

aag ctt cca cac ggc ctt gag acc aac atc tcc cgt gaa gag ctc ctg   1728
Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu
                565                 570                 575

gaa ctg gga cag gct ttc gcc aac acc cca gaa ggc ttc aac tac cac   1776
Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His
            580                 585                 590

cca cgt gtg gct ccc gtt gct aag aag cgc gtc tcc tct gtc acc gaa   1824
Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu
        595                 600                 605

ggt ggc atc gac tgg gca tgg ggc gag ctc ctc gcc ttc ggt tcc ctg   1872
Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu
    610                 615                 620

gct aac tcc ggc cgc ttg gtt cgc ctt gca ggt gaa gat tcc cgc cgc   1920
Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg
625                 630                 635                 640

ggt acc ttc acc cag cgc cac gca gtt gcc atc gac cca gcg acc gct   1968
Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala
                645                 650                 655

gaa gag ttc aac cca ctc cac gag ctt gca cag tcc aag ggc aac aac   2016
Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn
            660                 665                 670

ggt aag ttc ctg gtc tac aac tcc gca ctg acc gag tac gca ggc atg   2064
Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met
        675                 680                 685

ggc ttc gag tac ggc tac tcc gta gga aac gaa gac tcc atc gtt gca   2112
Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala
    690                 695                 700

tgg gaa gca cag ttc ggc gac ttc gcc aac ggc gct cag acc atc atc   2160
Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile
705                 710                 715                 720

gat gag tac gtc tcc tca ggc gaa gct aag tgg ggc cag acc tcc aag   2208
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Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys
                725                 730                 735

ctg atc ctt ctg ctg cct cac ggc tac gaa ggc cag ggc cca gac cac   2256
Leu Ile Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His
            740                 745                 750

tct tcc gca cgt atc gag cgc ttc ctg cag ctg tgc gct gag ggt tcc   2304
Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser
        755                 760                 765

atg act gtt gct cag cca tcc acc cca gca aac cac ttc cac cta ctg   2352
Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu
    770                 775                 780

cgt cgt cac gct ctg tcc gac ctg aag cgt cca ctg gtt atc ttc acc   2400
Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr
785                 790                 795                 800

ccg aag tcc atg ctg cgt aac aag gct gct gcc tcc gca cca gaa gac   2448
Pro Lys Ser Met Leu Arg Asn Lys Ala Ala Ala Ser Ala Pro Glu Asp
                805                 810                 815

ttc act gag gtc acc aag ttc cag tcc gtg atc aac gat cca aac gtt   2496
Phe Thr Glu Val Thr Lys Phe Gln Ser Val Ile Asn Asp Pro Asn Val
            820                 825                 830

gca gat gca gcc aag gtg aag aag gtc atg ctg gtc tcc ggc aag ctg   2544
Ala Asp Ala Ala Lys Val Lys Lys Val Met Leu Val Ser Gly Lys Leu
        835                 840                 845

tac tac gaa ttg gca aag cgc aag gag aag gac gga cgc gac gac atc   2592
Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile
    850                 855                 860

gcg atc gtt cgt atc gaa atg ctc cac cca att ccg ttc aac cgc atc   2640
Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile
865                 870                 875                 880

tcc gag gct ctt gcc ggc tac cct aac gct gag gaa gtc ctc ttc gtt   2688
Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val
                885                 890                 895

cag gat gag cca gca aac cag ggc cca tgg ccg ttc tac cag gag cac   2736
Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His
            900                 905                 910

ctc cca gag ctg atc ccg aac atg cca aag atg cgc cgc gtt tcc cgc   2784
Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg
        915                 920                 925

cgc gct cag tcc tcc acc gca act ggt gtt gcc aag gtg cac cag ctg   2832
Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu
    930                 935                 940

gag gag aag cag ctt atc gac gag gct ttc gag gct taagtcttta        2878
Glu Glu Lys Gln Leu Ile Asp Glu Ala Phe Glu Ala
945                 950                 955

tagtcctgca cta                                                   2891
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Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr
         35                  40                  45

Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg
     50                  55                  60

Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe
 65                  70                  75                  80

Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val
                 85                  90                  95

Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu
            100                 105                 110

Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser
        115                 120                 125

Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile
    130                 135                 140

Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val
145                 150                 155                 160

Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser
                165                 170                 175

Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His
            180                 185                 190

Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala
        195                 200                 205

Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys
    210                 215                 220

Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val
225                 230                 235                 240

Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu
                245                 250                 255

Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val
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Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile
        275                 280                 285
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Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met
    290                 295                 300

Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly
305                 310                 315                 320

Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val
                325                 330                 335

Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met
            340                 345                 350

Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp
        355                 360                 365

Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala
    370                 375                 380

Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly
385                 390                 395                 400

Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly
                405                 410                 415

Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp
            420                 425                 430

Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp
        435                 440                 445

Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg
    450                 455                 460

Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg
465                 470                 475                 480

Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr
                485                 490                 495

Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp
            500                 505                 510

Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val
        515                 520                 525

Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu
    530                 535                 540

Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln
545                 550                 555                 560

Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu
                565                 570                 575

Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His
            580                 585                 590

Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu
        595                 600                 605

Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu
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Replacement Sheet - 805

610 615 620

Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg
625 630 635 640

Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala
645 650 655

Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn
660 665 670

Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met
675 680 685

Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala
690 695 700

Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile
705 710 715 720

Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys
725 730 735

Leu Ile Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His
740 745 750

Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser
755 760 765

Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu
770 775 780

Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr
785 790 795 800

Pro Lys Ser Met Leu Arg Asn Lys Ala Ala Ala Ser Ala Pro Glu Asp
805 810 815

Phe Thr Glu Val Thr Lys Phe Gln Ser Val Ile Asn Asp Pro Asn Val
820 825 830

Ala Asp Ala Ala Lys Val Lys Lys Val Met Leu Val Ser Gly Lys Leu
835 840 845

Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile
850 855 860

Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile
865 870 875 880

Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val
885 890 895

Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His
900 905 910

Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg
915 920 925

Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu
930 935 940

Doc. Code: Appeal Brief

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  1               5                  10                  15

cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca   96
Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala Glu Glu Glu Ala
            20                  25                  30

gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag   144
Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
        35                  40                  45

gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa   192
Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
    50                  55                  60

atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg   240
Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
65                  70                  75                  80

ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag   288
Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
                85                  90                  95

gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc   336
Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
            100                 105                 110

acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc   384
Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
        115                 120                 125

gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc   432
Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala
    130                 135                 140

gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag   480
Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
145                 150                 155                 160

cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct   528
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
                165                 170                 175

act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac   576
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```
Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
            180                 185                 190

gtt cca tac gtc acc cca ctg gtg cgc aag ctt gct gaa aag cac ggc   624
Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly
        195                 200                 205

gtt gac ttg aac acc gtg acc ggt acc ggt atc ggt ggc cgt atc cgc   672
Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg
    210                 215                 220

aag cag gat gtt ttg gct gct gcg aac ggc gag gct gca cct gct gag   720
Lys Gln Asp Val Leu Ala Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu
225                 230                 235                 240

gct gct gct cct gtt tcc gct tgg tcc act aag tct gtt gac cct gag   768
Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu
                245                 250                 255

aag gct aag ctc cgt ggt acc act cag aag gtc aac cgc atc cgt gag   816
Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu
            260                 265                 270

atc acc gcg atg aag acc gtc gag gct ctg cag att tct gct cag ctc   864
Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu
        275                 280                 285

acc cag ctg cac gag gtc gat atg act cgc gtt gct gag ctg cgt aag   912
Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys
    290                 295                 300

aag aac aag ccc gcg ttc atc gag aag cac ggt gtg aac ctc act tac   960
Lys Asn Lys Pro Ala Phe Ile Glu Lys His Gly Val Asn Leu Thr Tyr
305                 310                 315                 320

ctg cca ttc ttc gtg aag gca gtt gtc gag gct ttg gtt tcc cat cca  1008
Leu Pro Phe Phe Val Lys Ala Val Val Glu Ala Leu Val Ser His Pro
                325                 330                 335

aac gtc aac gcg tct ttc aac gcg aag acc aag gag atg acc tac cac  1056
Asn Val Asn Ala Ser Phe Asn Ala Lys Thr Lys Glu Met Thr Tyr His
            340                 345                 350

tcc tcc gtt aac ctc tcc atc gct gtt gat acc cca gct ggt ctg ttg  1104
Ser Ser Val Asn Leu Ser Ile Ala Val Asp Thr Pro Ala Gly Leu Leu
        355                 360                 365

acc cca gtc att cac gat gct cag gat ctc tcc atc cca gag atc gca  1152
Thr Pro Val Ile His Asp Ala Gln Asp Leu Ser Ile Pro Glu Ile Ala
    370                 375                 380

aag gca att gtt gac ctg gct gat cgt tca cgc aac aac aag ctg aag  1200
Lys Ala Ile Val Asp Leu Ala Asp Arg Ser Arg Asn Asn Lys Leu Lys
385                 390                 395                 400

cca aac gat ctg tcc ggt ggc acc ttc acc atc acc aac att ggt tct  1248
Pro Asn Asp Leu Ser Gly Gly Thr Phe Thr Ile Thr Asn Ile Gly Ser
                405                 410                 415

gaa ggc gca ctg tct gat acc cca atc ctg gtt cca cca cag gct ggc  1296
Glu Gly Ala Leu Ser Asp Thr Pro Ile Leu Val Pro Pro Gln Ala Gly
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            420                 425                 430

atc ttg ggc acc ggc gcg atc gtg aag cgt cca gtt gtc atc acc gag   1344
Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu
        435                 440                 445

gat gga att gat tcc atc gcg atc cgt cag atg gtc ttc cta cca ctg   1392
Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu
    450                 455                 460

acc tac gac cac cag gtt gta gat ggc gca gat gct ggt cgc ttc ctg   1440
Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu
465                 470                 475                 480

acc acc atc aag gac cgc ctt gag acc gct aac ttc gaa ggc gat ctg   1488
Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu
                485                 490                 495

cag ctc taagatctct gcaagttaaa acc                                1517
Gln Leu
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09252004.090202

<210> 564
<211> 498
<212> PRT
<213> Corynebacterium glutamicum

<400> 564

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Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala
  1               5                  10                  15

Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala Glu Glu Glu Ala
             20                  25                  30

Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
         35                  40                  45

Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
     50                  55                  60

Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65                  70                  75                  80

Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
                 85                  90                  95

Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
            100                 105                 110

Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
        115                 120                 125

Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala
    130                 135                 140

Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
145                 150                 155                 160

Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
                165                 170                 175
```

```
Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
            180                 185                 190

Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly
        195                 200                 205

Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg
    210                 215                 220

Lys Gln Asp Val Leu Ala Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu
225                 230                 235                 240

Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu
                245                 250                 255

Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu
            260                 265                 270

Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu
        275                 280                 285

Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys
    290                 295                 300

Lys Asn Lys Pro Ala Phe Ile Glu Lys His Gly Val Asn Leu Thr Tyr
305                 310                 315                 320

Leu Pro Phe Phe Val Lys Ala Val Val Glu Ala Leu Val Ser His Pro
                325                 330                 335

Asn Val Asn Ala Ser Phe Asn Ala Lys Thr Lys Glu Met Thr Tyr His
            340                 345                 350

Ser Ser Val Asn Leu Ser Ile Ala Val Asp Thr Pro Ala Gly Leu Leu
        355                 360                 365

Thr Pro Val Ile His Asp Ala Gln Asp Leu Ser Ile Pro Glu Ile Ala
    370                 375                 380

Lys Ala Ile Val Asp Leu Ala Asp Arg Ser Arg Asn Asn Lys Leu Lys
385                 390                 395                 400

Pro Asn Asp Leu Ser Gly Gly Thr Phe Thr Ile Thr Asn Ile Gly Ser
                405                 410                 415

Glu Gly Ala Leu Ser Asp Thr Pro Ile Leu Val Pro Pro Gln Ala Gly
            420                 425                 430

Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu
        435                 440                 445

Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu
    450                 455                 460

Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu
465                 470                 475                 480

Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu
                485                 490                 495
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09625.0056-00000

Gln Leu

<210> 565
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(982)
<223> RXA00782

<400> 565
gggtatggat gcagcggctg atcacgctgc ccatttggcc aatcttgccc agcacggcca 60

gttcgcaacc gctaattagt taaggagcac ctgtttaatc atg tct att ttt ctc 115
Met Ser Ile Phe Leu
1 5

aat tca gat tcc cgc atc atc att cag ggc att acc ggt tcg gaa ggt 163
Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile Thr Gly Ser Glu Gly
10 15 20

tca gag cat gcg cgt cga att tta gcc tct ggt gcg aag ctc gtg ggt 211
Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly Ala Lys Leu Val Gly
25 30 35

ggc acc aac ccc cgc aaa gct ggg caa acc att ttg atc aat gac act 259
Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile Leu Ile Asn Asp Thr
40 45 50

gag ttg cct gta ttt ggc act gtt aag gaa gca atg gag gaa acg ggt 307
Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala Met Glu Glu Thr Gly
55 60 65

gcg gat gtc acc gta att ttc gtt cct cca gcc ttt gcc aaa gct gcg 355
Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala Phe Ala Lys Ala Ala
70 75 80 85

atc att gaa gct atc gac gct cac atc cca ctg tgc gtg att att act 403
Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu Cys Val Ile Ile Thr
90 95 100

gag ggc atc cca gtg cgt gac gct tct gag gcg tgg gct tat gcc aag 451
Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala Trp Ala Tyr Ala Lys
105 110 115

aag gtg gga cac acc cgc atc att ggc cct aac tgc cca ggc att att 499
Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn Cys Pro Gly Ile Ile
120 125 130

act ccc ggc gaa tct ctt gcg gga att acg ccg gca aac att gca ggt 547
Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro Ala Asn Ile Ala Gly
135 140 145

tcc ggc ccg atc ggg ttg atc tca aag tcg gga aca ctg act tat cag 595
Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly Thr Leu Thr Tyr Gln
150 155 160 165

```
atg atg tac gaa ctt tca gat att ggc att tct acg gcg att ggt att   643
Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser Thr Ala Ile Gly Ile
                170                 175                 180

ggc ggt gac cca atc atc ggt aca acc cat atc gac gct ctg gag gcc   691
Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile Asp Ala Leu Glu Ala
            185                 190                 195

ttt gaa gct gat cct gag acc aag gca atc gtc atg atc ggt gag atc   739
Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val Met Ile Gly Glu Ile
        200                 205                 210

ggt gga gat gca gag gaa cgc gct gct gac ttc att tct aag cac gtg   787
Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe Ile Ser Lys His Val
    215                 220                 225

aca aaa cca gtt gtg ggt tac gtg gca ggc ttt acc gcc cct gaa gga   835
Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly
230                 235                 240                 245

aag acc atg ggg cat gct ggc gcc atc gtg aca ggt tca gaa ggc act   883
Lys Thr Met Gly His Ala Gly Ala Ile Val Thr Gly Ser Glu Gly Thr
                250                 255                 260

gcg cga gca aag aag cat gca ttg gag gcc gtg ggt gtt cgc gtg gga   931
Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val Gly Val Arg Val Gly
            265                 270                 275

aca act ccg agt gaa acc gcg aag ctt atg cgt gag gta gtt gca gct   979
Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg Glu Val Val Ala Ala
        280                 285                 290

ttg taactaacag gccacagatc tta                                    1005
Leu
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09252010

<210> 566
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

<400> 566

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Met Ser Ile Phe Leu Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile
  1               5                  10                  15

Thr Gly Ser Glu Gly Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly
             20                  25                  30

Ala Lys Leu Val Gly Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile
         35                  40                  45

Leu Ile Asn Asp Thr Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala
     50                  55                  60

Met Glu Glu Thr Gly Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala
 65                  70                  75                  80

Phe Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu
                 85                  90                  95
```

```
Cys Val Ile Ile Thr Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala
            100                 105                 110

Trp Ala Tyr Ala Lys Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn
        115                 120                 125

Cys Pro Gly Ile Ile Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro
    130                 135                 140

Ala Asn Ile Ala Gly Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly
145                 150                 155                 160

Thr Leu Thr Tyr Gln Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser
                165                 170                 175

Thr Ala Ile Gly Ile Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile
            180                 185                 190

Asp Ala Leu Glu Ala Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val
        195                 200                 205

Met Ile Gly Glu Ile Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe
    210                 215                 220

Ile Ser Lys His Val Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe
225                 230                 235                 240

Thr Ala Pro Glu Gly Lys Thr Met Gly His Ala Gly Ala Ile Val Thr
                245                 250                 255

Gly Ser Glu Gly Thr Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val
            260                 265                 270

Gly Val Arg Val Gly Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg
        275                 280                 285

Glu Val Val Ala Ala Leu
    290
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09605420.030502

<210> 567
<211> 1395
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1372)
<223> RXA00783

<400> 567
aaagttccca aggggtgggg gctgagcacc acggatccaa ttttgttgca atttgcaaag 60

tttacagtgt tagacttcac aatacgatca tattggtgag ttg aaa cac tta ctt 115
                                                Leu Lys His Leu Leu
                                                  1   5

tta cgg gaa gac ttt gtt aaa gac gca gaa ggc tct aag cat ggg ccg 163
Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly Ser Lys His Gly Pro
                10   15   20

```
gaa atg gaa ttg gca gtg gat ctt ttt gaa tac caa gca cgg gac ctc   211
Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr Gln Ala Arg Asp Leu
             25                  30                  35

ttt gaa acc cat ggt gtg cca gtg ttg aag gga att gtg gca tca aca   259
Phe Glu Thr His Gly Val Pro Val Leu Lys Gly Ile Val Ala Ser Thr
         40                  45                  50

cca gag gcg gcg agg aaa gcg gct gag gaa atc ggc gga ctg acc gtc   307
Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile Gly Gly Leu Thr Val
     55                  60                  65

gtc aag gct cag gtc aag gtg ggc gga cgt ggc aag gcg ggt ggc gtc   355
Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly Lys Ala Gly Gly Val
 70                  75                  80                  85

cgt gtg gca ccg acg tcg gct cag gct ttt gat gct gcg gat gcg att   403
Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp Ala Ala Asp Ala Ile
                 90                  95                 100

ctc ggc atg gat atc aaa gga cac act gtt aat cag gtg atg gtg gcg   451
Leu Gly Met Asp Ile Lys Gly His Thr Val Asn Gln Val Met Val Ala
            105                 110                 115

cag ggc gct gac att gct gag gaa tac tat ttc tcc att ttg ttg gat   499
Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe Ser Ile Leu Leu Asp
        120                 125                 130

cgc gcg aat cgt tcg tat ctg gct atg tgc tct gtt gaa ggt ggc atg   547
Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser Val Glu Gly Gly Met
    135                 140                 145

gag atc gag atc ctg gcg aag gaa aag cct gaa gct ttg gca aag gtg   595
Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu Ala Leu Ala Lys Val
150                 155                 160                 165

gaa gtg gat ccc ctc act ggt att gat gag gac aaa gcg cgg gag att   643
Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp Lys Ala Arg Glu Ile
                170                 175                 180

gtc act gct gct ggc ttt gaa act gag gtg gca gag aaa gtc att ccg   691
Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala Glu Lys Val Ile Pro
            185                 190                 195

gtg ctg atc aag atc tgg cag gtg tat tac gaa gag gaa gca aca ctc   739
Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu Glu Glu Ala Thr Leu
        200                 205                 210

gtt gag gtg aac ccg ttg gtg ctc acg gat gac ggc gat gtg att gcg   787
Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp Gly Asp Val Ile Ala
    215                 220                 225

ctt gat ggc aag atc acg ctg gat gat aac gct gat ttc cgc cat gat   835
Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala Asp Phe Arg His Asp
230                 235                 240                 245

aac cgt ggt gcg ttg gct gaa tct gcc ggt ggc ttg gac att ttg gaa   883
Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly Leu Asp Ile Leu Glu
                250                 255                 260

ctg aag gcc aag aag aat gat ctg aac tac gtg aaa ctt gat ggc tct   931
```

```
Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser
            265                 270                 275

gtg ggc atc att ggc aat ggt gca ggt ttg gtg atg tcc acg ttg gat   979
Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp
        280                 285                 290

atc gtg gct gca gct ggt gaa cgc cat ggt ggg cag cgc ccc gcg aac   1027
Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly Gln Arg Pro Ala Asn
    295                 300                 305

ttc cta gac att ggt ggc gga gca tca gct gaa tcg atg gct gct ggt   1075
Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu Ser Met Ala Ala Gly
310                 315                 320                 325

ctc gat gtg atc ctt ggg gat agc cag gta cgc agt gtg ttt gtg aat   1123
Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg Ser Val Phe Val Asn
                330                 335                 340

gtg ttt ggt ggc atc acc gcg tgt gat gtg gtg gca aag gga atc gtt   1171
Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val Ala Lys Gly Ile Val
            345                 350                 355

gga gct ttg gat gtg ctc ggc gat caa gca acg aag cct ctt gtg gtg   1219
Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr Lys Pro Leu Val Val
        360                 365                 370

cgc ctt gat ggc aac aac gtg gtg gaa ggc aga cga atc ctc gcg gaa   1267
Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg Arg Ile Leu Ala Glu
    375                 380                 385

tat aac cac cct ttg gtc acc gtt gtg gag ggt atg gat gca gcg gct   1315
Tyr Asn His Pro Leu Val Thr Val Val Glu Gly Met Asp Ala Ala Ala
390                 395                 400                 405

gat cac gct gcc cat ttg gcc aat ctt gcc cag cac ggc cag ttc gca   1363
Asp His Ala Ala His Leu Ala Asn Leu Ala Gln His Gly Gln Phe Ala
                410                 415                 420

acc gct aat tagttaagga gcacctgttt aat                            1395
Thr Ala Asn
```

<210> 568
<211> 424
<212> PRT
<213> Corynebacterium glutamicum

<400> 568

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Leu Lys His Leu Leu Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly
  1               5                  10                  15

Ser Lys His Gly Pro Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr
            20                  25                  30

Gln Ala Arg Asp Leu Phe Glu Thr His Gly Val Pro Val Leu Lys Gly
        35                  40                  45

Ile Val Ala Ser Thr Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile
    50                  55                  60
```

```
Gly Gly Leu Thr Val Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly
 65                  70                  75                  80

Lys Ala Gly Gly Val Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp
                85                  90                  95

Ala Ala Asp Ala Ile Leu Gly Met Asp Ile Lys Gly His Thr Val Asn
            100                 105                 110

Gln Val Met Val Ala Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe
        115                 120                 125

Ser Ile Leu Leu Asp Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser
    130                 135                 140

Val Glu Gly Gly Met Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu
145                 150                 155                 160

Ala Leu Ala Lys Val Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp
                165                 170                 175

Lys Ala Arg Glu Ile Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala
            180                 185                 190

Glu Lys Val Ile Pro Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu
        195                 200                 205

Glu Glu Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp
    210                 215                 220

Gly Asp Val Ile Ala Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala
225                 230                 235                 240

Asp Phe Arg His Asp Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly
                245                 250                 255

Leu Asp Ile Leu Glu Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val
            260                 265                 270

Lys Leu Asp Gly Ser Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val
        275                 280                 285

Met Ser Thr Leu Asp Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly
    290                 295                 300

Gln Arg Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu
305                 310                 315                 320

Ser Met Ala Ala Gly Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg
                325                 330                 335

Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val
            340                 345                 350

Ala Lys Gly Ile Val Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr
        355                 360                 365

Lys Pro Leu Val Val Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg
    370                 375                 380
```

Doc. No. 0050-0001-0000

```
Arg Ile Leu Ala Glu Tyr Asn His Pro Leu Val Thr Val Val Glu Gly
385                 390                 395                 400

Met Asp Ala Ala Ala Asp His Ala Ala His Leu Ala Asn Leu Ala Gln
                405                 410                 415

His Gly Gln Phe Ala Thr Ala Asn
            420


<210> 569
<211> 1623
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1600)
<223> RXN01695

<400> 569
tatggccaac acttgcattc gggtgctggc gatcatttat gagatgacgc cttgtgttgg 60

tgttcggcag agaactcgcg gagataaaag gaagttgaac atg tca gat tcc ccg   115
                                            Met Ser Asp Ser Pro
                                              1               5

aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt   163
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly
                10                  15                  20

gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag   211
Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met Leu Arg Gln Leu Glu
            25                  30                  35

cca agc tgg act cag atc gtc ttc gag cgt ttg gat gga ccg gca caa   259
Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu Asp Gly Pro Ala Gln
        40                  45                  50

gag tcg tcc tcc ccg tgg aac aat gca gga acc ggc cac tct gct cta   307
Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr Gly His Ser Ala Leu
    55                  60                  65

tgc gag ctg aac tac acc cca gag gtt aag ggc aag gtt gaa att gcc   355
Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly Lys Val Glu Ile Ala
70                  75                  80                  85

aag gct gta gga atc aac gag aag ttc cag gtt tcc cgt cag ttc tgg   403
Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val Ser Arg Gln Phe Trp
                90                  95                  100

tct cac ctc gtt gaa gag gga gtg ctg tct gat cct aag gaa ttc atc   451
Ser His Leu Val Glu Glu Gly Val Leu Ser Asp Pro Lys Glu Phe Ile
            105                 110                 115

aac cct gtt cct cac gta tct ttc ggc cag ggc gca gat cag gtt gca   499
Asn Pro Val Pro His Val Ser Phe Gly Gln Gly Ala Asp Gln Val Ala
        120                 125                 130

tac atc aag gct cgc tac gaa gct ttg aag gat cac cca ctc ttc cag   547
Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp His Pro Leu Phe Gln
```

```
    135                 140                 145

ggc atg acc tac gct gac gat gaa gct acc ttc acc gag aag ctg cct   595
Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe Thr Glu Lys Leu Pro
150                 155                 160                 165

ttg atg gca aag ggc cgt gac ttc tct gat cca gta gca atc tct tgg   643
Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro Val Ala Ile Ser Trp
                170                 175                 180

atc gat gaa ggc acc gac atc aac tac ggt gct cag acc aag cag tac   691
Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala Gln Thr Lys Gln Tyr
            185                 190                 195

ctg gat gca gct gaa gtt gaa ggc act gaa atc cgc tat ggc cac gaa   739
Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile Arg Tyr Gly His Glu
        200                 205                 210

gtc aag agc atc aag gct gat ggc gca aag tgg atc gtg acc gtc aag   787
Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp Ile Val Thr Val Lys
    215                 220                 225

aac gta cac act ggc gac acc aag acc atc aag gca aac ttc gtg ttc   835
Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys Ala Asn Phe Val Phe
230                 235                 240                 245

gtc ggc gca ggc gga tac gca ctg gat ctg ctt cgc agc gca ggc atc   883
Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu Arg Ser Ala Gly Ile
                250                 255                 260

cca cag gtc aag ggc ttc gct gga ttc cca gta tcc ggc ctg tgg ctt   931
Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu
            265                 270                 275

cgt tgc acc aac gag gaa ctg atc gag cag cac gca gcc aag gta tat   979
Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr
        280                 285                 290

ggc aag gca tct gtt ggc gct cct cca atg tct gtt cct cac ctt gac   1027
Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser Val Pro His Leu Asp
    295                 300                 305

acc cgc gtt atc gag ggt gaa aag ggt ctg ctc ttt gga cct tac ggt   1075
Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu Phe Gly Pro Tyr Gly
310                 315                 320                 325

ggc tgg acc cct aag ttc ttg aag gaa ggc tcc tac ctg gac ctg ttc   1123
Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser Tyr Leu Asp Leu Phe
                330                 335                 340

aag tcc atc cgc cca gac aac att cct tcc tac ctt ggc gtt gct gct   1171
Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr Leu Gly Val Ala Ala
            345                 350                 355

cag gaa ttt gat ctg acc aag tac ctt gtc act gaa gtt ctc aag gac   1219
Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr Glu Val Leu Lys Asp
        360                 365                 370

cag gac aag cgt atg gat gct ctt cgc gag tac atg cca gag gca caa   1267
Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr Met Pro Glu Ala Gln
    375                 380                 385
```

US 09/726,760

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aac ggc gat tgg gag acc atc gtt gcc gga cag cgt gtt cag gtt att   1315
Asn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln Arg Val Gln Val Ile
390                 395                 400                 405

aag cct gca gga ttc cct aag ttc ggt tcc ctg gaa ttc ggc acc acc   1363
Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu Glu Phe Gly Thr Thr
                410                 415                 420

ttg atc aac aac tcc gaa ggc acc atc gcc gga ttg ctc ggt gct tcc   1411
Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly Leu Leu Gly Ala Ser
            425                 430                 435

cct gga gca tcc atc gca cct tcc gca atg atc gag ctg ctt gag cgt   1459
Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile Glu Leu Leu Glu Arg
        440                 445                 450

tgc ttc ggt gac cgc atg atc gag tgg ggc gac aag ctg aag gac atg   1507
Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp Lys Leu Lys Asp Met
    455                 460                 465

atc cct tcc tac ggc aag aag ctt gct tcc gag cca gca ctg ttt gag   1555
Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu Pro Ala Leu Phe Glu
470                 475                 480                 485

cag cag tgg gca cgc acc cag aag acc ctg aag ctt gag gaa gcc       1600
Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys Leu Glu Glu Ala
                490                 495                 500

taaatcttct aactgctttc ttt                                        1623
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<210> 570
<211> 500
<212> PRT
<213> Corynebacterium glutamicum

<400> 570

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Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp
  1               5                  10                  15

Val Val Leu Ile Gly Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met
            20                  25                  30

Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu
        35                  40                  45

Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
    50                  55                  60

Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly
65                  70                  75                  80

Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val
                85                  90                  95

Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp
            100                 105                 110

Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly
        115                 120                 125
```

```
Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp
    130                 135                 140

His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe
145                 150                 155                 160

Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro
                165                 170                 175

Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala
            180                 185                 190

Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile
        195                 200                 205

Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp
    210                 215                 220

Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys
225                 230                 235                 240

Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu
                245                 250                 255

Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val
            260                 265                 270

Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His
        275                 280                 285

Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser
    290                 295                 300

Val Pro His Leu Asp Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu
305                 310                 315                 320

Phe Gly Pro Tyr Gly Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser
                325                 330                 335

Tyr Leu Asp Leu Phe Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr
            340                 345                 350

Leu Gly Val Ala Ala Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr
        355                 360                 365

Glu Val Leu Lys Asp Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr
    370                 375                 380

Met Pro Glu Ala Gln Asn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln
385                 390                 395                 400

Arg Val Gln Val Ile Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu
                405                 410                 415

Glu Phe Gly Thr Thr Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly
            420                 425                 430

Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile
        435                 440                 445
```

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```
Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp
    450                 455                 460

Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu
465                 470                 475                 480

Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys
                485                 490                 495

Leu Glu Glu Ala
            500
```

<210> 571
<211> 1039
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1039)
<223> FRXA01615

<400> 571

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tatggccaac acttgcattc gggtgctggc gatcatttat gagatgacgc cttgtgttgg 60

tgttcggcag agaactcgcg gagataaaag gaagttgaac atg tca gat tcc ccg   115
                                            Met Ser Asp Ser Pro
                                              1               5

aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt   163
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly
                  10                  15                  20

gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag   211
Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met Leu Arg Gln Leu Glu
              25                  30                  35

cca agc tgg act cag atc gtc ttc gag cgt ttg gat gga ccg gca caa   259
Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu Asp Gly Pro Ala Gln
          40                  45                  50

gag tcg tcc tcc ccg tgg aac aat gca gga acc ggc cac tct gct cta   307
Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr Gly His Ser Ala Leu
      55                  60                  65

tgc gag ctg aac tac acc cca gag gtt aag ggc aag gtt gaa att gcc   355
Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly Lys Val Glu Ile Ala
  70                  75                  80                  85

aag gct gta gga atc aac gag aag ttc cag gtt tcc cgt cag ttc tgg   403
Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val Ser Arg Gln Phe Trp
                  90                  95                 100

tct cac ctc gtt gaa gag gga gtg ctg tct gat cct aag gaa ttc atc   451
Ser His Leu Val Glu Glu Gly Val Leu Ser Asp Pro Lys Glu Phe Ile
              105                 110                 115

aac cct gtt cct cac gta tct ttc ggc cag ggc gca gat cag gtt gca   499
Asn Pro Val Pro His Val Ser Phe Gly Gln Gly Ala Asp Gln Val Ala
          120                 125                 130
```

```
tac atc aag gct cgc tac gaa gct ttg aag gat cac cca ctc ttc cag   547
Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp His Pro Leu Phe Gln
    135                 140                 145

ggc atg acc tac gct gac gat gaa gct acc ttc acc gag aag ctg cct   595
Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe Thr Glu Lys Leu Pro
150                 155                 160                 165

ttg atg gca aag ggc cgt gac ttc tct gat cca gta gca atc tct tgg   643
Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro Val Ala Ile Ser Trp
                170                 175                 180

atc gat gaa ggc acc gac atc aac tac ggt gct cag acc aag cag tac   691
Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala Gln Thr Lys Gln Tyr
            185                 190                 195

ctg gat gca gct gaa gtt gaa ggc act gaa atc cgc tat ggc cac gaa   739
Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile Arg Tyr Gly His Glu
        200                 205                 210

gtc aag agc atc aag gct gat ggc gca aag tgg atc gtg acc gtc aag   787
Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp Ile Val Thr Val Lys
    215                 220                 225

aac gta cac act ggc gac acc aag acc atc aag gca aac ttc gtg ttc   835
Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys Ala Asn Phe Val Phe
230                 235                 240                 245

gtc ggc gca ggc gga tac gca ctg gat ctg ctt cgc agc gca ggc atc   883
Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu Arg Ser Ala Gly Ile
                250                 255                 260

cca cag gtc aag ggc ttc gct gga ttc cca gta tcc ggc ctg tgg ctt   931
Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu
            265                 270                 275

cgt tgc acc aac gag gaa ctg atc gag cag cac gca gcc aag gta tat   979
Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr
        280                 285                 290

ggc aag gca tct gtt ggc gct cct cca atg tct gtt cct cac ctt gac   1027
Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser Val Pro His Leu Asp
    295                 300                 305

acc cgc gtt atc                                                  1039
Thr Arg Val Ile
310
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<210> 572
<211> 313
<212> PRT
<213> Corynebacterium glutamicum

<400> 572

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Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp
  1               5                  10                  15

Val Val Leu Ile Gly Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met
             20                  25                  30
```

Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu
35 40 45

Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
50 55 60

Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly
65 70 75 80

Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val
85 90 95

Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp
100 105 110

Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly
115 120 125

Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp
130 135 140

His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe
145 150 155 160

Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro
165 170 175

Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala
180 185 190

Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile
195 200 205

Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp
210 215 220

Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys
225 230 235 240

Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu
245 250 255

Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val
260 265 270

Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His
275 280 285

Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser
290 295 300

Val Pro His Leu Asp Thr Arg Val Ile
305 310

<210> 573
<211> 233
<212> DNA
<213> Corynebacterium glutamicum

09625160.090502

<220>
<221> CDS
<222> (1)..(210)
<223> FRXA01695

<400> 573
gcc gga ttg ctc ggt gct tcc cct gga gca tcc atc gca cct tcc gca 48
Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala
1 5 10 15

atg atc gag ctg ctt gag cgt tgc ttc ggt gac cgc atg atc gag tgg 96
Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp
20 25 30

ggc gac aag ctg aag gac atg atc cct tcc tac ggc aag aag ctt gct 144
Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala
35 40 45

tcc gag cca gca ctg ttt gag cag cag tgg gca cgc acc cag aag acc 192
Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr
50 55 60

ctg aag ctt gag gaa gcc taaatcttct aactgctttc ttt 233
Leu Lys Leu Glu Glu Ala
65 70

<210> 574
<211> 70
<212> PRT
<213> Corynebacterium glutamicum

<400> 574
Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala
1 5 10 15

Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp
20 25 30

Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala
35 40 45

Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr
50 55 60

Leu Lys Leu Glu Glu Ala
65 70

<210> 575
<211> 1063
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1063)
<223> RXA00290

<400> 575
agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

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gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg   115
                                              Met Thr Ile Asp Leu
                                                1               5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac   163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
                10                  15                  20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg   211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
            25                  30                  35

cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa   259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
        40                  45                  50

gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga   307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly
    55                  60                  65

aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc   355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly
70                  75                  80                  85

gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag   403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln
                90                  95                  100

ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac   451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp
            105                 110                 115

gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct   499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro
        120                 125                 130

tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc   547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
    135                 140                 145

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac   595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
150                 155                 160                 165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac   643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
                170                 175                 180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att   691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
            185                 190                 195

tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac   739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
        200                 205                 210

gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac   787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
    215                 220                 225
```

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```
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag   835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
230                 235                 240                 245

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc   883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
                250                 255                 260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct   931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
            265                 270                 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca   979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
        280                 285                 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc   1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
    295                 300                 305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca                   1063
Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
310                 315                 320
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<210> 576
<211> 321
<212> PRT
<213> Corynebacterium glutamicum

<400> 576

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Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
  1               5                  10                  15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
             20                  25                  30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
         35                  40                  45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
     50                  55                  60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65                  70                  75                  80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
                 85                  90                  95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
            100                 105                 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
        115                 120                 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
    130                 135                 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
145                 150                 155                 160
```

```
Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
                165                 170                 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
            180                 185                 190

Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
        195                 200                 205

Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
    210                 215                 220

Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
225                 230                 235                 240

Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
                245                 250                 255

Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
            260                 265                 270

Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
        275                 280                 285

Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
    290                 295                 300

Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg
305                 310                 315                 320

Ser
```

US 2006/0160180 A1

<210> 577
<211> 1347
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1324)
<223> RXN01048

<400> 577
agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

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gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg   115
                                            Met Thr Ile Asp Leu
                                              1               5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac   163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
                10                  15                  20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg   211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
            25                  30                  35

cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa   259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
```

```
         40                  45                  50

gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga   307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly
     55                  60                  65

aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc   355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly
 70                  75                  80                  85

gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag   403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln
                 90                  95                 100

ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac   451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp
            105                 110                 115

gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct   499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro
        120                 125                 130

tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc   547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
    135                 140                 145

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac   595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
150                 155                 160                 165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac   643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
                170                 175                 180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att   691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
            185                 190                 195

tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac   739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
        200                 205                 210

gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac   787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
    215                 220                 225

gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag   835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
230                 235                 240                 245

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc   883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
                250                 255                 260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct   931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
            265                 270                 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca   979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
        280                 285                 290
```

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acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc   1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
    295                 300                 305

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg   1075
Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala
310                 315                 320                 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc   1123
Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile
                330                 335                 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag   1171
Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln
            345                 350                 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc   1219
Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro
        360                 365                 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc   1267
Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
    375                 380                 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg   1315
Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
390                 395                 400                 405

cca ata ttt taagagcaaa cttgaggccc aca                            1347
Pro Ile Phe
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<210> 578
<211> 408
<212> PRT
<213> Corynebacterium glutamicum

<400> 578

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Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
  1               5                  10                  15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
            20                  25                  30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
        35                  40                  45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
    50                  55                  60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
65                  70                  75                  80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
                85                  90                  95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
            100                 105                 110
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09251360

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
130 135 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
145 150 155 160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
165 170 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
180 185 190

Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
195 200 205

Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
210 215 220

Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
225 230 235 240

Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
245 250 255

Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
260 265 270

Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
275 280 285

Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
290 295 300

Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile
305 310 315 320

Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala
325 330 335

Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln
340 345 350

Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu
355 360 365

Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg
370 375 380

Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser
385 390 395 400

Leu Pro Val Glu Ala Pro Ile Phe
405

<210> 579
<211> 311
<212> DNA

Document: 09/502,176

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(288)
<223> FRXA01048

<400> 579
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cgc tct gac ttg cct aac cag atc aac aac gtg ctg gcg ttc cca gga   48
Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
  1               5                  10                  15

att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag   96
Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
             20                  25                  30

atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc   144
Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
         35                  40                  45

tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc   192
Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
     50                  55                  60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt   240
Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65                  70                  75                  80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt   288
Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
                 85                  90                  95

taagagcaaa cttgaggccc aca                                        311
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<210> 580
<211> 96
<212> PRT
<213> Corynebacterium glutamicum

<400> 580
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Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
  1               5                  10                  15

Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
             20                  25                  30

Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
         35                  40                  45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
     50                  55                  60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65                  70                  75                  80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
                 85                  90                  95
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<210> 581
<211> 1063
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1063)
<223> FRXA00290

<400> 581
agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
Met Thr Ile Asp Leu
1 5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
10 15 20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
25 30 35

cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
40 45 50

gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly
55 60 65

aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc 355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly
70 75 80 85

gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln
90 95 100

ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac 451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp
105 110 115

gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct 499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro
120 125 130

tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc 547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
135 140 145

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
150 155 160 165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn

```
                170                 175                 180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att   691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
            185                 190                 195

tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac   739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
        200                 205                 210

gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac   787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
    215                 220                 225

gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag   835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
230                 235                 240                 245

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc   883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
                250                 255                 260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct   931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
            265                 270                 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca   979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
        280                 285                 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc   1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
    295                 300                 305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca                   1063
Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
310                 315                 320
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<210> 582
<211> 321
<212> PRT
<213> Corynebacterium glutamicum

<400> 582

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Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
  1               5                  10                  15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
            20                  25                  30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
        35                  40                  45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
    50                  55                  60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
65                  70                  75                  80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
```

```
                85                  90                  95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
            100                 105                 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
        115                 120                 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
    130                 135                 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
145                 150                 155                 160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
                165                 170                 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
            180                 185                 190

Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
        195                 200                 205

Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
    210                 215                 220

Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
225                 230                 235                 240

Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
                245                 250                 255

Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
            260                 265                 270

Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
        275                 280                 285

Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
    290                 295                 300

Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg
305                 310                 315                 320

Ser
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09825160.1-09825160

<210> 583
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(582)
<223> RXN03101

<400> 583
atc ctt gca gac gaa gac gac acc gtc gac gtc ggc gca gtc atc gcc 48
Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala

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  1               5                  10                  15

cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca   96
Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala Glu Glu Glu Ala
             20                  25                  30

gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag   144
Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
         35                  40                  45

gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa   192
Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
     50                  55                  60

atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg   240
Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65                  70                  75                  80

ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag   288
Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
                 85                  90                  95

gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc   336
Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
            100                 105                 110

acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc   384
Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
        115                 120                 125

gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc   432
Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala
    130                 135                 140

gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag   480
Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
145                 150                 155                 160

cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct   528
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
                165                 170                 175

act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac   576
Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
            180                 185                 190

gtt cca                                                          582
Val Pro
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09525160.090502

<210> 584
<211> 194
<212> PRT
<213> Corynebacterium glutamicum

<400> 584

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Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala
  1               5                  10                  15

Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala Glu Glu Glu Ala
```

```
             20                  25                  30

Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
         35                  40                  45

Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
     50                  55                  60

Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65                  70                  75                  80

Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
                 85                  90                  95

Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
            100                 105                 110

Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
        115                 120                 125

Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala
    130                 135                 140

Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
145                 150                 155                 160

Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
                165                 170                 175

Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
            180                 185                 190

Val Pro
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<210> 585
<211> 540
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(517)
<223> RXN02046

<400> 585
tccgtgccat caccaccggc gagatcactg gcatcgtgga cgcaaaacaa acagcaacag 60

aaattattaa catccgacgc aacgcttcag gagagtcctc atg aaa gag aca ctg 115
                                                Met Lys Glu Thr Leu
                                                  1   5

acc acc ggt tta acc cac caa atg acc tac ata gtg cca gca aac cgc 163
Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile Val Pro Ala Asn Arg
                 10   15   20

aca gtt ccg cat ctg ctt ccc gaa gca gca gaa ttt gaa acc atg cca 211
Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu Phe Glu Thr Met Pro
             25   30   35

```
gat gtc ctg gcc act gga tat atg gtc ggc atc atc gag tgg gcc tgc   259
Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile Ile Glu Trp Ala Cys
         40                  45                  50

atg gaa ctt ctg cgt ccc cat ttg gac gac ggt gaa atc tcg ctg ggc   307
Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly Glu Ile Ser Leu Gly
     55                  60                  65

act cat gtg aac ttc tcc cac gca gct cca acg gtt cct gga tcc acg   355
Thr His Val Asn Phe Ser His Ala Ala Pro Thr Val Pro Gly Ser Thr
 70                  75                  80                  85

gtc acc atc gat gtt gag gtg aca gag atc aac cgt cgt gca gtt acc   403
Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn Arg Arg Ala Val Thr
                 90                  95                 100

ttc aac atc act gca gct gat gag ttc gcc acc atc agc acc ggc acc   451
Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr Ile Ser Thr Gly Thr
            105                 110                 115

cac cag cgc ggt gtg gtt aac cgt gag aag ttt gtc tcc cgt ctg cct   499
His Gln Arg Gly Val Val Asn Arg Glu Lys Phe Val Ser Arg Leu Pro
        120                 125                 130

gaa gca cct aag gaa aac taaatcatgg ccaagttgtt tga                 540
Glu Ala Pro Lys Glu Asn
    135
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<210> 586
<211> 139
<212> PRT
<213> Corynebacterium glutamicum

<400> 586

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Met Lys Glu Thr Leu Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile
  1               5                  10                  15

Val Pro Ala Asn Arg Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu
             20                  25                  30

Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile
         35                  40                  45

Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly
     50                  55                  60

Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr
 65                  70                  75                  80

Val Pro Gly Ser Thr Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn
                 85                  90                  95

Arg Arg Ala Val Thr Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr
            100                 105                 110

Ile Ser Thr Gly Thr His Gln Arg Gly Val Val Asn Arg Glu Lys Phe
        115                 120                 125

Val Ser Arg Leu Pro Glu Ala Pro Lys Glu Asn
    130                 135
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Document generated on 2025-09-05

<210> 587
<211> 1683
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1660)
<223> RXN00389

<400> 587
ccaccactgc gtaacctttc cgagcaagat atcgcggacc tgtcggattt gcttgccacc 60

tctggcgcag gttcctaccg ccttcagttg aggtgaaagc atg atc acc gca acc 115
Met Ile Thr Ala Thr
1 5

gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
10 15 20

aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
25 30 35

cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259
Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu Arg Ala Ala Thr Thr
40 45 50

tcg gcg aag cga gct ttt gaa agc tac cga ctc act act cca gag gtt 307
Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu Thr Thr Pro Glu Val
55 60 65

aga gca gat ttc ctg gat tcc atc gct gac aac atc gat gcg cta tcc 355
Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn Ile Asp Ala Leu Ser
70 75 80 85

ggc gag atc gtg caa cgg gcg agc ctg gag aca ggt ttg gga act acc 403
Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr Gly Leu Gly Thr Thr
90 95 100

cga ctc aca ggc gaa gta gcc cgc acc agc aac cag ctc cgc ctg ttt 451
Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn Gln Leu Arg Leu Phe
105 110 115

gca gaa acc gtg aga agc gga cag ttc cac cga gta cgc att gaa cga 499
Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg Val Arg Ile Glu Arg
120 125 130

gga ccg cgg att gat ctt cgc cag cgt cag gtt ccg ttg gga cca gtc 547
Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val Pro Leu Gly Pro Val
135 140 145

gcg gta ttc ggg gca agc aac ttc ccc gtc gct ttc tct act gct ggt 595
Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala Phe Ser Thr Ala Gly
150 155 160 165

ggc gat aca gca tca gcg ttg gct gca ggc tgc cct gtg gtt ttt aag 643
Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys Pro Val Val Phe Lys

```
                170                 175                 180

gcg cat aat gcg cac cct gga aca gct gag ctc gtc ggg caa gcg gtg   691
Ala His Asn Ala His Pro Gly Thr Ala Glu Leu Val Gly Gln Ala Val
            185                 190                 195

cgg gga gcc gtc gaa aag cat gag ttt gat gct ggt gtg ttt aac ctt   739
Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala Gly Val Phe Asn Leu
        200                 205                 210

gtc tac ggc cgt ggc gtg gaa att ggc cag gag ctg gct gcg gat ccg   787
Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu Leu Ala Ala Asp Pro
    215                 220                 225

aat atc acg gca atc ggt ttt acc ggt tca cgc cag ggt ggt ttg gca   835
Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg Gln Gly Gly Leu Ala
230                 235                 240                 245

ctg tca cag act gcg ttt agc cgc cca gtt ccc gtt cca gtc ttt gca   883
Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro Val Pro Val Phe Ala
                250                 255                 260

gaa atg agt gcc acc aac cct gtg ttc gtc ttc ccc ggc gcg ctg gcg   931
Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe Pro Gly Ala Leu Ala
            265                 270                 275

gat ttg gat gca tcg agt tcc ttg gct gag gcg ttt acc gct tcc gtc   979
Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala Phe Thr Ala Ser Val
        280                 285                 290

acc ggc agt tcc ggg caa ttg tgc acc aag cct ggc ctc gtt ttc atc  1027
Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile
    295                 300                 305

ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa  1075
Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys
310                 315                 320                 325

ttt aaa gaa acc acg ggt caa acg atg ctc acg caa ggc atc gct cag  1123
Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln
                330                 335                 340

gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa  1171
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys
            345                 350                 355

atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg  1219
Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro
        360                 365                 370

gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg  1267
Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu
    375                 380                 385

cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc  1315
Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser
390                 395                 400                 405

ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca  1363
Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr
                410                 415                 420
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gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt   1411
Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu
            425                 430                 435

atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg   1459
Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp
        440                 445                 450

cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat   1507
Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr
    455                 460                 465

ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc   1555
Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile
470                 475                 480                 485

gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg   1603
Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu
                490                 495                 500

ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa   1651
Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu
            505                 510                 515

ata gac cgt taatagctgg tctttacatt tgc                            1683
Ile Asp Arg
        520
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US09/925,359

<210> 588
<211> 520
<212> PRT
<213> Corynebacterium glutamicum

<400> 588

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Met Ile Thr Ala Thr Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu
  1               5                  10                  15

Trp Val Ala Gly Lys Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr
            20                  25                  30

Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu
        35                  40                  45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
    50                  55                  60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
65                  70                  75                  80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
                85                  90                  95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
            100                 105                 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
        115                 120                 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
```

```
    130                 135                 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
145                 150                 155                 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
                165                 170                 175

Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
            180                 185                 190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
        195                 200                 205

Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
    210                 215                 220

Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
225                 230                 235                 240

Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
                245                 250                 255

Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
            260                 265                 270

Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
        275                 280                 285

Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
    290                 295                 300

Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala
305                 310                 315                 320

Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr
                325                 330                 335

Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
            340                 345                 350

Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
        355                 360                 365

Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu
    370                 375                 380

Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val
385                 390                 395                 400

Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
                405                 410                 415

Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
            420                 425                 430

Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
        435                 440                 445

Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
    450                 455                 460
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His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
465                 470                 475                 480

Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr
                485                 490                 495

Phe Pro Ala Glu Leu Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp
            500                 505                 510

Ala Val Pro Arg Glu Ile Asp Arg
        515                 520


<210> 589
<211> 1467
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1444)
<223> RXN02399

<400> 589
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catcacgtcg aaacagtgac agtgcattag ctcatacttt gtg gtc ggc acc gcc   115
                                          Val Val Gly Thr Ala
                                            1               5

cat tgc gaa tca gca ctt aag gaa gtg act ttg atg tca aac gtt gga   163
His Cys Glu Ser Ala Leu Lys Glu Val Thr Leu Met Ser Asn Val Gly
                10                  15                  20

aag cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cct   211
Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro
            25                  30                  35

cgt tgg aac ggc atc acc cgc gac tac acc gca gac cag gta gct gat   259
Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Asp Gln Val Ala Asp
        40                  45                  50

ctg cag ggt tcc gtc atc gag gag cac act ctt gct cgc cgc ggc tca   307
Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu Ala Arg Arg Gly Ser
    55                  60                  65

gag atc ctc tgg gac gca gtc acc cag gaa ggt gac gga tac atc aac   355
Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly Asp Gly Tyr Ile Asn
70                  75                  80                  85

gcg ctt ggc gca ctc acc ggt aac cag gct gtt cag cag gtt cgt gca   403
Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val Gln Gln Val Arg Ala
                90                  95                  100

ggc ctg aag gct gtc tac ctg tcc ggt tgg cag gtc gca ggt gac gcc   451
Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala
            105                 110                 115

aac ctc tcc ggc cac acc tac cct gac cag tcc ctc tac cca gcg aac   499
Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn
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        120                 125                 130

tcc gtt cca agc gtc gtt cgt cgc atc aac aac gca ctg ctg cgt tcc   547
Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn Ala Leu Leu Arg Ser
    135                 140                 145

gat gaa atc gca cgc acc gaa ggc gac acc tcc gtt gac aac tgg gtt   595
Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser Val Asp Asn Trp Val
150                 155                 160                 165

gtc cca atc gtc gcg gac ggc gaa gct ggc ttc ggt gga gca ctc aac   643
Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn
                170                 175                 180

gtc tac gaa ctc cag aag gca atg atc gca gct ggc gct gca ggc acc   691
Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala Gly Ala Ala Gly Thr
            185                 190                 195

cac tgg gaa gac cag ctc gct tct gaa aag aag tgt ggc cac ctc ggc   739
His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly
        200                 205                 210

ggc aag gtt ctg atc cca acc cag cag cac atc cgc acc ctg aac tct   787
Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser
    215                 220                 225

gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca   835
Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala
230                 235                 240                 245

cgt acc gac gct gag gca gca acc ctg atc acc tct gac gtt gat gag   883
Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu
                250                 255                 260

cgc gac caa cca ttc atc acc ggt gag cgc acc gca gaa ggc tac tac   931
Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr
            265                 270                 275

cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac   979
His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr
        280                 285                 290

gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg   1027
Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu
    295                 300                 305

gag ctc gct aag aag ttc gct gaa ggc gtt cgc tct gag ttc cca gac   1075
Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp
310                 315                 320                 325

cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac   1123
Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His
                330                 335                 340

ctc gag gca gat gag atc gct aag ttc cag aag gaa ctc ggc gca atg   1171
Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met
            345                 350                 355

ggc ttc aag ttc cag ttc atc acc ctc gca ggc ttc cac tcc ctc aac   1219
Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn
        360                 365                 370
```

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tac ggc atg ttc gac ctg gct tac gga tac gct cgc gaa ggc atg acc   1267
Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Thr
    375                 380                 385

tcc ttc gtt gac ctg cag aac cgt gag ttc aag gca gct gaa gag cgt   1315
Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg
390                 395                 400                 405

ggc ttc acc gct gtt aag cac cag cgt gag gtt ggc gca ggc tac ttc   1363
Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe
                410                 415                 420

gac cag atc gca acc acc gtt gac ccg aac tct tct acc acc gct ttg   1411
Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu
            425                 430                 435

aag ggt tcc act gaa gaa ggc cag ttc cac aac taggacctac aggttctgac 1464
Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn
        440                 445

aat                                                               1467
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<210> 590
<211> 448
<212> PRT
<213> Corynebacterium glutamicum

<400> 590

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Val Val Gly Thr Ala His Cys Glu Ser Ala Leu Lys Glu Val Thr Leu
  1               5                  10                  15

Met Ser Asn Val Gly Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp
             20                  25                  30

Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala
         35                  40                  45

Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu
     50                  55                  60

Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly
 65                  70                  75                  80

Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
                 85                  90                  95

Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
            100                 105                 110

Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser
        115                 120                 125

Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn
    130                 135                 140

Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser
145                 150                 155                 160

Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
```

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                165                 170                 175

Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala
            180                 185                 190

Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
        195                 200                 205

Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
    210                 215                 220

Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
225                 230                 235                 240

Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
                245                 250                 255

Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr
            260                 265                 270

Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala
        275                 280                 285

Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
    290                 295                 300

Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
305                 310                 315                 320

Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
                325                 330                 335

Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
            340                 345                 350

Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
        355                 360                 365

Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
    370                 375                 380

Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
385                 390                 395                 400

Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
                405                 410                 415

Gly Ala Gly Tyr Phe Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser
            420                 425                 430

Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn
        435                 440                 445
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<210> 591
<211> 1419
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1396)
<223> FRXA02399

<400> 591
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caccgcccat tgcgaatcag cacttaagga agtgactttg atg tca aac gtt gga 115
Met Ser Asn Val Gly
1 5

aag cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cct 163
Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro
10 15 20

cgt tgg aac ggc atc acc cgc gac tac acc gca gac cag gta gct gat 211
Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Asp Gln Val Ala Asp
25 30 35

ctg cag ggt tcc gtc atc gag gag cac act ctt gct cgc cgc ggc tca 259
Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu Ala Arg Arg Gly Ser
40 45 50

gag atc ctc tgg gac gca gtc acc cag gaa ggt gac gga tac atc aac 307
Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly Asp Gly Tyr Ile Asn
55 60 65

gcg ctt ggc gca ctc acc ggt aac cag gct gtt cag cag gtt cgt gca 355
Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val Gln Gln Val Arg Ala
70 75 80 85

ggc ctg aag gct gtc tac ctg tcc ggt tgg cag gtc gca ggt gac gcc 403
Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala
90 95 100

aac ctc tcc ggc cac acc tac cct gac cag tcc ctc tac cca gcg aac 451
Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn
105 110 115

tcc gtt cca agc gtc gtt cgt cgc atc aac aac gca ctg ctg cgt tcc 499
Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn Ala Leu Leu Arg Ser
120 125 130

gat gaa atc gca cgc acc gaa ggc gac acc tcc gtt gac aac tgg gtt 547
Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser Val Asp Asn Trp Val
135 140 145

gtc cca atc gtc gcg gac ggc gaa gct ggc ttc ggt gga gca ctc aac 595
Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn
150 155 160 165

gtc tac gaa ctc cag aag gca atg atc gca gct ggc gct gca ggc acc 643
Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala Gly Ala Ala Gly Thr
170 175 180

cac tgg gaa gac cag ctc gct tct gaa aag aag tgt ggc cac ctc ggc 691
His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly
185 190 195

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ggc aag gtt ctg atc cca acc cag cag cac atc cgc acc ctg aac tct   739
Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser
        200                 205                 210

gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca   787
Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala
    215                 220                 225

cgt acc gac gct gag gca gca acc ctg atc acc tct gac gtt gat gag   835
Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu
230                 235                 240                 245

cgc gac caa cca ttc atc acc ggt gag cgc acc gca gaa ggc tac tac   883
Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr
                250                 255                 260

cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac   931
His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr
            265                 270                 275

gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg   979
Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu
        280                 285                 290

gag ctc gct aag aag ttc gct gaa ggc gtt cgc tct gag ttc cca gac   1027
Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp
    295                 300                 305

cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac   1075
Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His
310                 315                 320                 325

ctc gag gca gat gag atc gct aag ttc cag aag gaa ctc ggc gca atg   1123
Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met
                330                 335                 340

ggc ttc aag ttc cag ttc atc acc ctc gca ggc ttc cac tcc ctc aac   1171
Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn
            345                 350                 355

tac ggc atg ttc gac ctg gct tac gga tac gct cgc gaa ggc atg acc   1219
Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Thr
        360                 365                 370

tcc ttc gtt gac ctg cag aac cgt gag ttc aag gca gct gaa gag cgt   1267
Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg
    375                 380                 385

ggc ttc acc gct gtt aag cac cag cgt gag gtt ggc gca ggc tac ttc   1315
Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe
390                 395                 400                 405

gac cag atc gca acc acc gtt gac ccg aac tct tct acc acc gct ttg   1363
Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu
                410                 415                 420

aag ggt tcc act gaa gaa ggc cag ttc cac aac taggacctac aggttctgac 1416
Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn
            425                 430

aat                                                               1419
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Doc. No. 0626N2PCT.ST25

<210> 592
<211> 432
<212> PRT
<213> Corynebacterium glutamicum

<400> 592

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Met Ser Asn Val Gly Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp
  1               5                  10                  15

Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala
             20                  25                  30

Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu
         35                  40                  45

Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly
     50                  55                  60

Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
 65                  70                  75                  80

Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
                 85                  90                  95

Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser
            100                 105                 110

Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn
        115                 120                 125

Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser
    130                 135                 140

Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
145                 150                 155                 160

Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala
                165                 170                 175

Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
            180                 185                 190

Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
        195                 200                 205

Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
    210                 215                 220

Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
225                 230                 235                 240

Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr
                245                 250                 255

Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala
            260                 265                 270

Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
        275                 280                 285
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Doc No. 1-0000-0000

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Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
    290                 295                 300

Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
305                 310                 315                 320

Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
                325                 330                 335

Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
            340                 345                 350

Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
        355                 360                 365

Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
    370                 375                 380

Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
385                 390                 395                 400

Gly Ala Gly Tyr Phe Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser
                405                 410                 415

Ser Thr Thr Ala Leu Lys Gly Ser Thr Glu Glu Gly Gln Phe His Asn
            420                 425                 430
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09/25/2003 15:29:00

<210> 593
<211> 2340
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2317)
<223> RXN02404

<400> 593

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cacaggtcat ctaaaaccca tgctttaaaa ggagccttca atg act gaa cag gaa   115
                                            Met Thr Glu Gln Glu
                                              1               5

ctg ttg tct gct cag act gcc gac aac gct gga act gac agc acc gaa   163
Leu Leu Ser Ala Gln Thr Ala Asp Asn Ala Gly Thr Asp Ser Thr Glu
                  10                  15                  20

cgc gtt gac gcg ggc gga atg cag gtt gca aaa gtt ctc tac gac ttt   211
Arg Val Asp Ala Gly Gly Met Gln Val Ala Lys Val Leu Tyr Asp Phe
              25                  30                  35

gta acc gaa gcg gta ctc cct cgc gtg ggt gtg gat gcg gaa aag ttc   259
Val Thr Glu Ala Val Leu Pro Arg Val Gly Val Asp Ala Glu Lys Phe
          40                  45                  50
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```
tgg tcc gga ttc gcc gcc atc gcc cgg gac ctc acc cca cgc aac cgc   307
Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg
     55                  60                  65

gag ctg ctt gct cgc cgc gat gaa ctg cag atg ctt atc gac gac tac   355
Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr
 70                  75                  80                  85

cac cgc aac aac tcc ggc acc atc gac caa gag gcg tac gag gat ttc   403
His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe
                 90                  95                 100

ctc aaa gaa atc gga tac ttg gtt gag gag cca gaa gct gca gaa atc   451
Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro Glu Ala Ala Glu Ile
            105                 110                 115

cgt acc caa aac gtc gat acg gaa atc tcc agc acc gca gga cct cag   499
Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln
        120                 125                 130

ctg gtt gtt cca att ctg aac gca cgc ttc gcg ctg aac gct gcc aat   547
Leu Val Val Pro Ile Leu Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn
    135                 140                 145

gct cgc tgg ggt tcc ctc tac gat gcg ttg tac ggc acc aac gcc atc   595
Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile
150                 155                 160                 165

cca gaa act gat ggc gct gaa aag ggc aag gag tac aac ccg gtc cgc   643
Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg
                170                 175                 180

ggc cag aag gtc atc gag tgg ggt cgt gaa ttc ctc gac agc gtt gtc   691
Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe Leu Asp Ser Val Val
            185                 190                 195

cca ctg gac ggt gct tcg cat gcc gat gtt gag aag tac aac atc acc   739
Pro Leu Asp Gly Ala Ser His Ala Asp Val Glu Lys Tyr Asn Ile Thr
        200                 205                 210

gat gga aag ctt gca gcc cac att gga gat agc gtc tac cga ctg aaa   787
Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser Val Tyr Arg Leu Lys
    215                 220                 225

aac cgt gaa tcc tac cgt ggc ttc acc ggc aac ttc ctt gat cca gaa   835
Asn Arg Glu Ser Tyr Arg Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu
230                 235                 240                 245

gca atc ctg ctg gaa acc aac ggc ctg cac atc gag ctg cag atc gat   883
Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile Glu Leu Gln Ile Asp
                250                 255                 260

cct gtc cac cca atc ggc aag gca gac aag act ggt ctc aaa gac atc   931
Pro Val His Pro Ile Gly Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile
            265                 270                 275

gtt ttg gaa tct gcg atc acc acg atc atg gac ttc gaa gac tcc gtt   979
Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp Phe Glu Asp Ser Val
        280                 285                 290

gca gct gtt gat gct gaa gac aag acc tta ggt tac tct aac tgg ttc   1027
```

```
Ala Ala Val Asp Ala Glu Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe
    295                 300                 305

gga ctc aac acc ggc gaa ctg aaa gaa gag atg tcc aag aac gga cgc   1075
Gly Leu Asn Thr Gly Glu Leu Lys Glu Glu Met Ser Lys Asn Gly Arg
310                 315                 320                 325

atc ttc acc cgt gag ctc aac aag gac cgc gtc tac att ggc cgc aat   1123
Ile Phe Thr Arg Glu Leu Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn
                330                 335                 340

ggt acc gag ctg gtt ctg cac ggt cgt tcc ctg ctg ttc gtc cgc aac   1171
Gly Thr Glu Leu Val Leu His Gly Arg Ser Leu Leu Phe Val Arg Asn
            345                 350                 355

gtt ggt cac ctc atg caa aac cca tcc atc ttg att gat ggc gag gag   1219
Val Gly His Leu Met Gln Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu
        360                 365                 370

atc ttc gaa ggc atc atg gat gct gtc ttg acc act gtt tgt gcc atc   1267
Ile Phe Glu Gly Ile Met Asp Ala Val Leu Thr Thr Val Cys Ala Ile
    375                 380                 385

cca gga att gct ccg cag aac aag atg cgc aat tcc cgc aag ggc tcc   1315
Pro Gly Ile Ala Pro Gln Asn Lys Met Arg Asn Ser Arg Lys Gly Ser
390                 395                 400                 405

atc tac atc gtg aag cct aag cag cac ggc cct gaa gaa gtc gcg ttc   1363
Ile Tyr Ile Val Lys Pro Lys Gln His Gly Pro Glu Glu Val Ala Phe
                410                 415                 420

acc aac gag ctc ttc ggc cgc gtt gag gat ctg ctt gat ctg cca cgc   1411
Thr Asn Glu Leu Phe Gly Arg Val Glu Asp Leu Leu Asp Leu Pro Arg
            425                 430                 435

cac acc ttg aag gtt ggt gtt atg gat gag gag cgt cgc acg tcc gtg   1459
His Thr Leu Lys Val Gly Val Met Asp Glu Glu Arg Arg Thr Ser Val
        440                 445                 450

aac ctg gat gcc agc atc atg gaa gtt gct gac cgc ttg gca ttc atc   1507
Asn Leu Asp Ala Ser Ile Met Glu Val Ala Asp Arg Leu Ala Phe Ile
    455                 460                 465

aac act ggc ttc ctg gac cgc acc ggc gat gaa atc cac acc tcc atg   1555
Asn Thr Gly Phe Leu Asp Arg Thr Gly Asp Glu Ile His Thr Ser Met
470                 475                 480                 485

gaa gca ggc gcc atg gtg cgc aag gct gat atg cag acc gca ccg tgg   1603
Glu Ala Gly Ala Met Val Arg Lys Ala Asp Met Gln Thr Ala Pro Trp
                490                 495                 500

aag cag gcc tac gag aac aac aac gtt gat gca ggt att cag cgt ggt   1651
Lys Gln Ala Tyr Glu Asn Asn Asn Val Asp Ala Gly Ile Gln Arg Gly
            505                 510                 515

ctt cct ggc aag gct cag atc ggt aag ggc atg tgg gcg atg act gaa   1699
Leu Pro Gly Lys Ala Gln Ile Gly Lys Gly Met Trp Ala Met Thr Glu
        520                 525                 530

ctc atg gca gaa atg ctg gag aag aag atc ggc cag cca cgc gaa ggc   1747
Leu Met Ala Glu Met Leu Glu Lys Lys Ile Gly Gln Pro Arg Glu Gly
```

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    535                 540                 545

gcc aac act gca tgg gtt cct tca cca act ggt gcg acg ctg cac gca   1795
Ala Asn Thr Ala Trp Val Pro Ser Pro Thr Gly Ala Thr Leu His Ala
550                 555                 560                 565

acg cac tac cac ttg gtt gat gtg ttc aag gtt caa gac gaa ctg cgt   1843
Thr His Tyr His Leu Val Asp Val Phe Lys Val Gln Asp Glu Leu Arg
                570                 575                 580

gct gcc ggc cgc cgc gac agc ctg cgc aac att ctc acc att tca acc   1891
Ala Ala Gly Arg Arg Asp Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr
            585                 590                 595

gca cca aac acc aat tgg tct gag gaa gag aag aag gaa gag atg gac   1939
Ala Pro Asn Thr Asn Trp Ser Glu Glu Glu Lys Lys Glu Glu Met Asp
        600                 605                 610

aac aac tgc cag tcc atc ctc gga tac gtt gtg cgc tgg gtt gag cac   1987
Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val Arg Trp Val Glu His
    615                 620                 625

ggt gtt ggt tgc tcc aag gtt cca gac atc cat gac atc gac ctc atg   2035
Gly Val Gly Cys Ser Lys Val Pro Asp Ile His Asp Ile Asp Leu Met
630                 635                 640                 645

gaa gac cgc gca acg ctg cgt att tcc tcg cag atg ctg gcc aac tgg   2083
Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln Met Leu Ala Asn Trp
                650                 655                 660

atc cgc cat gat gtt gtc tcg aag gag cag gtc ttg gag tca ctg gaa   2131
Ile Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu
            665                 670                 675

cga atg gca gtg gtc gtc gac aag caa aat gcg ggc gac gag gcc tac   2179
Arg Met Ala Val Val Val Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr
        680                 685                 690

cgc gat atg gcg ccg aag tac gac gcc tcc ctc gcc ttc cag gcg gct   2227
Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala
    695                 700                 705

aag gac ttg att ttc gaa ggc acc aag tcc cca tcg ggc tac acc gag   2275
Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu
710                 715                 720                 725

ccc atc ttg cac gca cgc cgc cgc gag ttc aaa gca aaa aac           2317
Pro Ile Leu His Ala Arg Arg Arg Glu Phe Lys Ala Lys Asn
                730                 735

taagcacgct tttcgacgct tac                                        2340
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<210> 594
<211> 739
<212> PRT
<213> Corynebacterium glutamicum

<400> 594

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Met Thr Glu Gln Glu Leu Leu Ser Ala Gln Thr Ala Asp Asn Ala Gly
  1               5                  10                  15
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Thr Asp Ser Thr Glu Arg Val Asp Ala Gly Gly Met Gln Val Ala Lys
            20                  25                  30

Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu Pro Arg Val Gly Val
        35                  40                  45

Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu
    50                  55                  60

Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met
65                  70                  75                  80

Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu
                85                  90                  95

Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro
            100                 105                 110

Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser
        115                 120                 125

Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu Asn Ala Arg Phe Ala
    130                 135                 140

Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr
145                 150                 155                 160

Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu
                165                 170                 175

Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe
            180                 185                 190

Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser His Ala Asp Val Glu
        195                 200                 205

Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser
    210                 215                 220

Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg Gly Phe Thr Gly Asn
225                 230                 235                 240

Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile
                245                 250                 255

Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly Lys Ala Asp Lys Thr
            260                 265                 270

Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp
        275                 280                 285

Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu Asp Lys Thr Leu Gly
    290                 295                 300

Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu Leu Lys Glu Glu Met
305                 310                 315                 320

Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu Asn Lys Asp Arg Val
                325                 330                 335
```

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Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu His Gly Arg Ser Leu
340 345 350

Leu Phe Val Arg Asn Val Gly His Leu Met Gln Asn Pro Ser Ile Leu
355 360 365

Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met Asp Ala Val Leu Thr
370 375 380

Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln Asn Lys Met Arg Asn
385 390 395 400

Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro Lys Gln His Gly Pro
405 410 415

Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly Arg Val Glu Asp Leu
420 425 430

Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly Val Met Asp Glu Glu
435 440 445

Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile Met Glu Val Ala Asp
450 455 460

Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp Arg Thr Gly Asp Glu
465 470 475 480

Ile His Thr Ser Met Glu Ala Gly Ala Met Val Arg Lys Ala Asp Met
485 490 495

Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn Asn Asn Val Asp Ala
500 505 510

Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln Ile Gly Lys Gly Met
515 520 525

Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu Glu Lys Lys Ile Gly
530 535 540

Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val Pro Ser Pro Thr Gly
545 550 555 560

Ala Thr Leu His Ala Thr His Tyr His Leu Val Asp Val Phe Lys Val
565 570 575

Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp Ser Leu Arg Asn Ile
580 585 590

Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp Ser Glu Glu Glu Lys
595 600 605

Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val Val
610 615 620

Arg Trp Val Glu His Gly Val Gly Cys Ser Lys Val Pro Asp Ile His
625 630 635 640

Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln
645 650 655

Met Leu Ala Asn Trp Ile Arg His Asp Val Val Ser Lys Glu Gln Val

```
            660                 665                 670

Leu Glu Ser Leu Glu Arg Met Ala Val Val Val Asp Lys Gln Asn Ala
        675                 680                 685

Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu
    690                 695                 700

Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro
705                 710                 715                 720

Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg Arg Arg Glu Phe Lys
                725                 730                 735

Ala Lys Asn
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<210> 595
<211> 2159
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(2136)
<223> FRXA02404

<400> 595

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atg cag gtt gca aaa gtt ctc tac gac ttt gta acc gaa gcg gta ctc   48
Met Gln Val Ala Lys Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu
  1               5                  10                  15

cct cgc gtg ggt gtg gat gcg gaa aag ttc tgg tcc gga ttc gcc gcc   96
Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala
             20                  25                  30

atc gcc cgg gac ctc acc cca cgc aac cgc gag ctg ctt gct cgc cgc   144
Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg
         35                  40                  45

gat gaa ctg cag atg ctt atc gac gac tac cac cgc aac aac tcc ggc   192
Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly
     50                  55                  60

acc atc gac caa gag gcg tac gag gat ttc ctc aaa gaa atc gga tac   240
Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr
 65                  70                  75                  80

ttg gtt gag gag cca gaa gct gca gaa atc cgt acc caa aac gtc gat   288
Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp
                85                  90                  95

acg gaa atc tcc agc acc gca gga cct cag ctg gtt gtt cca att ctg   336
Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu
            100                 105                 110

aac gca cgc ttc gcg ctg aac gct gcc aat gct cgc tgg ggt tcc ctc   384
Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu
        115                 120                 125
```

```
tac gat gcg ttg tac ggc acc aac gcc atc cca gaa act gat ggc gct   432
Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala
    130                 135                 140

gaa aag ggc aag gag tac aac ccg gtc cgc ggc cag aag gtc atc gag   480
Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu
145                 150                 155                 160

tgg ggt cgt gaa ttc ctc gac agc gtt gtc cca ctg gac ggt gct tcg   528
Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser
                165                 170                 175

cat gcc gat gtt gag aag tac aac atc acc gat gga aag ctt gca gcc   576
His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala
            180                 185                 190

cac att gga gat agc gtc tac cga ctg aaa aac cgt gaa tcc tac cgt   624
His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg
        195                 200                 205

ggc ttc acc ggc aac ttc ctt gat cca gaa gca atc ctg ctg gaa acc   672
Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr
    210                 215                 220

aac ggc ctg cac atc gag ctg cag atc gat cct gtc cac cca atc ggc   720
Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly
225                 230                 235                 240

aag gca gac aag act ggt ctc aaa gac atc gtt ttg gaa tct gcg atc   768
Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile
                245                 250                 255

acc acg atc atg gac ttc gaa gac tcc gtt gca gct gtt gat gct gaa   816
Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu
            260                 265                 270

gac aag acc tta ggt tac tct aac tgg ttc gga ctc aac acc ggc gaa   864
Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu
        275                 280                 285

ctg aaa gaa gag atg tcc aag aac gga cgc atc ttc acc cgt gag ctc   912
Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu
    290                 295                 300

aac aag gac cgc gtc tac att ggc cgc aat ggt acc gag ctg gtt ctg   960
Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu
305                 310                 315                 320

cac ggt cgt tcc ctg ctg ttc gtc cgc aac gtt ggt cac ctc atg caa  1008
His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln
                325                 330                 335

aac cca tcc atc ttg att gat ggc gag gag atc ttc gaa ggc atc atg  1056
Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met
            340                 345                 350

gat gct gtc ttg acc act gtt tgt gcc atc cca gga att gct ccg cag  1104
Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln
        355                 360                 365

aac aag atg cgc aat tcc cgc aag ggc tcc atc tac atc gtg aag cct  1152
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09603460.090302

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Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro
    370                 375                 380

aag cag cac ggc cct gaa gaa gtc gcg ttc acc aac gag ctc ttc ggc  1200
Lys Gln His Gly Pro Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly
385                 390                 395                 400

cgc gtt gag gat ctg ctt gat ctg cca cgc cac acc ttg aag gtt ggt  1248
Arg Val Glu Asp Leu Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly
                405                 410                 415

gtt atg gat gag gag cgt cgc acg tcc gtg aac ctg gat gcc agc atc  1296
Val Met Asp Glu Glu Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile
            420                 425                 430

atg gaa gtt gct gac cgc ttg gca ttc atc aac act ggc ttc ctg gac  1344
Met Glu Val Ala Asp Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp
        435                 440                 445

cgc acc ggc gat gaa atc cac acc tcc atg gaa gca ggc gcc atg gtg  1392
Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu Ala Gly Ala Met Val
    450                 455                 460

cgc aag gct gat atg cag acc gca ccg tgg aag cag gcc tac gag aac  1440
Arg Lys Ala Asp Met Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn
465                 470                 475                 480

aac aac gtt gat gca ggt att cag cgt ggt ctt cct ggc aag gct cag  1488
Asn Asn Val Asp Ala Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln
                485                 490                 495

atc ggt aag ggc atg tgg gcg atg act gaa ctc atg gca gaa atg ctg  1536
Ile Gly Lys Gly Met Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu
            500                 505                 510

gag aag aag atc ggc cag cca cgc gaa ggc gcc aac act gca tgg gtt  1584
Glu Lys Lys Ile Gly Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val
        515                 520                 525

cct tca cca act ggt gcg acg ctg cac gca acg cac tac cac ttg gtt  1632
Pro Ser Pro Thr Gly Ala Thr Leu His Ala Thr His Tyr His Leu Val
    530                 535                 540

gat gtg ttc aag gtt caa gac gaa ctg cgt gct gcc ggc cgc cgc gac  1680
Asp Val Phe Lys Val Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp
545                 550                 555                 560

agc ctg cgc aac att ctc acc att tca acc gca cca aac acc aat tgg  1728
Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp
                565                 570                 575

tct gag gaa gag aag aag gaa gag atg gac aac aac tgc cag tcc atc  1776
Ser Glu Glu Glu Lys Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile
            580                 585                 590

ctc gga tac gtt gtg cgc tgg gtt gag cac ggt gtt ggt tgc tcc aag  1824
Leu Gly Tyr Val Val Arg Trp Val Glu His Gly Val Gly Cys Ser Lys
        595                 600                 605

gtt cca gac atc cat gac atc gac ctc atg gaa gac cgc gca acg ctg  1872
Val Pro Asp Ile His Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu
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    610                 615                 620

cgt att tcc tcg cag atg ctg gcc aac tgg atc cgc cat gat gtt gtc   1920
Arg Ile Ser Ser Gln Met Leu Ala Asn Trp Ile Arg His Asp Val Val
625                 630                 635                 640

tcg aag gag cag gtc ttg gag tca ctg gaa cga atg gca gtg gtc gtc   1968
Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val
                645                 650                 655

gac aag caa aat gcg ggc gac gag gcc tac cgc gat atg gcg ccg aag   2016
Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys
            660                 665                 670

tac gac gcc tcc ctc gcc ttc cag gcg gct aag gac ttg att ttc gaa   2064
Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu
        675                 680                 685

ggc acc aag tcc cca tcg ggc tac acc gag ccc atc ttg cac gca cgc   2112
Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg
    690                 695                 700

cgc cgc gag ttc aaa gca aaa aac taagcacgct tttcgacgct tac         2159
Arg Arg Glu Phe Lys Ala Lys Asn
705                 710
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US20050260729A1

<210> 596
<211> 712
<212> PRT
<213> Corynebacterium glutamicum

<400> 596

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Met Gln Val Ala Lys Val Leu Tyr Asp Phe Val Thr Glu Ala Val Leu
  1               5                  10                  15

Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala
             20                  25                  30

Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg
         35                  40                  45

Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly
     50                  55                  60

Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr
 65                  70                  75                  80

Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp
                 85                  90                  95

Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu
            100                 105                 110

Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu
        115                 120                 125

Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala
    130                 135                 140

Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu
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145                 150                 155                 160

Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser
                165                 170                 175

His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala
            180                 185                 190

His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg
        195                 200                 205

Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr
    210                 215                 220

Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly
225                 230                 235                 240

Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile
                245                 250                 255

Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu
            260                 265                 270

Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu
        275                 280                 285

Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu
    290                 295                 300

Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu
305                 310                 315                 320

His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln
                325                 330                 335

Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met
            340                 345                 350

Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln
        355                 360                 365

Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro
    370                 375                 380

Lys Gln His Gly Pro Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly
385                 390                 395                 400

Arg Val Glu Asp Leu Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly
                405                 410                 415

Val Met Asp Glu Glu Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile
            420                 425                 430

Met Glu Val Ala Asp Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp
        435                 440                 445

Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu Ala Gly Ala Met Val
    450                 455                 460

Arg Lys Ala Asp Met Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn
465                 470                 475                 480
```

Asn Asn Val Asp Ala Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln
485 490 495

Ile Gly Lys Gly Met Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu
500 505 510

Glu Lys Lys Ile Gly Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val
515 520 525

Pro Ser Pro Thr Gly Ala Thr Leu His Ala Thr His Tyr His Leu Val
530 535 540

Asp Val Phe Lys Val Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp
545 550 555 560

Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp
565 570 575

Ser Glu Glu Glu Lys Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile
580 585 590

Leu Gly Tyr Val Val Arg Trp Val Glu His Gly Val Gly Cys Ser Lys
595 600 605

Val Pro Asp Ile His Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu
610 615 620

Arg Ile Ser Ser Gln Met Leu Ala Asn Trp Ile Arg His Asp Val Val
625 630 635 640

Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val
645 650 655

Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys
660 665 670

Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu
675 680 685

Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg
690 695 700

Arg Arg Glu Phe Lys Ala Lys Asn
705 710

<210> 597
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(850)
<223> RXA01089

<400> 597
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attagactca aggcacatca cattgaagga gcttcttatc ttg tct cga ttt gct 115

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                                                    Leu Ser Arg Phe Ala
                                                      1               5

gcc aac ctg tca ttg act ttt act gag cta gat ttc ctg gat cgt ttt   163
Ala Asn Leu Ser Leu Thr Phe Thr Glu Leu Asp Phe Leu Asp Arg Phe
                 10                  15                  20

gat gcc gct tcg aag cat gct ttc agt gcc gtg gag ttt cag tac cct   211
Asp Ala Ala Ser Lys His Ala Phe Ser Ala Val Glu Phe Gln Tyr Pro
             25                  30                  35

tac gat ttc gat gtt caa gag att aaa cag cgt gct gat tcc gca ggt   259
Tyr Asp Phe Asp Val Gln Glu Ile Lys Gln Arg Ala Asp Ser Ala Gly
         40                  45                  50

ctg ccc att gaa ctg ttc aat gcc cca cct ggg gat act ttt ggt ctt   307
Leu Pro Ile Glu Leu Phe Asn Ala Pro Pro Gly Asp Thr Phe Gly Leu
     55                  60                  65

gcg gca ctg gct tcc cct gaa gac ttt caa caa tcc atc gag cag gcc   355
Ala Ala Leu Ala Ser Pro Glu Asp Phe Gln Gln Ser Ile Glu Gln Ala
 70                  75                  80                  85

atc acg tac gcc aca gtg ttg aag cca aag aag atg cat gtc atg gct   403
Ile Thr Tyr Ala Thr Val Leu Lys Pro Lys Lys Met His Val Met Ala
                 90                  95                 100

ggc atc gcg gac gta acc tca gaa acc acg gcg cgc tat gtg gag aat   451
Gly Ile Ala Asp Val Thr Ser Glu Thr Thr Ala Arg Tyr Val Glu Asn
             105                 110                 115

att cgc tgg gct gcg cag caa cta gac aag ctc gac gtt gtc gtt gtt   499
Ile Arg Trp Ala Ala Gln Gln Leu Asp Lys Leu Asp Val Val Val Val
         120                 125                 130

att gaa cca att aat cac tat tcg gtt ccc ggt tat ttc ctg cac act   547
Ile Glu Pro Ile Asn His Tyr Ser Val Pro Gly Tyr Phe Leu His Thr
     135                 140                 145

tta gag cag gcg tat tgg ctt atc gac agc att gcc cac ccc aat gtg   595
Leu Glu Gln Ala Tyr Trp Leu Ile Asp Ser Ile Ala His Pro Asn Val
 150                 155                 160                 165

aag atc tta ttc gat act ttc cac ctt cag cag att cat ggc aat ctc   643
Lys Ile Leu Phe Asp Thr Phe His Leu Gln Gln Ile His Gly Asn Leu
                 170                 175                 180

acc cgc cgc ctg cgc gag gtt cat ggc gca ggt ctt ttg gga cac gtg   691
Thr Arg Arg Leu Arg Glu Val His Gly Ala Gly Leu Leu Gly His Val
             185                 190                 195

caa gtg gcc tca gtt cct gat cga cac gaa cct ggc act ggc gaa gtc   739
Gln Val Ala Ser Val Pro Asp Arg His Glu Pro Gly Thr Gly Glu Val
         200                 205                 210

aat gcg gcg tat atc ttc caa ctc cta agc gaa ctg gga tat gac ggt   787
Asn Ala Ala Tyr Ile Phe Gln Leu Leu Ser Glu Leu Gly Tyr Asp Gly
     215                 220                 225

gtc atc gct ggc gaa tac cac cct gct ggt gaa act aca gcc ggt ttg   835
Val Ile Ala Gly Glu Tyr His Pro Ala Gly Glu Thr Thr Ala Gly Leu
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DOCSNET

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230                 235                 240                 245

ggc tgg ttg gag ctc tagatcgtaa gtggtgtcgt acc                    873
Gly Trp Leu Glu Leu
               250


<210> 598
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 598
Leu Ser Arg Phe Ala Ala Asn Leu Ser Leu Thr Phe Thr Glu Leu Asp
  1               5                  10                  15

Phe Leu Asp Arg Phe Asp Ala Ala Ser Lys His Ala Phe Ser Ala Val
             20                  25                  30

Glu Phe Gln Tyr Pro Tyr Asp Phe Asp Val Gln Glu Ile Lys Gln Arg
         35                  40                  45

Ala Asp Ser Ala Gly Leu Pro Ile Glu Leu Phe Asn Ala Pro Pro Gly
     50                  55                  60

Asp Thr Phe Gly Leu Ala Ala Leu Ala Ser Pro Glu Asp Phe Gln Gln
 65                  70                  75                  80

Ser Ile Glu Gln Ala Ile Thr Tyr Ala Thr Val Leu Lys Pro Lys Lys
                 85                  90                  95

Met His Val Met Ala Gly Ile Ala Asp Val Thr Ser Glu Thr Thr Ala
            100                 105                 110

Arg Tyr Val Glu Asn Ile Arg Trp Ala Ala Gln Gln Leu Asp Lys Leu
        115                 120                 125

Asp Val Val Val Val Ile Glu Pro Ile Asn His Tyr Ser Val Pro Gly
    130                 135                 140

Tyr Phe Leu His Thr Leu Glu Gln Ala Tyr Trp Leu Ile Asp Ser Ile
145                 150                 155                 160

Ala His Pro Asn Val Lys Ile Leu Phe Asp Thr Phe His Leu Gln Gln
                165                 170                 175

Ile His Gly Asn Leu Thr Arg Arg Leu Arg Glu Val His Gly Ala Gly
            180                 185                 190

Leu Leu Gly His Val Gln Val Ala Ser Val Pro Asp Arg His Glu Pro
        195                 200                 205

Gly Thr Gly Glu Val Asn Ala Ala Tyr Ile Phe Gln Leu Leu Ser Glu
    210                 215                 220

Leu Gly Tyr Asp Gly Val Ile Ala Gly Glu Tyr His Pro Ala Gly Glu
225                 230                 235                 240

Thr Thr Ala Gly Leu Gly Trp Leu Glu Leu
                245                 250
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<210> 599
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXA01886

<400> 599
gcgaagctgc acgcaccgca ctactcatcg cactcggcgc catccgaagc gtagaaaccg 60

gcgcaaccat caaccttgct gaaagcatcg aggtttaacc atg act ttt aaa ctc 115
Met Thr Phe Lys Leu
1 5

gca gca tgc gca gag atg atc tac cag gac ctg cct ttc gag gag agg 163
Ala Ala Cys Ala Glu Met Ile Tyr Gln Asp Leu Pro Phe Glu Glu Arg
10 15 20

gtc aag acg atc tct gat cag gga ttc ctc gtg gaa att tgg gac tgg 211
Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val Glu Ile Trp Asp Trp
25 30 35

tcc aca aaa gac atc gat gcg ctc gtg gca aca ggc gcg gaa ttt tcc 259
Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr Gly Ala Glu Phe Ser
40 45 50

tcc atg acg ggc tac ctg cgc ggg gat ctg att act gaa cag ggc cgc 307
Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile Thr Glu Gln Gly Arg
55 60 65

gcg gag ctc ttg gca acc gct tcg gag tcc ttg gcg gtg gcg gaa aag 355
Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu Ala Val Ala Glu Lys
70 75 80 85

ctc aac tgc ccc cgg ctg aat ctg cat gga act ggc ctt gga ccg cag 403
Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr Gly Leu Gly Pro Gln
90 95 100

gga cta cct gtt act ccc att gaa gtg gtt acc cca gaa atg tgg ctc 451
Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr Pro Glu Met Trp Leu
105 110 115

tac gct gct gaa acg ctc cgc cag atc gct gag ctg ggg gag cgc gca 499
Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu Leu Gly Glu Arg Ala
120 125 130

ggc aag gtt ttc gtg ctg gaa aac ctc aac ctc gca gtc gat cac ccc 547
Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu Ala Val Asp His Pro
135 140 145

ggc act cct ttt gcc aag gcc act gac act ttg gcg ctg gtc aag gct 595
Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu Ala Leu Val Lys Ala
150 155 160 165

gtc aat cac ccg aat ctg cgc ctc aac ctg gat ttg tac cac gcc cag 643
Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp Leu Tyr His Ala Gln
170 175 180

```
att ggc gaa gga aac ctc att gag ctg ctc cgt gag gcg cag cca ttc   691
Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg Glu Ala Gln Pro Phe
            185                 190                 195

atc ggc gaa atc cag gtt gcc gat gtc ccc ggc cgc atg gaa ccc ggc   739
Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly Arg Met Glu Pro Gly
        200                 205                 210

acc ggc gag atc aac tac cag ggc gtc gcg aaa gct ctc gcc gcg atg   787
Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys Ala Leu Ala Ala Met
    215                 220                 225

ggc tac gac ggc gtc atc ggc atg gag gcg tgg gca tcg ggc gac tcc   835
Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp Ala Ser Gly Asp Ser
230                 235                 240                 245

agc gac gcg ctg cag gcg ttg aag tca gcg ttc acg gtc taaattgctt    884
Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe Thr Val
                250                 255

atcgacgcac ccc                                                   897
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Sequence Listing

<210> 600
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 600

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Met Thr Phe Lys Leu Ala Ala Cys Ala Glu Met Ile Tyr Gln Asp Leu
  1               5                  10                  15

Pro Phe Glu Glu Arg Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val
            20                  25                  30

Glu Ile Trp Asp Trp Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr
        35                  40                  45

Gly Ala Glu Phe Ser Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile
    50                  55                  60

Thr Glu Gln Gly Arg Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu
65                  70                  75                  80

Ala Val Ala Glu Lys Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr
                85                  90                  95

Gly Leu Gly Pro Gln Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr
            100                 105                 110

Pro Glu Met Trp Leu Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu
        115                 120                 125

Leu Gly Glu Arg Ala Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu
    130                 135                 140

Ala Val Asp His Pro Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu
145                 150                 155                 160

Ala Leu Val Lys Ala Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp
```

```
                165                 170                 175

Leu Tyr His Ala Gln Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg
            180                 185                 190

Glu Ala Gln Pro Phe Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly
        195                 200                 205

Arg Met Glu Pro Gly Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys
    210                 215                 220

Ala Leu Ala Ala Met Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp
225                 230                 235                 240

Ala Ser Gly Asp Ser Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe
                245                 250                 255

Thr Val
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<210> 601
<211> 1575
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (41)..(1552)
<223> RXN03117

<400> 601

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tgtgcaacat tagttcgtta agaagagtca cattccagcc atg att acc cac gaa   55
                                            Met Ile Thr His Glu
                                              1               5

gtg cgc acc cac cgt tct gcg gaa gag ttc ccg tac aag aag cac ctg   103
Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro Tyr Lys Lys His Leu
                  10                  15                  20

gct cac aag atg gct cgc gtt gca gcc gac cca gtt gag gtt gct gcg   151
Ala His Lys Met Ala Arg Val Ala Ala Asp Pro Val Glu Val Ala Ala
              25                  30                  35

gac act cag gaa atg atc atc acc cgc atc atc gac aat gca tcg gtg   199
Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile Asp Asn Ala Ser Val
          40                  45                  50

cag gca gct tcc gtg ttg cgt cga cca gtt agc tct gcc cgt gcg atg   247
Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser Ser Ala Arg Ala Met
      55                  60                  65

gca cag gtc agg cca gtt acc gat ggt cgg ggt gca tct gtt ttc ggt   295
Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly Ala Ser Val Phe Gly
  70                  75                  80                  85

ctg cca gga cgt tat gcc gcg gaa tgg gct gcg ctt gct aac ggc act   343
Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala Leu Ala Asn Gly Thr
                  90                  95                 100

gcg gtg cgt gag ctt gat ttc cat gac acg ttc ctc gct gcg gaa tac   391
```

```
Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr
            105                 110                 115

tcc cac cca gga gat aac att cct ccg att ttg gct gca gca cag cag   439
Ser His Pro Gly Asp Asn Ile Pro Pro Ile Leu Ala Ala Ala Gln Gln
        120                 125                 130

gct gga aaa ggt ggc aag gat ctg atc cgt ggc atc gct act ggg tat   487
Ala Gly Lys Gly Gly Lys Asp Leu Ile Arg Gly Ile Ala Thr Gly Tyr
    135                 140                 145

gag att cag gtt aac ttg gtg cgt gga atg tgc ctg cat gag cac aag   535
Glu Ile Gln Val Asn Leu Val Arg Gly Met Cys Leu His Glu His Lys
150                 155                 160                 165

att gat cac gtt gct cat ctt gga cca tca gcg gct gct ggt atc gga   583
Ile Asp His Val Ala His Leu Gly Pro Ser Ala Ala Ala Gly Ile Gly
                170                 175                 180

acc ttg cta gac cta gat gtg gac acc atc tac cag gca att ggt cag   631
Thr Leu Leu Asp Leu Asp Val Asp Thr Ile Tyr Gln Ala Ile Gly Gln
            185                 190                 195

gca ttg cac acc acc acg gcg acg agg cag tcc cgt aaa ggt gcg att   679
Ala Leu His Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Ala Ile
        200                 205                 210

tct tca tgg aag gca ttt gct cct gcg ttt gcg ggc aag atg tcc atc   727
Ser Ser Trp Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ser Ile
    215                 220                 225

gag gca gta gat cgc gca atg cgt ggc gag ggc gca ccg tca cca atc   775
Glu Ala Val Asp Arg Ala Met Arg Gly Glu Gly Ala Pro Ser Pro Ile
230                 235                 240                 245

tgg gaa ggc gaa gac ggc gta atc gcg tgg ctg ctg tcc ggt ctt gat   823
Trp Glu Gly Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Leu Asp
                250                 255                 260

cac atc tac acc att cct ttg cct gca gaa ggt gaa gcc aaa cga gca   871
His Ile Tyr Thr Ile Pro Leu Pro Ala Glu Gly Glu Ala Lys Arg Ala
            265                 270                 275

atc ttg gat acc tac acc aag gaa cac tcg gcg gaa tac cag tca cag   919
Ile Leu Asp Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln
        280                 285                 290

gca ccg atc gac ttg gcg cgc agc atg ggg gag aag ctg gca gca cag   967
Ala Pro Ile Asp Leu Ala Arg Ser Met Gly Glu Lys Leu Ala Ala Gln
    295                 300                 305

ggc ttg gac ctg cgt gat gtg gac tcc atc gtt ttg cac acc tcc cac   1015
Gly Leu Asp Leu Arg Asp Val Asp Ser Ile Val Leu His Thr Ser His
310                 315                 320                 325

cac act cac tac gtg atc ggc acc gga tct aat gat cca cag aag ttc   1063
His Thr His Tyr Val Ile Gly Thr Gly Ser Asn Asp Pro Gln Lys Phe
                330                 335                 340

gat cca gat gca tcg cga gaa acc ctt gat cac tcc atc atg tac att   1111
Asp Pro Asp Ala Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile
```

```
            345                 350                 355

ttc gct gtc gcg ctg aag gat cgc gcg tgg cac cac gag cgt tcc tat   1159
Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His His Glu Arg Ser Tyr
        360                 365                 370

gct cct gag cga gcc cac cgc cga gag acc atc gag ctg tgg aac aag   1207
Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile Glu Leu Trp Asn Lys
    375                 380                 385

att tcc acg gtg gag gat cct gaa tgg acc agg cgt tac cac tcc gtt   1255
Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Val
390                 395                 400                 405

gat cct gca gaa aag gcc ttc ggc gca cgc gca gtg atc acc ttc aag   1303
Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala Val Ile Thr Phe Lys
                410                 415                 420

gat gga acc gtc gtg gaa gat gaa ctg gct gtg gcg aat gcg cat cct   1351
Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val Ala Asn Ala His Pro
            425                 430                 435

ctg gga gca cgg cct ttc gct agg gag cag tac att cag aaa ttc cgc   1399
Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr Ile Gln Lys Phe Arg
        440                 445                 450

acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa cag gat cgc ttc ttg   1447
Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu Gln Asp Arg Phe Leu
    455                 460                 465

gat gcg gca cag cgt acg cac gag ctt gag gat ctt tca gaa ctc aac   1495
Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp Leu Ser Glu Leu Asn
470                 475                 480                 485

att gaa ttg gat gcc gat att ttg gcc aag gct cct gtg att ccg gaa   1543
Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala Pro Val Ile Pro Glu
                490                 495                 500

gga ctg ttc tgatggcggg tttgttttcc tct                            1575
Gly Leu Phe
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<210> 602
<211> 504
<212> PRT
<213> Corynebacterium glutamicum

<400> 602

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Met Ile Thr His Glu Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro
  1               5                  10                  15

Tyr Lys Lys His Leu Ala His Lys Met Ala Arg Val Ala Ala Asp Pro
             20                  25                  30

Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile
         35                  40                  45

Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser
     50                  55                  60
```

```
Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly
 65                  70                  75                  80

Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala
                 85                  90                  95

Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe
            100                 105                 110

Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro Ile Leu
        115                 120                 125

Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile Arg Gly
    130                 135                 140

Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly Met Cys
145                 150                 155                 160

Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro Ser Ala
                165                 170                 175

Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr Ile Tyr
            180                 185                 190

Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg Gln Ser
        195                 200                 205

Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala Phe Ala
    210                 215                 220

Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly Glu Gly
225                 230                 235                 240

Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala Trp Leu
                245                 250                 255

Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala Glu Gly
            260                 265                 270

Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His Ser Ala
        275                 280                 285

Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met Gly Glu
    290                 295                 300

Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser Ile Val
305                 310                 315                 320

Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly Ser Asn
                325                 330                 335

Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu Asp His
            340                 345                 350

Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His
        355                 360                 365

His Glu Arg Ser Tyr Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile
    370                 375                 380

Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg
```

Replacement Sheet

```
385                 390                 395                 400

Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
                405                 410                 415

Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
            420                 425                 430

Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
        435                 440                 445

Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
    450                 455                 460

Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
465                 470                 475                 480

Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
                485                 490                 495

Pro Val Ile Pro Glu Gly Leu Phe
            500
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09529_seq_list

<210> 603
<211> 975
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(975)
<223> FRXA00406

<400> 603

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gac cca gtt gag gtt gct gcg gac act cag gaa atg atc atc acc cgc   48
Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg
  1               5                  10                  15

atc atc gac aat gca tcg gtg cag gca gct tcc gtg ttg cgt cga cca   96
Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro
             20                  25                  30

gtt agc tct gcc cgt gcg atg gca cag gtc agg cca gtt acc gat ggt  144
Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly
         35                  40                  45

cgg ggt gca tct gtt ttc ggt ctg cca gga cgt tat gcc gcg gaa tgg  192
Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp
     50                  55                  60

gct gcg ctt gct aac ggc act gcg gtg cgt gag ctt gat ttc cat gac  240
Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp
 65                  70                  75                  80

acg ttc ctc gct gcg gaa tac tcc cac cca gga gat aac att cct ccg  288
Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro
                 85                  90                  95

att ttg gct gca gca cag cag gct gga aaa ggt ggc aag gat ctg atc  336
Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile
```

```
            100                 105                 110

cgt ggc atc gct act ggg tat gag att cag gtt aac ttg gtg cgt gga   384
Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly
        115                 120                 125

atg tgc ctg cat gag cac aag att gat cac gtt gct cat ctt gga cca   432
Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro
    130                 135                 140

tca gcg gct gct ggt atc gga acc ttg cta gac cta gat gtg gac acc   480
Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr
145                 150                 155                 160

atc tac cag gca att ggt cag gca ttg cac acc acc acg gcg acg agg   528
Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg
                165                 170                 175

cag tcc cgt aaa ggt gcg att tct tca tgg aag gca ttt gct cct gcg   576
Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala
            180                 185                 190

ttt gcg ggc aag atg tcc atc gag gca gta gat cgc gca atg cgt ggc   624
Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly
        195                 200                 205

gag ggc gca ccg tca cca atc tgg gaa ggc gaa gac ggc gta atc gcg   672
Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala
    210                 215                 220

tgg ctg ctg tcc ggt ctt gat cac atc tac acc att cct ttg cct gca   720
Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala
225                 230                 235                 240

gaa ggt gaa gcc aaa cga gca atc ttg gat acc tac acc aag gaa cac   768
Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His
                245                 250                 255

tcg gcg gaa tac cag tca cag gca ccg atc gac ttg gcg cgc agc atg   816
Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met
            260                 265                 270

ggg gag aag ctg gca gca cag ggc ttg gac ctg cgt gat gtg gac tcc   864
Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser
        275                 280                 285

atc gtt ttg cac acc tcc cac cac act cac tac gtg atc ggc acc gga   912
Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly
    290                 295                 300

tct aat gat cca cag aag ttc gat cca gat gca tcg cga gaa acc ctt   960
Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu
305                 310                 315                 320

gat cac tcc atc atg                                              975
Asp His Ser Ile Met
                325
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<210> 604
<211> 325

<212> PRT
<213> Corynebacterium glutamicum

<400> 604

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Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg
  1               5                  10                  15

Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro
             20                  25                  30

Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly
         35                  40                  45

Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp
     50                  55                  60

Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp
 65                  70                  75                  80

Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro
                 85                  90                  95

Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile
            100                 105                 110

Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly
        115                 120                 125

Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro
    130                 135                 140

Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr
145                 150                 155                 160

Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg
                165                 170                 175

Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala
            180                 185                 190

Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly
        195                 200                 205

Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala
    210                 215                 220

Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala
225                 230                 235                 240

Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His
                245                 250                 255

Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met
            260                 265                 270

Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser
        275                 280                 285

Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly
    290                 295                 300
```

```
Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu
305                 310                 315                 320

Asp His Ser Ile Met
                325


<210> 605
<211> 431
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(408)
<223> FRXA00514

<400> 605
cac gag cgt tcc tat gct cct gag cga gcc ctc cgc cga gag acc atc   48
His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile
  1               5                  10                  15

gag ctg tgg aac aag att tcc acg gtg gag gat cct gaa tgg acc agg   96
Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg
             20                  25                  30

cgt tac cac tcc gtt gat cct gca gaa aag gcc ttc ggc gca cgc gca   144
Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
         35                  40                  45

gtg atc acc ttc aag gat gga acc gtc gtg gaa gat gaa ctg gct gtg   192
Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
     50                  55                  60

gcg aat gcg cat cct ctg gga gca cgg cct ttc gct agg gag cag tac   240
Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
 65                  70                  75                  80

att cag aaa ttc cgc acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa   288
Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
                 85                  90                  95

cag gat cgc ttc ttg gat gcg gca cag cgt acg cac gag ctt gag gat   336
Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
            100                 105                 110

ctt tca gaa ctc aac att gaa ttg gat gcc gat att ttg gcc aag gct   384
Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
        115                 120                 125

cct gtg att ccg gaa gga ctg ttc tgatggcggg tttgttttcc tct         431
Pro Val Ile Pro Glu Gly Leu Phe
    130                 135


<210> 606
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 606
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His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile
 1               5                  10                  15

Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg
            20                  25                  30

Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
        35                  40                  45

Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
    50                  55                  60

Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
65                  70                  75                  80

Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
                85                  90                  95

Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
            100                 105                 110

Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
        115                 120                 125

Pro Val Ile Pro Glu Gly Leu Phe
    130                 135
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09602760 - 060308

<210> 607
<211> 718
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(718)
<223> RXA00512

<400> 607
tacaacgagt acaacgcttt cgaccagcaa gtattcacct attccgctga cagctacaag 60

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cccatcttct aacccgccta tatataagga gtgaatcacc atg tcc agc gcc aca   115
                                            Met Ser Ser Ala Thr
                                              1               5

acc act gat gtt cgc aaa ggg ctc tac gga gtc atc gcc gat tac acg   163
Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val Ile Ala Asp Tyr Thr
                  10                  15                  20

gcc gtt tcc aaa gtc atg cca gag acc aat tca ctg acc tac cgt ggc   211
Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser Leu Thr Tyr Arg Gly
              25                  30                  35

tac gcg gtg gaa gat ttg gtg gaa aac tgc agc ttc gag gag gtg ttt   259
Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Phe
          40                  45                  50

tac ctc ctg tgg cac ggc gag ctg ccc act gcg caa caa ctt gcg gag   307
Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala Gln Gln Leu Ala Glu
      55                  60                  65
```

```
ttc aat gag cgt ggc cgt tcc tac cgc tcc ctg gat gcc ggt ttg atc   355
Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile
 70                  75                  80                  85

tcc ctg atc cac tct ttg ccc aaa gaa gcc cac ccg atg gat gtt atg   403
Ser Leu Ile His Ser Leu Pro Lys Glu Ala His Pro Met Asp Val Met
                90                  95                 100

cgc acc gcg gtg tcc tac atg ggc acc aag gat tcc gag tat ttc acc   451
Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp Ser Glu Tyr Phe Thr
            105                 110                 115

acc gat tct gag cac atc cgc aaa gtt ggc cac acc ttg ttg gcg cag   499
Thr Asp Ser Glu His Ile Arg Lys Val Gly His Thr Leu Leu Ala Gln
        120                 125                 130

ctt ccg atg gtg cta gcc atg gat att cgt cgc cgc aag ggc ctc gat   547
Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg Arg Lys Gly Leu Asp
    135                 140                 145

atc atc gcc cct gac tcc agc aag tca gtc gcc gaa aac ctg ctg tct   595
Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala Glu Asn Leu Leu Ser
150                 155                 160                 165

atg gtg ttt ggt act ggc ccg gaa tca cct gca tcc aac cca gct gac   643
Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala Ser Asn Pro Ala Asp
                170                 175                 180

gtc cgc gat ttt gag aaa tca ctg atc ctc tac gcc gag cac tcc ttc   691
Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr Ala Glu His Ser Phe
            185                 190                 195

aac gcc tcc acc ttc acc gcc cgc gtg                              718
Asn Ala Ser Thr Phe Thr Ala Arg Val
        200                 205
```

<210> 608
<211> 206
<212> PRT
<213> Corynebacterium glutamicum

<400> 608

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Met Ser Ser Ala Thr Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val
  1               5                  10                  15

Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
            20                  25                  30

Leu Thr Tyr Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser
        35                  40                  45

Phe Glu Glu Val Phe Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala
    50                  55                  60

Gln Gln Leu Ala Glu Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu
65                  70                  75                  80

Asp Ala Gly Leu Ile Ser Leu Ile His Ser Leu Pro Lys Glu Ala His
                85                  90                  95
```

```
Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
            100                 105                 110

Ser Glu Tyr Phe Thr Thr Asp Ser Glu His Ile Arg Lys Val Gly His
        115                 120                 125

Thr Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg
    130                 135                 140

Arg Lys Gly Leu Asp Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala
145                 150                 155                 160

Glu Asn Leu Leu Ser Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala
                165                 170                 175

Ser Asn Pro Ala Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr
            180                 185                 190

Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ala Arg Val
        195                 200                 205
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<210> 609
<211> 320
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(297)
<223> RXA00518

<400> 609

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gtc ctt ccg gta tta gct gcc cgc cac gac ggc gaa aag tgg gtt gcc   48
Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala
  1               5                  10                  15

atg tat gaa aac atg cgc gac gcc atg gac gcc cgc acc ggc atc aag   96
Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys
             20                  25                  30

ccg aat ctc gat ttc cct gct ggc cct gcc tac cac ctg ctc ggt ttc   144
Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe
         35                  40                  45

ccg gtc gat ttc ttc acc ccg ctg ttc gtc atc gcc cgc gtc gcc ggc   192
Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly
     50                  55                  60

tgg acg gcc cac atc gtg gag cag tac gaa aac aac tcg ctc atc cgc   240
Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg
 65                  70                  75                  80

cca ctg tcc gag tac aac ggc gag gag cag cgc gag gtc gcg ccc att   288
Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile
                 85                  90                  95

gaa aag cgc taaaagattt tcgcttttcg acg                            320
Glu Lys Arg
```

<210> 610
<211> 99
<212> PRT
<213> Corynebacterium glutamicum

<400> 610
Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala
1 5 10 15

Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys
20 25 30

Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe
35 40 45

Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly
50 55 60

Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg
65 70 75 80

Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile
85 90 95

Glu Lys Arg

<210> 611
<211> 1494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1471)
<223> RXA01077

<400> 611
tctatgactt gatccacaat gtgatgcaaa tcattgaccc tcaccccgga ccaagcgctt 60

aatgaaggca agccaaactt aactagtaga taggattgca atg acc gaa tcg caa 115
Met Thr Glu Ser Gln
1 5

gat ctc gcc gca ttc gtg gaa gct gcc aaa ctc aat gat gca agc ccc 163
Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu Asn Asp Ala Ser Pro
10 15 20

gaa gcc gta gag caa ttg aaa atc aga gtg cta gac acc gta ggc gtt 211
Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu Asp Thr Val Gly Val
25 30 35

gcc att ggc gca ctg gat gcc gaa ccg att gtc gcc att cga gga ctc 259
Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val Ala Ile Arg Gly Leu
40 45 50

ctg gaa gac ctc ggg gga acc gaa cag tca aca ctt att ggt ggt ggc 307
Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr Leu Ile Gly Gly Gly
55 60 65

```
aaa acc agt ccg gaa cgt gca gca ttt ttc aac agc gca tta agc cgc   355
Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn Ser Ala Leu Ser Arg
 70                  75                  80                  85

tac ctc gac ttc atg gac gcc tac cta gca aag ggc gaa acc aac cac   403
Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys Gly Glu Thr Asn His
                 90                  95                 100

ccc tcg gat aac ttc gga gca gtg ctc gct gca gcc gaa agc gtt ggc   451
Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala Ala Glu Ser Val Gly
            105                 110                 115

gcc tct gga aaa gac ctg ctc acc gca ttc gcc gtg gcc tac cag gta   499
Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala Val Ala Tyr Gln Val
        120                 125                 130

cac acc aga ctt tca gat gtc gca cca gtt cgc gcc aaa ggt ttc gat   547
His Thr Arg Leu Ser Asp Val Ala Pro Val Arg Ala Lys Gly Phe Asp
    135                 140                 145

cac acc acc caa gga gca ttc gca gcg ggc gca tct gct gcc aag gca   595
His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala Ser Ala Ala Lys Ala
150                 155                 160                 165

ctg ggt ttg cca gct gat caa atc gcc aac gca ctg gcc atc gca gga   643
Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala Leu Ala Ile Ala Gly
                170                 175                 180

aca gcc aat gtt gca ctt cgt gtc act cgc act gga aac ttg agc cac   691
Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr Gly Asn Leu Ser His
            185                 190                 195

tgg aaa ggc ctt gcc tac cca cac gtg tcc aaa gaa gga acc tgg gca   739
Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys Glu Gly Thr Trp Ala
        200                 205                 210

gca ctg ctc gca agc cga ggt att acc ggt ccg gaa gaa gtc ttc gaa   787
Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro Glu Glu Val Phe Glu
    215                 220                 225

ggc aac aag gga ttc aaa gag tcc gtc tcc gga ccg ttc gag atc gat   835
Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly Pro Phe Glu Ile Asp
230                 235                 240                 245

tgg tcc aag gaa gac ttg gaa agc gtt aag cgc acc atc atc aag aaa   883
Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg Thr Ile Ile Lys Lys
                250                 255                 260

cac aac gcg gaa att cac tcg cag tca gcg ctt gat gca gcc caa gaa   931
His Asn Ala Glu Ile His Ser Gln Ser Ala Leu Asp Ala Ala Gln Glu
            265                 270                 275

ata cgc gca caa gaa ggc ttc aat gtg gac aac att gaa aag att cac   979
Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn Ile Glu Lys Ile His
        280                 285                 290

ctg act act ttc gac gtt gcc tac tcc atc att ggc ggc ggc gaa gaa  1027
Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile Gly Gly Gly Glu Glu
    295                 300                 305
```

```
ggc gac aaa cag ctt att cgc acc aaa gaa gaa gcc gat cac tca ctg   1075
Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu Ala Asp His Ser Leu
310                 315                 320                 325

ccg tgg atg ctc gct gta gtt ctg ctg gat ggt cag ctc aat ccc gaa   1123
Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly Gln Leu Asn Pro Glu
                330                 335                 340

cag tac gaa cca tca cgc atc gtt gct gat gat gta caa acc ttg atg   1171
Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp Val Gln Thr Leu Met
            345                 350                 355

aag aaa atc gaa atc aca ccg tca gat gaa ttc tct gat cgc ttc cct   1219
Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe Ser Asp Arg Phe Pro
        360                 365                 370

gac cac atg cca gct gat cta gaa gtc aca cta aac gat ggc tcg gtg   1267
Asp His Met Pro Ala Asp Leu Glu Val Thr Leu Asn Asp Gly Ser Val
    375                 380                 385

ttc aaa gct tca caa gat agc tac tta ggc ttc cac gac aat ccc cta   1315
Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe His Asp Asn Pro Leu
390                 395                 400                 405

gat tgg gac aac gcg cgc aag aaa ttc gat gcc ctt gtc aca cca ttc   1363
Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala Leu Val Thr Pro Phe
                410                 415                 420

acc ggt gaa gaa cta cgt gaa gaa atc gcc acg atc att cac gag ctc   1411
Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr Ile Ile His Glu Leu
            425                 430                 435

gat agc cga cag gtt tct gaa ctc aca gaa gcc ctg gcc aaa gtc tcc   1459
Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala Leu Ala Lys Val Ser
        440                 445                 450

acc acc cgc agc taaaactttt tgaaaggagc tca                        1494
Thr Thr Arg Ser
    455
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<210> 612
<211> 457
<212> PRT
<213> Corynebacterium glutamicum

<400> 612

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Met Thr Glu Ser Gln Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu
  1               5                  10                  15

Asn Asp Ala Ser Pro Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu
             20                  25                  30

Asp Thr Val Gly Val Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val
         35                  40                  45

Ala Ile Arg Gly Leu Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr
     50                  55                  60

Leu Ile Gly Gly Gly Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn
 65                  70                  75                  80
```

Ser Ala Leu Ser Arg Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys
85 90 95

Gly Glu Thr Asn His Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala
100 105 110

Ala Glu Ser Val Gly Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala
115 120 125

Val Ala Tyr Gln Val His Thr Arg Leu Ser Asp Val Ala Pro Val Arg
130 135 140

Ala Lys Gly Phe Asp His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala
145 150 155 160

Ser Ala Ala Lys Ala Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala
165 170 175

Leu Ala Ile Ala Gly Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr
180 185 190

Gly Asn Leu Ser His Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys
195 200 205

Glu Gly Thr Trp Ala Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro
210 215 220

Glu Glu Val Phe Glu Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly
225 230 235 240

Pro Phe Glu Ile Asp Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg
245 250 255

Thr Ile Ile Lys Lys His Asn Ala Glu Ile His Ser Gln Ser Ala Leu
260 265 270

Asp Ala Ala Gln Glu Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn
275 280 285

Ile Glu Lys Ile His Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile
290 295 300

Gly Gly Gly Glu Glu Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu
305 310 315 320

Ala Asp His Ser Leu Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly
325 330 335

Gln Leu Asn Pro Glu Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp
340 345 350

Val Gln Thr Leu Met Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe
355 360 365

Ser Asp Arg Phe Pro Asp His Met Pro Ala Asp Leu Glu Val Thr Leu
370 375 380

Asn Asp Gly Ser Val Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe
385 390 395 400

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```
His Asp Asn Pro Leu Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala
                405                 410                 415

Leu Val Thr Pro Phe Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr
            420                 425                 430

Ile Ile His Glu Leu Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala
        435                 440                 445

Leu Ala Lys Val Ser Thr Thr Arg Ser
    450                 455
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<210> 613
<211> 923
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(900)
<223> RXN03144

<400> 613

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acc acg acg gct acc agg cag tcg cga aaa ggt gag att tcc agc tgg   48
Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp
  1               5                  10                  15

aag gcg ttc gcg cca gcg ttt gcg gga aag atg gcc att gag gcg atg   96
Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met
            20                  25                  30

gat cgt gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc  144
Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly
        35                  40                  45

gaa gac ggg gtc atc gcg tgg ctg tta tcg ggc aaa gat cat gtt tat  192
Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr
    50                  55                  60

cat gtg cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag  240
His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu
65                  70                  75                  80

act tac aca aag gaa cat tca gcg gaa tat caa tcg cag gca ccg att  288
Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile
                85                  90                  95

gat ctg gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg  336
Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr
            100                 105                 110

gaa cac att gca gag att gtg ctg cgc acc agt cac cac acg cat tat  384
Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr
        115                 120                 125

gtg att ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc  432
Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala
    130                 135                 140

tcg cgt gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg  480
```

```
Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala
145                 150                 155                 160

ctt caa gat ggc gtg tgg cac cac gag ttt tcc tac acc cgc aag cgt   528
Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg
                165                 170                 175

tcc acc cgc ccg gaa act gtg gag ctg tgg cac aag att cgc acc gtg   576
Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val
            180                 185                 190

gag gat cct gaa tgg acg cgc cga tac cat tct gat gat cct gca aaa   624
Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys
        195                 200                 205

aag gcc ttt ggt gcg aaa gca gtg atc aca atg gct gat ggc acc gtg   672
Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val
    210                 215                 220

att gag gat gaa ttg gct gtc gcg gat gcc cac ccg ctg ggt gct cgg   720
Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg
225                 230                 235                 240

ccg ttt gcg cgg gag aat tac att gaa aaa ttc cgc aca ctc gcg cag   768
Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln
                245                 250                 255

ggg att gtc att gat tca gaa cag gaa cgc ttc ttg cat gcc gtg caa   816
Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln
            260                 265                 270

agc ctg cct gac ctg gat gat ctt gat cag ctc aac atc gaa gtc gac   864
Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp
        275                 280                 285

ata agc aac cag gcc gcg acg aaa gcg ggg ctg tta tgaatctctt        910
Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu
    290                 295                 300

ttcgaatggt gtt                                                   923
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<210> 614
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 614

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Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp
  1               5                  10                  15

Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met
            20                  25                  30

Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly
        35                  40                  45

Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr
    50                  55                  60

His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu
```

65 70 75 80

Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile
85 90 95

Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr
100 105 110

Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr
115 120 125

Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala
130 135 140

Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala
145 150 155 160

Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg
165 170 175

Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val
180 185 190

Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys
195 200 205

Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val
210 215 220

Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg
225 230 235 240

Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln
245 250 255

Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln
260 265 270

Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp
275 280 285

Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu
290 295 300

<210> 615
<211> 511
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> FRXA02322

<400> 615
cgcgcagagc taaactgcgt gaggttgtgg cctgtcacac ataatcggcc tagggtggga 60

ctttaaggaa acagtgcaca aataaatctc aaggagcccc atg cgc atc cac gat 115
Met Arg Ile His Asp
1 5

09509369.090902

```
gtt tat acc cac ctt tcg gcc gat aac ttt ccc aaa gca gag cac ctt   163
Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro Lys Ala Glu His Leu
                10                  15                  20

gcg tgg aaa ttc tcc gag ctt gcc acc gac ccc gtg gag gtg aca ccg   211
Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro Val Glu Val Thr Pro
            25                  30                  35

gat gtt tcg gag atg atc atc aac cgg atc atc gac aac gcg gcg gtg   259
Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile Asp Asn Ala Ala Val
        40                  45                  50

tct gcc gcg tcg gtg ttg cgc cgg cct gtg act gtg gcc agg caa caa   307
Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr Val Ala Arg Gln Gln
    55                  60                  65

gcg cag tcc cat ccg cgg gaa aag ggc gga aaa gtt ttt gga att tca   355
Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys Val Phe Gly Ile Ser
70                  75                  80                  85

ggc agc tac tca cca gag tgg gct gcc ttt gct aat ggt gtg gcc gta   403
Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala Asn Gly Val Ala Val
                90                  95                  100

cgt gaa ttg gac ttc cac gat aca ttt tta gca gct gaa tac tcc cat   451
Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr Ser His
            105                 110                 115

ccc ggc gac aat att cca cca ctt ctt gca gta gcg cag gct cag aga   499
Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val Ala Gln Ala Gln Arg
        120                 125                 130

agc agc ggc agg                                                  511
Ser Ser Gly Arg
    135
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<210> 616
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 616

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Met Arg Ile His Asp Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro
  1               5                  10                  15

Lys Ala Glu His Leu Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro
            20                  25                  30

Val Glu Val Thr Pro Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile
        35                  40                  45

Asp Asn Ala Ala Val Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr
    50                  55                  60

Val Ala Arg Gln Gln Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys
65                  70                  75                  80

Val Phe Gly Ile Ser Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala
                85                  90                  95
```

```
Asn Gly Val Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala
            100                 105                 110

Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val
        115                 120                 125

Ala Gln Ala Gln Arg Ser Ser Gly Arg
    130                 135


<210> 617
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(603)
<223> RXA02329

<400> 617
acg gct acc agg cag tcg cga aaa ggt gag att tcc agc tgg aag gcg   48
Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp Lys Ala
  1               5                  10                  15

ttc gcg cca gcg ttt gcg gga aag atg gcc att gag gcg atg gat cgt   96
Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg
             20                  25                  30

gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc gaa gac  144
Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp
         35                  40                  45

ggg gtc atc gcg tgg ctg tta tcg ggc aaa gat cat gtt tat cat gtg  192
Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val
     50                  55                  60

cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag act tac  240
Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr
 65                  70                  75                  80

aca aag gaa cat tca gcg gaa tat caa tcg cag gca ccg att gat ctg  288
Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu
                 85                  90                  95

gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg gaa cac  336
Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His
            100                 105                 110

att gca gag att gtg ctg cgc acc agt cac cac acg cat tat gtg att  384
Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile
        115                 120                 125

ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc tcg cgt  432
Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg
    130                 135                 140

gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg ctt caa  480
Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln
145                 150                 155                 160
```

```
gat ggc gtg tgg cac cac gag ttt tcc tac acc cgc aag cgt tcc acc   528
Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr
                165                 170                 175

cgc ccg gaa act gtg gag ctg tgg cac aag att cgc acc gtg gag gat   576
Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp
            180                 185                 190

cct gaa tgg acg cgc cga tac cat tct                              603
Pro Glu Trp Thr Arg Arg Tyr His Ser
        195                 200
```

<210> 618
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 618

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Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp Lys Ala
  1               5                  10                  15

Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg
            20                  25                  30

Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp
        35                  40                  45

Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val
    50                  55                  60

Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr
65                  70                  75                  80

Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu
                85                  90                  95

Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His
            100                 105                 110

Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile
        115                 120                 125

Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg
    130                 135                 140

Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln
145                 150                 155                 160

Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr
                165                 170                 175

Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp
            180                 185                 190

Pro Glu Trp Thr Arg Arg Tyr His Ser
        195                 200
```

<210> 619

<211> 1266
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1243)
<223> RXA02332

<400> 619
gaccgcatgc aacaccgcag cagattatat gagctcctgc gatacgaaga ctacaacgtc 60

tttgaccagc acattttcac ctacagaaaa ggagaaaaca atg agt gac agc caa 115
Met Ser Asp Ser Gln
1 5

gtc cgc aaa gga ctc aac ggc gtc atc tct gac tac aca agc att tcc 163
Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp Tyr Thr Ser Ile Ser
10 15 20

aaa gtg atg cca gag agc aac tcg ctg act tac cgt ggc tac gcc gtg 211
Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr Arg Gly Tyr Ala Val
25 30 35

gag gat ttg gtg gaa aac tgc agc ttt gaa gaa gtg atc tac ctc ctg 259
Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Ile Tyr Leu Leu
40 45 50

tgg ttt ggg gag ctg ccc acc act gaa caa ctc cgg acc ttc aac acg 307
Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu Arg Thr Phe Asn Thr
55 60 65

aca ggt cga agc tac cgc tca ctc gac gcc gga ctg att tcc ctc atc 355
Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile Ser Leu Ile
70 75 80 85

cac tcc tta ccc aac acc tgc cac ccc atg gac gtg ctg cgc acc gca 403
His Ser Leu Pro Asn Thr Cys His Pro Met Asp Val Leu Arg Thr Ala
90 95 100

gtg tcc tac atg ggt acc ttt gat ccc gat ccg ttt acc cgc gat gcc 451
Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro Phe Thr Arg Asp Ala
105 110 115

gat cat atc cga agc att gga cac aac ctg ctt gcg cag ctt ccc atg 499
Asp His Ile Arg Ser Ile Gly His Asn Leu Leu Ala Gln Leu Pro Met
120 125 130

gtg gtt gcc atg gat atc cgc agg cga agt ggg gaa gag atc atc gca 547
Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly Glu Glu Ile Ile Ala
135 140 145

cct gac cac aac aaa ggt atc gct tcg aat ttc tta tcc atg gtg ttt 595
Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe Leu Ser Met Val Phe
150 155 160 165

ggc aat gat gat ggt tct gta gcc aac tcc gca gat gac atc cgc gat 643
Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala Asp Asp Ile Arg Asp
170 175 180

ttt gaa cgc tcc ctc atc ctc tac gcc gag cac tcc ttc aac gcc tcc 691

```
Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His Ser Phe Asn Ala Ser
            185                 190                 195

aca ttc tca gcc cgc gtg atc tca tca acg cga tcc gat acg tat tcg   739
Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg Ser Asp Thr Tyr Ser
        200                 205                 210

gcg atc aca ggt gcg atc ggt gct ctc aaa ggc cca ctg cac gga ggt   787
Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Leu His Gly Gly
    215                 220                 225

gcc aat gag ttt gtc atg cac acc atg ctg gat atc gac gat ccc aac   835
Ala Asn Glu Phe Val Met His Thr Met Leu Asp Ile Asp Asp Pro Asn
230                 235                 240                 245

aat gct gcc gac tgg atg ggc aag gcg ttg gat cgt aaa gaa cgc atc   883
Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp Arg Lys Glu Arg Ile
                250                 255                 260

atg gga ttc ggg cac cgc gtg tac aaa aac ggc gac tcc agg gtc ccc   931
Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly Asp Ser Arg Val Pro
            265                 270                 275

tcc atg gag aaa tcc atg cgc tcc ctt gct gct cgt cac cgt ggt caa   979
Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala Arg His Arg Gly Gln
        280                 285                 290

aaa tgg gtg cac atg tat gag tcg atg caa gaa gtc atg gag gct cgc  1027
Lys Trp Val His Met Tyr Glu Ser Met Gln Glu Val Met Glu Ala Arg
    295                 300                 305

act ggc att aaa ccc aac ctc gac ttc ccg gcc ggc cct gcc tat tac  1075
Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr Tyr
310                 315                 320                 325

atg ctg gga ttc ccc gtc gac ttc ttc aca cca ctg ttt gtg ctg gcc  1123
Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro Leu Phe Val Leu Ala
                330                 335                 340

cga gtg tca ggg tgg acg gca cac atc gtg gag caa ttt gaa aac aat  1171
Arg Val Ser Gly Trp Thr Ala His Ile Val Glu Gln Phe Glu Asn Asn
            345                 350                 355

gcg ctg atc cga cca ttg tct gcc tac aac gga gtg gaa gaa agg gag  1219
Ala Leu Ile Arg Pro Leu Ser Ala Tyr Asn Gly Val Glu Glu Arg Glu
        360                 365                 370

gtg gtg ccc att tcg gag aga acc taatcagtga ggctgatttc taa        1266
Val Val Pro Ile Ser Glu Arg Thr
    375                 380


<210> 620
<211> 381
<212> PRT
<213> Corynebacterium glutamicum

<400> 620
Met Ser Asp Ser Gln Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp
  1               5                  10                  15
```

Tyr Thr Ser Ile Ser Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr
20 25 30

Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu
35 40 45

Val Ile Tyr Leu Leu Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu
50 55 60

Arg Thr Phe Asn Thr Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly
65 70 75 80

Leu Ile Ser Leu Ile His Ser Leu Pro Asn Thr Cys His Pro Met Asp
85 90 95

Val Leu Arg Thr Ala Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro
100 105 110

Phe Thr Arg Asp Ala Asp His Ile Arg Ser Ile Gly His Asn Leu Leu
115 120 125

Ala Gln Leu Pro Met Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly
130 135 140

Glu Glu Ile Ile Ala Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe
145 150 155 160

Leu Ser Met Val Phe Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala
165 170 175

Asp Asp Ile Arg Asp Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His
180 185 190

Ser Phe Asn Ala Ser Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg
195 200 205

Ser Asp Thr Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly
210 215 220

Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr Met Leu Asp
225 230 235 240

Ile Asp Asp Pro Asn Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp
245 250 255

Arg Lys Glu Arg Ile Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly
260 265 270

Asp Ser Arg Val Pro Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala
275 280 285

Arg His Arg Gly Gln Lys Trp Val His Met Tyr Glu Ser Met Gln Glu
290 295 300

Val Met Glu Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala
305 310 315 320

Gly Pro Ala Tyr Tyr Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro
325 330 335

Leu Phe Val Leu Ala Arg Val Ser Gly Trp Thr Ala His Ile Val Glu

Sequence Listing

```
            340                 345                 350

Gln Phe Glu Asn Asn Ala Leu Ile Arg Pro Leu Ser Ala Tyr Asn Gly
        355                 360                 365

Val Glu Glu Arg Glu Val Val Pro Ile Ser Glu Arg Thr
    370                 375                 380


<210> 621
<211> 1038
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1015)
<223> RXN02333

<400> 621
tcttgcatgc cgtgcaaagc ctgcctgacc tggatgatct tgatcagctc aacatcgaag 60

tcgacataag caaccaggcc gcgacgaaag cggggctgtt atg aat ctc ttt tcg   115
                                          Met Asn Leu Phe Ser
                                            1               5

aat ggt gtt gat gtg ggg agg cgt cga caa gca ttt aaa gcg gca ctc   163
Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala Phe Lys Ala Ala Leu
                10                  15                  20

gcc gca ccc cac atc gcc cgg ctg ccc ggc gca ttc tcc cct ctg att   211
Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala Phe Ser Pro Leu Ile
            25                  30                  35

gcg cgc tcc atc gaa gaa gcc ggc ttc gaa ggc gtc tac gtt tcc ggc   259
Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly Val Tyr Val Ser Gly
        40                  45                  50

gcc gtc ata gct gct gac ctg gca cta ccc gat atc ggc ttg acg acg   307
Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp Ile Gly Leu Thr Thr
    55                  60                  65

ctg acc gaa gtc gcc cac cgc gcg cgg caa att gcg cgc gtc aca gac   355
Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile Ala Arg Val Thr Asp
70                  75                  80                  85

cta gga gtg ctt gtc gac gcc gac acc ggc ttt ggc gaa ccc atg tcg   403
Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe Gly Glu Pro Met Ser
                90                  95                  100

gcc gca cgc acc gtc gcc gaa ttg gag gac gcc ggt gtg gcc gga tgc   451
Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala Gly Val Ala Gly Cys
            105                 110                 115

cac ctt gaa gac caa gtc aac ccc aaa cgt tgc ggg cac ttg gac ggc   499
His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys Gly His Leu Asp Gly
        120                 125                 130

aaa gaa gtc gtg cgc aca gac gtg atg gtt cga cgc atc gca gcc gcc   547
Lys Glu Val Val Arg Thr Asp Val Met Val Arg Arg Ile Ala Ala Ala
    135                 140                 145
```

```
gtc tcg gcc cgg cgc gac ccg aac ttt gtc atc tgc gcc cgc acc gac   595
Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile Cys Ala Arg Thr Asp
150                 155                 160                 165

gcc gct gga gtg gaa gga atc gac gcc gcc att gag cgc gcg aaa gcc   643
Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile Glu Arg Ala Lys Ala
                170                 175                 180

tac tta gat gcg ggc gcc gac atg att ttc acc gaa gcc ctc cac agc   691
Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr Glu Ala Leu His Ser
            185                 190                 195

gaa gcc gac ttc cga tac ttc cgg cac gcc atc cct gat gcc ttg ttg   739
Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile Pro Asp Ala Leu Leu
        200                 205                 210

ctg gcg aat atg acc gaa ttt ggc aaa acg acg ctg ctg tca gcc gac   787
Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr Leu Leu Ser Ala Asp
    215                 220                 225

gtg ttg gaa gag att ggc tac aac gcc gtg atc tac ccc gtg acc acg   835
Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr
230                 235                 240                 245

ctg cgt att gcc atg gga caa gta gaa caa gca cta gcc gaa atc aaa   883
Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys
                250                 255                 260

gaa cac ggt acc caa gaa gga tgg ctg gac cgc atg caa cac cgc agc   931
Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser
            265                 270                 275

aga tta tat gag ctc ctg cga tac gaa gac tac aac gtc ttt gac cag   979
Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln
        280                 285                 290

cac att ttc acc tac aga aaa gga gaa aac aat gag tgacagccaa       1025
His Ile Phe Thr Tyr Arg Lys Gly Glu Asn Asn Glu
    295                 300                 305

gtccgcaaag gac                                                  1038
```

<210> 622
<211> 305
<212> PRT
<213> Corynebacterium glutamicum

<400> 622

```
Met Asn Leu Phe Ser Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala
  1               5                  10                  15

Phe Lys Ala Ala Leu Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala
             20                  25                  30

Phe Ser Pro Leu Ile Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly
         35                  40                  45

Val Tyr Val Ser Gly Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp
     50                  55                  60
```

```
Ile Gly Leu Thr Thr Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile
 65                  70                  75                  80

Ala Arg Val Thr Asp Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe
                 85                  90                  95

Gly Glu Pro Met Ser Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala
            100                 105                 110

Gly Val Ala Gly Cys His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys
        115                 120                 125

Gly His Leu Asp Gly Lys Glu Val Val Arg Thr Asp Val Met Val Arg
    130                 135                 140

Arg Ile Ala Ala Ala Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile
145                 150                 155                 160

Cys Ala Arg Thr Asp Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile
                165                 170                 175

Glu Arg Ala Lys Ala Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr
            180                 185                 190

Glu Ala Leu His Ser Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile
        195                 200                 205

Pro Asp Ala Leu Leu Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr
    210                 215                 220

Leu Leu Ser Ala Asp Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile
225                 230                 235                 240

Tyr Pro Val Thr Thr Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala
                245                 250                 255

Leu Ala Glu Ile Lys Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg
            260                 265                 270

Met Gln His Arg Ser Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr
        275                 280                 285

Asn Val Phe Asp Gln His Ile Phe Thr Tyr Arg Lys Gly Glu Asn Asn
    290                 295                 300

Glu
305
```

<210> 623
<211> 242
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(219)
<223> FRXA02333

<400> 623

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gag att ggc tac aac gcc gtg atc tac ccc gtg acc acg ctg cgt att   48
Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr Leu Arg Ile
  1               5                  10                  15

gcc atg gga caa gta gaa caa gca cta gcc gaa atc aaa gaa cac ggt   96
Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys Glu His Gly
             20                  25                  30

acc caa gaa gga tgg ctg gac cgc atg caa cac cgc agc aga tta tat  144
Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser Arg Leu Tyr
         35                  40                  45

gag ctc ctg cga tac gaa gac tac aac gtc ttt gac cag cac att ttc  192
Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln His Ile Phe
     50                  55                  60

acc tac aga aaa gga gaa aac aat gag tgacagccaa gtccgcaaag        239
Thr Tyr Arg Lys Gly Glu Asn Asn Glu
 65                  70

gac                                                             242
```

09622960.1

<210> 624
<211> 73
<212> PRT
<213> Corynebacterium glutamicum

<400> 624
Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr Leu Arg Ile
  1   5   10   15

Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys Glu His Gly
             20   25   30

Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser Arg Leu Tyr
         35   40   45

Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln His Ile Phe
     50   55   60

Thr Tyr Arg Lys Gly Glu Asn Asn Glu
 65   70

<210> 625
<211> 513
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> RXA00030

<400> 625
taaaaacgcc actttggtgt cgataacacc gaacttccga acataaaaga tgcgttggtg 60

ctctctgcac aatgtttctt tcggaactat tctggcgacc atg cga att gaa atc   115
                                        Met Arg Ile Glu Ile
                                          1   5

```
aca agc gta ttt gtt gat gac cag gcc aaa gca ctc gat ttc tac acc   163
Thr Ser Val Phe Val Asp Asp Gln Ala Lys Ala Leu Asp Phe Tyr Thr
                10                  15                  20

acg aag ctc gga ttt gag ctc aaa cac gat gta act gct ggt gac tac   211
Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val Thr Ala Gly Asp Tyr
            25                  30                  35

cgc tgg ttg act gtt gtt gat cca gaa aac cca gat ggt gtg cag ctt   259
Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro Asp Gly Val Gln Leu
        40                  45                  50

ttg ttg gaa cca aac cag cac cca gat gca gcg act tac caa gct gga   307
Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala Thr Tyr Gln Ala Gly
    55                  60                  65

att aaa cga gac ggt att ccc gct aca cag ttt tat gtt gat gat gtg   355
Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe Tyr Val Asp Asp Val
70                  75                  80                  85

cag gaa gaa tat gac agc ctc aag gat aaa ggc gtg gat ttc atc atg   403
Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly Val Asp Phe Ile Met
                90                  95                  100

gaa cca acc gat gtg ggc cct tca gtg att gcc att ctc gat gac acc   451
Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala Ile Leu Asp Asp Thr
            105                 110                 115

gta gga aac cta att cag att gtt caa ttg aag cag aac taaccccgtg   500
Val Gly Asn Leu Ile Gln Ile Val Gln Leu Lys Gln Asn
        120                 125                 130

gaatgacaaa atc                                                  513
```

<210> 626
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 626

```
Met Arg Ile Glu Ile Thr Ser Val Phe Val Asp Asp Gln Ala Lys Ala
  1               5                  10                  15

Leu Asp Phe Tyr Thr Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val
            20                  25                  30

Thr Ala Gly Asp Tyr Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro
        35                  40                  45

Asp Gly Val Gln Leu Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala
    50                  55                  60

Thr Tyr Gln Ala Gly Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe
65                  70                  75                  80

Tyr Val Asp Asp Val Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly
                85                  90                  95

Val Asp Phe Ile Met Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala
```

```
            100                 105                 110

Ile Leu Asp Asp Thr Val Gly Asn Leu Ile Gln Ile Val Gln Leu Lys
        115                 120                 125

Gln Asn
    130


<210> 627
<211> 2334
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2311)
<223> RXN00148

<400> 627
ctttgagggc agcgcgcatg cgcccgatgg ttatttgaac atgacaattg atgccgcggc 60

gacgctggct gacctgctag atgctttggg agcttaaatc atg acg tcg atc cct   115
                                        Met Thr Ser Ile Pro
                                          1               5

aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca   163
Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser
                10                  15                  20

cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat   211
His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
            25                  30                  35

gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg   259
Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
        40                  45                  50

gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggg   307
Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
    55                  60                  65

ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac   355
Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
70                  75                  80                  85

gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat cgg agg aac   403
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn
                90                  95                  100

ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc   451
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr
            105                 110                 115

cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt   499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly
        120                 125                 130

atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt   547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe
    135                 140                 145
```

```
gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc   595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly
150                 155                 160                 165

gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa   643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln
                170                 175                 180

ggt gtg ggt ccg gag cag ctt gcg ggc acg atc cag aat gac atc ttg   691
Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu
            185                 190                 195

aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg   739
Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser
        200                 205                 210

atg cgc atc att tcc aac atc ttt gag tac acc tcc ttg aag atg cca   787
Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr Ser Leu Lys Met Pro
    215                 220                 225

cgt ttt aac tcc att tcg att tct ggc tat cac atc cag gaa gcg gga   835
Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His Ile Gln Glu Ala Gly
230                 235                 240                 245

gcg act gcc gat ttg gag ctg gcc tac act ctg gcg gat ggt att gaa   883
Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu Ala Asp Gly Ile Glu
                250                 255                 260

tac atc cgt gca ggt aaa gag gta ggc ctt gac gtg gat aag ttc gcg   931
Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp Val Asp Lys Phe Ala
            265                 270                 275

cct cgt ctg tcc ttc ttc tgg ggt att tct atg tac acc ttc atg gag   979
Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu
        280                 285                 290

atc gca aag ctg cgt gcg gga cga ctg ctg tgg agc gag ttg gtg gca   1027
Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp Ser Glu Leu Val Ala
    295                 300                 305

aaa ttc gat ccg aaa aac gcc aag tcc cag tcg ctg cgc acg cac tcg   1075
Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser
310                 315                 320                 325

cag acc tct ggt tgg tcg ttg acc gcg cag gat gtg tac aac aac gtc   1123
Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp Val Tyr Asn Asn Val
                330                 335                 340

gcc cgc acc gcg att gag gcg atg gct gca acc cag ggc cac acc cag   1171
Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr Gln Gly His Thr Gln
            345                 350                 355

tcg ctg cac acc aat gca ctt gat gag gcg ttg gcg ctg ccc acc gat   1219
Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu Ala Leu Pro Thr Asp
        360                 365                 370

ttc tct gct cgt atc gcc cga aac acc cag ctg ttg ctg cag cag gaa   1267
Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu Leu Leu Gln Gln Glu
    375                 380                 385
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tct ggc acg gtg cgt cca gtt gat cca tgg gcg ggc tcc tat tac gtg   1315
Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala Gly Ser Tyr Tyr Val
390                 395                 400                 405

gag tgg ttg acc aat gag ctg gct aac cgc gcg cgc aag cac atc gat   1363
Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala Arg Lys His Ile Asp
                410                 415                 420

gag gtg gag gaa gcc ggc gga atg gcg cag gcc acc gcg cag gga att   1411
Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala Thr Ala Gln Gly Ile
            425                 430                 435

cct aag ctg cgc att gag gaa tca gcg gca cgc acc cag gct cgc att   1459
Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg Thr Gln Ala Arg Ile
        440                 445                 450

gat tcc ggc cgc cag gcg ctg atc ggc gtg aat cgc tac gtg gcg gaa   1507
Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn Arg Tyr Val Ala Glu
    455                 460                 465

gaa gat gag gaa att gaa gtc ctc aag gtt gac aac acc aag gtt cgc   1555
Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg
470                 475                 480                 485

gca gaa cag ttg gct aaa ctc gcg caa ctg aaa gca gag cgc aac gat   1603
Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp
                490                 495                 500

gcg gaa gtc aag gct gcg ctg gat gcg ttg aca gct gct gcc cgc aac   1651
Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Ala Arg Asn
            505                 510                 515

gag cat aaa gag cca ggg gat ttg gat cag aac ctg ctc aaa ctt gcc   1699
Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala
        520                 525                 530

gtc gat gct gcg cgc gca aaa gct acc att gga gag atc tcc gat gct   1747
Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly Glu Ile Ser Asp Ala
    535                 540                 545

ttg gaa gtt gtc ttt ggc cgc cac gaa gca gaa atc agg acg ctg tct   1795
Leu Glu Val Val Phe Gly Arg His Glu Ala Glu Ile Arg Thr Leu Ser
550                 555                 560                 565

ggc gtg tac aag gat gag gtt gga aag gaa ggc aca gtg agc aac gtc   1843
Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly Thr Val Ser Asn Val
                570                 575                 580

gaa cgc gcg atc gcc ctg gct gac gcc ttt gag gct gag gaa ggc cgc   1891
Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg
            585                 590                 595

cgc cca cgt atc ttt att gcc aag atg ggc cag gat gga cat gac cgt   1939
Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg
        600                 605                 610

gga cag aag gtt gtc gcg tct gcc tat gct gac ctg ggc atg gac gtg   1987
Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp Leu Gly Met Asp Val
    615                 620                 625

gat gtt gga ccg ctg ttt caa act cca gcc gaa gct gcc cgc gcc gcc   2035
```

```
Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Ala Arg Ala Ala
630                 635                 640                 645

gtg gac gcc gat gtt cac gtg gtg ggt atg tct tcg ctg gca gca ggc   2083
Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly
                650                 655                 660

cac ctc acc ttg ctg ccc gag ctg aag aaa gaa ctt gca gct ctt ggc   2131
His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu Leu Ala Ala Leu Gly
            665                 670                 675

cgc gat gac att ctg gtc acc gtg ggc ggc gtc att ccg ccg ggc gat   2179
Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val Ile Pro Pro Gly Asp
        680                 685                 690

ttc cag gat ctc tac gat atg ggt gcc gcc gcg att tac cct tca gga   2227
Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala Ile Tyr Pro Ser Gly
    695                 700                 705

acc gtc atc gcg gag tcg gcg atc gat ctg atc acc cga ctc gcc gca   2275
Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile Thr Arg Leu Ala Ala
710                 715                 720                 725

cac ctg ggc ttt gac ctg gat gtg gat gtg aat gaa tgatcacggt        2321
His Leu Gly Phe Asp Leu Asp Val Asp Val Asn Glu
                730                 735

ttcctagaag aca                                                   2334
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<210> 628
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<213> Corynebacterium glutamicum

<400> 628

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Met Thr Ser Ile Pro Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr
  1               5                  10                  15

Arg Ala Ser Glu Ser His Asn Val Asp Ala Gly Lys Val Trp Asn Thr
            20                  25                  30

Pro Glu Gly Ile Asp Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp
        35                  40                  45

Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
    50                  55                  60

Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
65                  70                  75                  80

Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
                85                  90                  95

Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
            100                 105                 110

Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
        115                 120                 125

Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp
```

```
    130                 135                 140

Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser
145                 150                 155                 160

Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val
                165                 170                 175

Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile
            180                 185                 190

Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr
        195                 200                 205

Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr
    210                 215                 220

Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His
225                 230                 235                 240

Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu
                245                 250                 255

Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp
            260                 265                 270

Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met
        275                 280                 285

Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp
    290                 295                 300

Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser
305                 310                 315                 320

Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp
                325                 330                 335

Val Tyr Asn Asn Val Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr
            340                 345                 350

Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu
        355                 360                 365

Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu
    370                 375                 380

Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala
385                 390                 395                 400

Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala
                405                 410                 415

Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala
            420                 425                 430

Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg
        435                 440                 445

Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn
    450                 455                 460
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Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp
465 470 475 480

Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys
485 490 495

Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr
500 505 510

Ala Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn
515 520 525

Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly
530 535 540

Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu
545 550 555 560

Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly
565 570 575

Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu
580 585 590

Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln
595 600 605

Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp
610 615 620

Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu
625 630 635 640

Ala Ala Arg Ala Ala Val Asp Ala Asp Val His Val Val Gly Met Ser
645 650 655

Ser Leu Ala Ala Gly His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu
660 665 670

Leu Ala Ala Leu Gly Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val
675 680 685

Ile Pro Pro Gly Asp Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala
690 695 700

Ile Tyr Pro Ser Gly Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile
705 710 715 720

Thr Arg Leu Ala Ala His Leu Gly Phe Asp Leu Asp Val Asp Val Asn
725 730 735

Glu

<210> 629
<211> 2098
<212> DNA
<213> Corynebacterium glutamicum

09502360 - 09502360

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<222> (101)..(2098)
<223> FRXA00148

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gacgctggct gacctgctag atgctttggg agcttaaatc atg acg tcg atc cct 115
Met Thr Ser Ile Pro
1 5

aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca 163
Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser
10 15 20

cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat 211
His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
25 30 35

gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg 259
Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
40 45 50

gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggg 307
Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
55 60 65

ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac 355
Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
70 75 80 85

gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat cgg agg aac 403
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn
90 95 100

ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc 451
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr
105 110 115

cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt 499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly
120 125 130

atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt 547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe
135 140 145

gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc 595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly
150 155 160 165

gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa 643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln
170 175 180

ggt gtg ggt ccg gag cag ctt gcg ggc acg atc cag aat gac atc ttg 691
Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu
185 190 195

aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg 739

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Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser
        200                 205                 210

atg cgc atc att tcc aac atc ttt gag tac acc tcc ttg aag atg cca   787
Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr Ser Leu Lys Met Pro
    215                 220                 225

cgt ttt aac tcc att tcg att tct ggc tat cac atc cag gaa gcg gga   835
Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His Ile Gln Glu Ala Gly
230                 235                 240                 245

gcg act gcc gat ttg gag ctg gcc tac act ctg gcg gat ggt att gaa   883
Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu Ala Asp Gly Ile Glu
                250                 255                 260

tac atc cgt gca ggt aaa gag gta ggc ctt gac gtg gat aag ttc gcg   931
Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp Val Asp Lys Phe Ala
            265                 270                 275

cct cgt ctg tcc ttc ttc tgg ggt att tct atg tac acc ttc atg gag   979
Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu
        280                 285                 290

atc gca aag ctg cgt gcg gga cga ctg ctg tgg agc gag ttg gtg gca   1027
Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp Ser Glu Leu Val Ala
    295                 300                 305

aaa ttc gat ccg aaa aac gcc aag tcc cag tcg ctg cgc acg cac tcg   1075
Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser
310                 315                 320                 325

cag acc tct ggt tgg tcg ttg acc gcg cag gat gtg tac aac aac gtc   1123
Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp Val Tyr Asn Asn Val
                330                 335                 340

gcc cgc acc gcg att gag gcg atg gct gca acc cag ggc cac acc cag   1171
Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr Gln Gly His Thr Gln
            345                 350                 355

tcg ctg cac acc aat gca ctt gat gag gcg ttg gcg ctg ccc acc gat   1219
Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu Ala Leu Pro Thr Asp
        360                 365                 370

ttc tct gct cgt atc gcc cga aac acc cag ctg ttg ctg cag cag gaa   1267
Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu Leu Leu Gln Gln Glu
    375                 380                 385

tct ggc acg gtg cgt cca gtt gat cca tgg gcg ggc tcc tat tac gtg   1315
Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala Gly Ser Tyr Tyr Val
390                 395                 400                 405

gag tgg ttg acc aat gag ctg gct aac cgc gcg cgc aag cac atc gat   1363
Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala Arg Lys His Ile Asp
                410                 415                 420

gag gtg gag gaa gcc ggc gga atg gcg cag gcc acc gcg cag gga att   1411
Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala Thr Ala Gln Gly Ile
            425                 430                 435

cct aag ctg cgc att gag gaa tca gcg gca cgc acc cag gct cgc att   1459
Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg Thr Gln Ala Arg Ile
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        440                 445                 450

gat tcc ggc cgc cag gcg ctg atc ggc gtg aat cgc tac gtg gcg gaa   1507
Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn Arg Tyr Val Ala Glu
    455                 460                 465

gaa gat gag gaa att gaa gtc ctc aag gtt gac aac acc aag gtt cgc   1555
Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg
470                 475                 480                 485

gca gaa cag ttg gct aaa ctc gcg caa ctg aaa gca gag cgc aac gat   1603
Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp
                490                 495                 500

gcg gaa gtc aag gct gcg ctg gat gcg ttg aca gct gct gcc cgc aac   1651
Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Ala Arg Asn
            505                 510                 515

gag cat aaa gag cca ggg gat ttg gat cag aac ctg ctc aaa ctt gcc   1699
Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala
        520                 525                 530

gtc gat gct gcg cgc gca aaa gct acc att gga gag atc tcc gat gct   1747
Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly Glu Ile Ser Asp Ala
    535                 540                 545

ttg gaa gtt gtc ttt ggc cgc cac gaa gca gaa atc agg acg ctg tct   1795
Leu Glu Val Val Phe Gly Arg His Glu Ala Glu Ile Arg Thr Leu Ser
550                 555                 560                 565

ggc gtg tac aag gat gag gtt gga aag gaa ggc aca gtg agc aac gtc   1843
Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly Thr Val Ser Asn Val
                570                 575                 580

gaa cgc gcg atc gcc ctg gct gac gcc ttt gag gct gag gaa ggc cgc   1891
Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg
            585                 590                 595

cgc cca cgt atc ttt att gcc aag atg ggc cag gat gga cat gac cgt   1939
Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg
        600                 605                 610

gga cag aag gtt gtc gcg tct gcc tat gct gac ctg ggc atg gac gtg   1987
Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp Leu Gly Met Asp Val
    615                 620                 625

gat gtt gga ccg ctg ttt caa act cca gcc gaa gct gcc cgc gcc gcc   2035
Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Ala Arg Ala Ala
630                 635                 640                 645

gtg gac gcc gat gtt cac gtg gtg ggt atg tct tcg ctg gca gca ggc   2083
Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly
                650                 655                 660

cac ctc acc ttg ctg                                             2098
His Leu Thr Leu Leu
            665
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<210> 630
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<212> PRT
<213> Corynebacterium glutamicum

<400> 630

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Met Thr Ser Ile Pro Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr
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Arg Ala Ser Glu Ser His Asn Val Asp Ala Gly Lys Val Trp Asn Thr
            20                  25                  30

Pro Glu Gly Ile Asp Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp
        35                  40                  45

Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
    50                  55                  60

Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
65                  70                  75                  80

Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
                85                  90                  95

Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
            100                 105                 110

Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
        115                 120                 125

Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp
    130                 135                 140

Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser
145                 150                 155                 160

Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val
                165                 170                 175

Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile
            180                 185                 190

Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr
        195                 200                 205

Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr
    210                 215                 220

Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His
225                 230                 235                 240

Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu
                245                 250                 255

Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp
            260                 265                 270

Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met
        275                 280                 285

Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp
    290                 295                 300
```

```
Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser
305                 310                 315                 320

Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp
                325                 330                 335

Val Tyr Asn Asn Val Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr
            340                 345                 350

Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu
        355                 360                 365

Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu
    370                 375                 380

Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala
385                 390                 395                 400

Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala
                405                 410                 415

Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala
            420                 425                 430

Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg
        435                 440                 445

Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn
    450                 455                 460

Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp
465                 470                 475                 480

Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys
                485                 490                 495

Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr
            500                 505                 510

Ala Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn
        515                 520                 525

Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly
    530                 535                 540

Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu
545                 550                 555                 560

Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly
                565                 570                 575

Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu
            580                 585                 590

Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln
        595                 600                 605

Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp
    610                 615                 620

Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu
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625 630 635 640

Ala Ala Arg Ala Ala Val Asp Ala Asp Val His Val Val Gly Met Ser
645 650 655

Ser Leu Ala Ala Gly His Leu Thr Leu Leu
660 665

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<211> 1971
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1948)
<223> RXA00149

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Leu Thr Asp Leu Thr
1 5

aag act gcg gtg ccc gag gaa ctt tca gag aac ctc gaa act tgg tac 163
Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn Leu Glu Thr Trp Tyr
10 15 20

aag gct gtg gcc ggt gtt ttc gcg cgc aca cag aaa aaa gac atc ggc 211
Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln Lys Lys Asp Ile Gly
25 30 35

gac att gcc gta gat gtg tgg aag aaa ctc atc gtc act aca ccg gat 259
Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile Val Thr Thr Pro Asp
40 45 50

ggt gtt gat atc aat ccg ctg tac acc aga gca gat gag tcc cag agg 307
Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala Asp Glu Ser Gln Arg
55 60 65

aaa ttc act gag gtt cct ggt gag ttt ccc ttc act agg gga acc act 355
Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe Thr Arg Gly Thr Thr
70 75 80 85

gtt gat ggt gaa cgc gtt ggt tgg ggt gtt act gag act ttc gga cat 403
Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr Glu Thr Phe Gly His
90 95 100

gac agc ccg aag aat atc aac gct gcg gtg ctg aat gct ctg aat tct 451
Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu Asn Ala Leu Asn Ser
105 110 115

ggc acc acc aca ttg ggt ttt gag ttc tct gag gaa ttc acg gca gct 499
Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu Glu Phe Thr Ala Ala
120 125 130

gat ctt aaa gtt gct ctc gaa ggc gtg tat ctc aac atg gct ccg ttg 547
Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu Asn Met Ala Pro Leu
135 140 145

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ctg att cat gcg ggt gga tcc acg tca gag gtt gca gcg gcg ttg tat   595
Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val Ala Ala Ala Leu Tyr
150                 155                 160                 165

acg ttg gcg gag gaa gcc gga acg ttt ttt gct gcg ttg acc ttg ggt   643
Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala Ala Leu Thr Leu Gly
                170                 175                 180

tct cgt cct ttg acg gcg cag gtt gat ggt tcg cac agt gac acc att   691
Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser His Ser Asp Thr Ile
            185                 190                 195

gaa gaa gca gtt cag ttg gca gtg aat gct tcc aag cgt gcg aat gtg   739
Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser Lys Arg Ala Asn Val
        200                 205                 210

cgc gct atc ttg gtg gat ggt tcc agt ttt tcc aac cag ggc gcg tcg   787
Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser Asn Gln Gly Ala Ser
    215                 220                 225

gat gct caa gaa att ggt cta agt atc gcc gcc ggt gtg gat tat gtc   835
Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala Gly Val Asp Tyr Val
230                 235                 240                 245

cgt cgc ttg gtc gat gca ggc ctt tcc acg gaa gct gca ctt aag cag   883
Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu Ala Ala Leu Lys Gln
                250                 255                 260

gtg gcg ttc cgt ttt gcg gtc acc gat gag cag ttc gcg cag att tct   931
Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln Phe Ala Gln Ile Ser
            265                 270                 275

aag ctg cgt gtg gct cga cgt ctg tgg gcc agg gtg tgt gag gtg ctt   979
Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg Val Cys Glu Val Leu
        280                 285                 290

ggt ttt cca gag ctg gcc gta gca cca cag cat gcg gtg act gca cga   1027
Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His Ala Val Thr Ala Arg
    295                 300                 305

gcg atg ttt agc cag cgt gat ccg tgg gtg aat atg ctg cgc agt act   1075
Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn Met Leu Arg Ser Thr
310                 315                 320                 325

gtt gca gct ttc gct gca ggc gtc ggt gga gca acc gat gtg gag gtt   1123
Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala Thr Asp Val Glu Val
                330                 335                 340

cgt act ttt gat gat gcg atc cca gat gga gtt cct gga gtg tcg agg   1171
Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val Pro Gly Val Ser Arg
            345                 350                 355

aat ttc gct cac cgc atc gcg cgc aat act aat ttg ttg ttg cta gaa   1219
Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn Leu Leu Leu Leu Glu
        360                 365                 370

gag tca cat ctt ggt cac gtg gtt gat cct gct ggt gga tca tat ttc   1267
Glu Ser His Leu Gly His Val Val Asp Pro Ala Gly Gly Ser Tyr Phe
    375                 380                 385
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gtg gag agc ttc acc gat gat cta gcg gag aag gcg tgg gct gtg ttc   1315
Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys Ala Trp Ala Val Phe
390                 395                 400                 405

agt ggc atc gaa gct gag ggc gga tac agt gca gct tgt gca tcc ggc   1363
Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala Ala Cys Ala Ser Gly
                410                 415                 420

acg gtg act gcc atg ctt gat cag acg tgg gag cag act cgc gct gat   1411
Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu Gln Thr Arg Ala Asp
            425                 430                 435

gtg gcg tcg aga aag aag aag ctc act gga att aat gag ttc ccg aac   1459
Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile Asn Glu Phe Pro Asn
        440                 445                 450

ttg gcg gag tct ccg ctg cca gct gat cgt cgg gta gaa cct gca ggt   1507
Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg Val Glu Pro Ala Gly
    455                 460                 465

gtg cgt cga tgg gca gcg gat ttt gaa gcg ctg cgc aat cgt tcg gat   1555
Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu Arg Asn Arg Ser Asp
470                 475                 480                 485

gct ttc ttg gaa aag aac ggc gcg agg cca cag atc acg atg att cct   1603
Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln Ile Thr Met Ile Pro
                490                 495                 500

ctg gga ccg ttg tcc aag cac aat att cgc act ggt ttt act tcc aac   1651
Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr Gly Phe Thr Ser Asn
            505                 510                 515

ctg ttg gct tcc ggt ggc att gaa gca atc aac ccg ggt caa ctt gtt   1699
Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn Pro Gly Gln Leu Val
        520                 525                 530

ccc ggc act gac gct ttt gca gaa gct gca cag gcc gca ggc att gta   1747
Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln Ala Ala Gly Ile Val
    535                 540                 545

gtg gtg tgt gga acg gac caa gag tat gcc gaa acg ggg gag gga gcc   1795
Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu Thr Gly Glu Gly Ala
550                 555                 560                 565

gtc gaa aag ctc cgc gaa gcg ggc gtt gag cgc atc ctg ctt gct ggc   1843
Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg Ile Leu Leu Ala Gly
                570                 575                 580

gcg ccg aag agc ttt gag ggc agc gcg cat gcg ccc gat ggt tat ttg   1891
Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala Pro Asp Gly Tyr Leu
            585                 590                 595

aac atg aca att gat gcc gcg gcg acg ctg gct gac ctg cta gat gct   1939
Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala Asp Leu Leu Asp Ala
        600                 605                 610

ttg gga gct taaatcatga cgtcgatccc taa                            1971
Leu Gly Ala
    615
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<210> 632
<211> 616
<212> PRT
<213> Corynebacterium glutamicum

<400> 632
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1 5 10 15

Leu Glu Thr Trp Tyr Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln
20 25 30

Lys Lys Asp Ile Gly Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile
35 40 45

Val Thr Thr Pro Asp Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala
50 55 60

Asp Glu Ser Gln Arg Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe
65 70 75 80

Thr Arg Gly Thr Thr Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr
85 90 95

Glu Thr Phe Gly His Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu
100 105 110

Asn Ala Leu Asn Ser Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu
115 120 125

Glu Phe Thr Ala Ala Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu
130 135 140

Asn Met Ala Pro Leu Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val
145 150 155 160

Ala Ala Ala Leu Tyr Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala
165 170 175

Ala Leu Thr Leu Gly Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser
180 185 190

His Ser Asp Thr Ile Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser
195 200 205

Lys Arg Ala Asn Val Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser
210 215 220

Asn Gln Gly Ala Ser Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala
225 230 235 240

Gly Val Asp Tyr Val Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu
245 250 255

Ala Ala Leu Lys Gln Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln
260 265 270

Phe Ala Gln Ile Ser Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg
275 280 285

Val Cys Glu Val Leu Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His

290 295 300

Ala Val Thr Ala Arg Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn
305 310 315 320

Met Leu Arg Ser Thr Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala
325 330 335

Thr Asp Val Glu Val Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val
340 345 350

Pro Gly Val Ser Arg Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn
355 360 365

Leu Leu Leu Leu Glu Glu Ser His Leu Gly His Val Val Asp Pro Ala
370 375 380

Gly Gly Ser Tyr Phe Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys
385 390 395 400

Ala Trp Ala Val Phe Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala
405 410 415

Ala Cys Ala Ser Gly Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu
420 425 430

Gln Thr Arg Ala Asp Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile
435 440 445

Asn Glu Phe Pro Asn Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg
450 455 460

Val Glu Pro Ala Gly Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu
465 470 475 480

Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln
485 490 495

Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr
500 505 510

Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn
515 520 525

Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln
530 535 540

Ala Ala Gly Ile Val Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu
545 550 555 560

Thr Gly Glu Gly Ala Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg
565 570 575

Ile Leu Leu Ala Gly Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala
580 585 590

Pro Asp Gly Tyr Leu Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala
595 600 605

Asp Leu Leu Asp Ala Leu Gly Ala
610 615

US 9,580,486 B2

<210> 633
<211> 777
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(754)
<223> RXN00317

<400> 633
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gtctagccaa gccttgaaaa attctggcaa ggttaatggt gtg act acg cct tct 115
Val Thr Thr Pro Ser
1 5

aag aaa act ctg ctc ttt gat ctc gac gga acc ctc gtc gat tct ttc 163
Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe
10 15 20

ccc ggt atc cgc act tca ttc ctt cac acc ctg cac gaa aag aac tgg 211
Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu His Glu Lys Asn Trp
25 30 35

gaa atc ccc tct gag gaa cgc atc tcg caa gtt cca gga cct ccc atg 259
Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val Pro Gly Pro Pro Met
40 45 50

gaa tgg acg ttc cag gat ttg ggc atg act cca gag cag gca caa gac 307
Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro Glu Gln Ala Gln Asp
55 60 65

gct ctg cag acc tac ctt gag cat tac ggc cag gtg ggt tgg gat ctt 355
Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln Val Gly Trp Asp Leu
70 75 80 85

tcc gaa gca ttc ccc ggc atg cga gat ttg ctg atc cgc ttg aaa tac 403
Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Arg Leu Lys Tyr
90 95 100

gaa ggt ttc cgt ctg tgc acc gcc acc tcc aag ggc gag ttc ttt gcg 451
Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys Gly Glu Phe Phe Ala
105 110 115

gag aag gta ctt cgc aaa ttc gag atg ttc gat ctc ttc gaa ttc atg 499
Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp Leu Phe Glu Phe Met
120 125 130

ggt gcc gcc acc gac agc ggc aac cga cgc agc aaa tct gcc gtg atc 547
Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser Lys Ser Ala Val Ile
135 140 145

aaa cat gtc ctc gac agc gtt ggg ttg gac gaa cca aat gat att ttg 595
Lys His Val Leu Asp Ser Val Gly Leu Asp Glu Pro Asn Asp Ile Leu
150 155 160 165

atg att ggt gat cga tca cac gat att gaa ggt tcg agt gaa ttc ggc 643
Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly Ser Ser Glu Phe Gly

```
                170                 175                 180

atc gat tgt gtt gcc gta acc tgg ggc tac ggc agc aaa act gaa tgg   691
Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly Ser Lys Thr Glu Trp
            185                 190                 195

gac gct gcc cgc tac acc gtg agc acc gca gaa gaa tta gaa agg atc   739
Asp Ala Ala Arg Tyr Thr Val Ser Thr Ala Glu Glu Leu Glu Arg Ile
        200                 205                 210

atc cat gac tgg gcc taaaacttcg ctacctgtgg aaa                    777
Ile His Asp Trp Ala
    215
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<210> 634
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 634

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Val Thr Thr Pro Ser Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr
  1               5                  10                  15

Leu Val Asp Ser Phe Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu
             20                  25                  30

His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val
         35                  40                  45

Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro
     50                  55                  60

Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln
 65                  70                  75                  80

Val Gly Trp Asp Leu Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu
                 85                  90                  95

Ile Arg Leu Lys Tyr Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys
            100                 105                 110

Gly Glu Phe Phe Ala Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp
        115                 120                 125

Leu Phe Glu Phe Met Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser
    130                 135                 140

Lys Ser Ala Val Ile Lys His Val Leu Asp Ser Val Gly Leu Asp Glu
145                 150                 155                 160

Pro Asn Asp Ile Leu Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly
                165                 170                 175

Ser Ser Glu Phe Gly Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly
            180                 185                 190

Ser Lys Thr Glu Trp Asp Ala Ala Arg Tyr Thr Val Ser Thr Ala Glu
        195                 200                 205

Glu Leu Glu Arg Ile Ile His Asp Trp Ala
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210 215

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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(439)
<223> FRXA00317

<400> 635
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gtcaagccaa gccttgaaaa attctggcaa ggttaatggt gtg act acg cct tct 115
Val Thr Thr Pro Ser
1 5

aag aaa act ctg ctc ttt gat ctc gac gga acc ctc gtc gat tct ttc 163
Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe
10 15 20

ccc ggt atc cgc act tca ttc ctt cac acc ctg cac gaa aag aac tgg 211
Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu His Glu Lys Asn Trp
25 30 35

gaa atc ccc tct gag gaa cgc atc tcg caa gtt cca gga cct ccc atg 259
Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val Pro Gly Pro Pro Met
40 45 50

gaa tgg acg ttc cag gat ttg ggc atg act cca gag cag gca caa gac 307
Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro Glu Gln Ala Gln Asp
55 60 65

gct ctg cag acc tac ctt gag cat tac ggc cag gtg ggt tgg gat ctt 355
Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln Val Gly Trp Asp Leu
70 75 80 85

tcc gaa gca ttc ccc ggc atg cga gat ttg ctg atc ccc ttg ata tac 403
Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Pro Leu Ile Tyr
90 95 100

gaa ggt ttt cgt ctg tgc acc gcc acc ttt caa ggg 439
Glu Gly Phe Arg Leu Cys Thr Ala Thr Phe Gln Gly
105 110

<210> 636
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 636
Val Thr Thr Pro Ser Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr
1 5 10 15

Leu Val Asp Ser Phe Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu
20 25 30

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His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val
         35                  40                  45

Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro
     50                  55                  60

Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln
 65                  70                  75                  80

Val Gly Trp Asp Leu Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu
                 85                  90                  95

Ile Pro Leu Ile Tyr Glu Gly Phe Arg Leu Cys Thr Ala Thr Phe Gln
            100                 105                 110

Gly
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<210> 637
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXA02196

<400> 637

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tctaccaccc agaggcaaag tactttaacg tctaacacct ttgagaggga aaactttccc 60

gcacattgca gatcgtgcca ctttaactaa ggttgacggc atg att aag gcg att   115
                                          Met Ile Lys Ala Ile
                                            1               5

ttc tgg gac atg gac ggc acg atg gtg gac tct gag cca cag tgg ggc   163
Phe Trp Asp Met Asp Gly Thr Met Val Asp Ser Glu Pro Gln Trp Gly
                 10                  15                  20

att gct acc tac gag ctc agc gaa gcc atg ggc cgc cgc ctc acc ccg   211
Ile Ala Thr Tyr Glu Leu Ser Glu Ala Met Gly Arg Arg Leu Thr Pro
             25                  30                  35

gag ctc cgg gaa ctc acc gtc ggc tcg agc ctg ccg cgc acc atg cgc   259
Glu Leu Arg Glu Leu Thr Val Gly Ser Ser Leu Pro Arg Thr Met Arg
         40                  45                  50

tta tgc gca gag cac gca ggc att aca ttg agc gac gcg gac tac gag   307
Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser Asp Ala Asp Tyr Glu
     55                  60                  65

cgc tac cgg gct ggc atg ttc gcc cgg gtc cat gag ctt ttc gac gaa   355
Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His Glu Leu Phe Asp Glu
 70                  75                  80                  85

tcc ctc gtc cca aat cca ggc gtc acc gaa ctc ctg aca gag ttg aag   403
Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu Leu Thr Glu Leu Lys
                 90                  95                 100

gcc ctc gag atc ccc atg ttg gtc acc acc aac aca gag cgc gat ctc   451
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```
Ala Leu Glu Ile Pro Met Leu Val Thr Thr Asn Thr Glu Arg Asp Leu
            105                 110                 115

gcg acc cgt tca gtc gca gcc gtg gga aat gag ttc ttc atc ggt tct   499
Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu Phe Phe Ile Gly Ser
        120                 125                 130

atc gct ggt gat gaa gtc cca aca gca aag cca gcc ccc gac atg tac   547
Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro Ala Pro Asp Met Tyr
    135                 140                 145

ctc gaa gca gca cga cgt gtg ggc ttt gac cca tca gag tgc ctc gtg   595
Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro Ser Glu Cys Leu Val
150                 155                 160                 165

ttc gaa gat tcc tac aac ggc atg ctg ggc gct gtt act gca ggt tgc   643
Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala Val Thr Ala Gly Cys
                170                 175                 180

cgc gtc att ggt ctg cac cca gaa gaa gtc caa gcg cca gaa ggt gta   691
Arg Val Ile Gly Leu His Pro Glu Glu Val Gln Ala Pro Glu Gly Val
            185                 190                 195

gtg cct ttg cgt tcc ctc cac ggt aaa aac tct ttc gaa ggt gtc acc   739
Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser Phe Glu Gly Val Thr
        200                 205                 210

gct gag atg gtc act gcc tgg tac cac cag atc gag ccg gca ggt gtc   787
Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile Glu Pro Ala Gly Val
    215                 220                 225

gca aaa taaaaccagg tgggggagtg aaa                                 816
Ala Lys
230
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09025160

<210> 638
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 638

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Met Ile Lys Ala Ile Phe Trp Asp Met Asp Gly Thr Met Val Asp Ser
  1               5                  10                  15

Glu Pro Gln Trp Gly Ile Ala Thr Tyr Glu Leu Ser Glu Ala Met Gly
             20                  25                  30

Arg Arg Leu Thr Pro Glu Leu Arg Glu Leu Thr Val Gly Ser Ser Leu
         35                  40                  45

Pro Arg Thr Met Arg Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser
     50                  55                  60

Asp Ala Asp Tyr Glu Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His
 65                  70                  75                  80

Glu Leu Phe Asp Glu Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu
                 85                  90                  95

Leu Thr Glu Leu Lys Ala Leu Glu Ile Pro Met Leu Val Thr Thr Asn
```

```
            100                 105                 110

Thr Glu Arg Asp Leu Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu
        115                 120                 125

Phe Phe Ile Gly Ser Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro
    130                 135                 140

Ala Pro Asp Met Tyr Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro
145                 150                 155                 160

Ser Glu Cys Leu Val Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala
                165                 170                 175

Val Thr Ala Gly Cys Arg Val Ile Gly Leu His Pro Glu Glu Val Gln
            180                 185                 190

Ala Pro Glu Gly Val Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser
        195                 200                 205

Phe Glu Gly Val Thr Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile
    210                 215                 220

Glu Pro Ala Gly Val Ala Lys
225                 230


<210> 639
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXN02461

<400> 639
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acgactatta tgtcacgaag aaaccaaaga aagggaaata atg cgc gga cta att   115
                                              Met Arg Gly Leu Ile
                                                1               5

gtt gac tac gct gga gta cta gac gga acc gat gag gac cag cgt cgc   163
Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp Glu Asp Gln Arg Arg
                  10                  15                  20

tgg cgc aac ctg ctc gcc gca gca aag aaa aat ggc gtc gga acc gtg   211
Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn Gly Val Gly Thr Val
              25                  30                  35

atc ctc agc aac gat cca ggt ggg ctc ggc gca gcg ccg atc cgg gaa   259
Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu
          40                  45                  50

ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt   307
Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu
      55                  60                  65

ggc gtc gaa aag cca gag gaa gca gct ttc cag gcc gcc gca gac gcc   355
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Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln Ala Ala Ala Asp Ala
 70                  75                  80                  85

atc gac ctg ccc atg cgt gac tgc gtg ctt gtc gac gac tcg atc ctc   403
Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val Asp Asp Ser Ile Leu
                 90                  95                 100

aac gtg cgc ggc gcc gtc gaa gcc gga ctc gta ggc gtc tac tac cag   451
Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val Gly Val Tyr Tyr Gln
            105                 110                 115

caa ttt gac cgt gca gtc gtc gaa atc gtc gga ctg ttc ggg cta gaa   499
Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly Leu Phe Gly Leu Glu
        120                 125                 130

gga gaa ttc taatcttgcg cgtctacatc cca                            531
Gly Glu Phe
    135


<210> 640
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 640
Met Arg Gly Leu Ile Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp
  1               5                  10                  15

Glu Asp Gln Arg Arg Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn
             20                  25                  30

Gly Val Gly Thr Val Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala
         35                  40                  45

Ala Pro Ile Arg Glu Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu
     50                  55                  60

Leu Ser Gly Glu Leu Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln
 65                  70                  75                  80

Ala Ala Ala Asp Ala Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val
                 85                  90                  95

Asp Asp Ser Ile Leu Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val
            100                 105                 110

Gly Val Tyr Tyr Gln Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly
        115                 120                 125

Leu Phe Gly Leu Glu Gly Glu Phe
    130                 135


<210> 641
<211> 1662
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
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<222> (101)..(1639)
<223> RXN01744

<400> 641
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gttcctgtca acctgcaatg gaagaggaag tgtacctagc gtg gat gtc gtc gac 115
Val Asp Val Val Asp
1 5

atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt 163
Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe
10 15 20

gtc cca ctg acc att ggc tta gcg ccg ctg gtc gca atc atg caa acg 211
Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr
25 30 35

ttt tgg caa gtt acc ggc aaa gag cac tgg tat cgg gcc aca aga ttt 259
Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr Arg Ala Thr Arg Phe
40 45 50

ttt ggc act gtg ctg ctc atc aac ttc gcg gtt ggt gta gca acg ggc 307
Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val Gly Val Ala Thr Gly
55 60 65

att gtg cag gag ttc cag ttc ggt atg aac tgg tcg gaa tat tcg cgt 355
Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp Ser Glu Tyr Ser Arg
70 75 80 85

ttc gtc ggt gat gtt ttc ggc gga ccg ctg gct ttg gag ggt ctt atc 403
Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala Leu Glu Gly Leu Ile
90 95 100

gcg ttc ttc ctt gag tct gta ttc ctg gga ctg tgg att ttc gga tgg 451
Ala Phe Phe Leu Glu Ser Val Phe Leu Gly Leu Trp Ile Phe Gly Trp
105 110 115

ggg aag att cct ggt tgg ttg cac act gca tcc att tgg atc gtt gct 499
Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser Ile Trp Ile Val Ala
120 125 130

att gcg acg aat att tct gcc tat ttc atc atc gtg gcc aac tcg ttt 547
Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile Val Ala Asn Ser Phe
135 140 145

atg cag cat ccg gtg ggt gct gag tat aac cct gag act ggt cgt gcg 595
Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro Glu Thr Gly Arg Ala
150 155 160 165

gag ctt act gat ttt tgg gct ctt ctc aca aac tcc acc gcg ctg gct 643
Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr Asn Ser Thr Ala Leu Ala
170 175 180

gcg ttc ccg cat gct gtt gcc ggt ggt ttt tta aca gct gga act ttc 691
Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu Thr Ala Gly Thr Phe
185 190 195

gtt ctc gga att tcg ggt tgg tgg att att cgt gcg cac cgt cag gcc 739
Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg Ala His Arg Gln Ala
200 205 210

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aag aag gct gag tcg gaa atc gag tcg aag cat tcg atg cac agg ccc   787
Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His Ser Met His Arg Pro
    215                 220                 225

gcg ttg tgg gtt ggt tgg tgg acc aca gtt gtc tct tcc gtg gcg ctg   835
Ala Leu Trp Val Gly Trp Trp Thr Thr Val Val Ser Ser Val Ala Leu
230                 235                 240                 245

ttc atc act ggc gat atc cag gcg aag ctc atg ttc gtg caa cag cca   883
Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu Met Phe Val Gln Gln Pro
                250                 255                 260

atg aag atg gcg tcg gcg gaa tcc ttg tgt gaa acc gcc aca gat cca   931
Met Lys Met Ala Ser Ala Glu Ser Leu Cys Glu Thr Ala Thr Asp Pro
            265                 270                 275

aac ttc tcc att ctg aca att ggt acg cac aac aac tgc gat acg gta   979
Asn Phe Ser Ile Leu Thr Ile Gly Thr His Asn Asn Cys Asp Thr Val
        280                 285                 290

acc cac ctg atc gat gtt ccg ttt gtg ctt cca ttc ttg gct gaa gga   1027
Thr His Leu Ile Asp Val Pro Phe Val Leu Pro Phe Leu Ala Glu Gly
    295                 300                 305

aaa ttc acc ggt gtg act ttg cag ggt gta aac cag ctc caa gct gca   1075
Lys Phe Thr Gly Val Thr Leu Gln Gly Val Asn Gln Leu Gln Ala Ala
310                 315                 320                 325

gcg gag caa gca tac ggt cct ggc aac tac tcc cct aac ttg ttt gtc   1123
Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr Ser Pro Asn Leu Phe Val
                330                 335                 340

acc tac tgg tca ttc cgc gca atg atc ggc ctg atg ctt ggt tct ttg   1171
Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu Met Leu Gly Ser Leu
            345                 350                 355

gct atc gct gcg att gcg tgg ctg ttg ctg cgt aag aag cgc aca cca   1219
Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg Lys Lys Arg Thr Pro
        360                 365                 370

act gga aag att gct cgt ctg ttc cag atc ggc agc ctc att gct atc   1267
Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly Ser Leu Ile Ala Ile
    375                 380                 385

ccg ttc cca ttc ttg gcc aac tct gct ggt tgg atc ttc acc gag atg   1315
Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp Ile Phe Thr Glu Met
390                 395                 400                 405

ggc cgc cag cct tgg gtg gtg cac ccg aac cct gaa tct gcc ggc gat   1363
Gly Arg Gln Pro Trp Val Val His Pro Asn Pro Glu Ser Ala Gly Asp
                410                 415                 420

gcc cga aca gag atg atc cgg atg act gtt gat atg ggt gta tct gat   1411
Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp Met Gly Val Ser Asp
            425                 430                 435

cat gcg cca tgg caa gtc tgg ctg act ctc att ggc ttc acg att ctc   1459
His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile Gly Phe Thr Ile Leu
        440                 445                 450
```

```
tat ctc att ttg ttc gtg gtg tgg gtg tgg ctg att cgc cgc gca gtt   1507
Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu Ile Arg Arg Ala Val
    455                 460                 465

ctg atc gga cca cca gag gaa ggc gct cca tcc gtg gag gca aag act   1555
Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser Val Glu Ala Lys Thr
470                 475                 480                 485

gga ccg gca acc ccg att ggt tca gat atg ccc atg aca ccg ctg caa   1603
Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro Met Thr Pro Leu Gln
                490                 495                 500

ttt act gcc gct gcc cca acc aca ggt gaa aag gaa taaccatgga        1649
Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys Glu
            505                 510

tctcaatacc ttt                                                   1662
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<210> 642
<211> 513
<212> PRT
<213> Corynebacterium glutamicum

<400> 642

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Val Asp Val Val Asp Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val
  1               5                  10                  15

Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val
            20                  25                  30

Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr
        35                  40                  45

Arg Ala Thr Arg Phe Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val
    50                  55                  60

Gly Val Ala Thr Gly Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp
65                  70                  75                  80

Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala
                85                  90                  95

Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly Leu
            100                 105                 110

Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser
        115                 120                 125

Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile
    130                 135                 140

Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro
145                 150                 155                 160

Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr Asn
                165                 170                 175

Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu
            180                 185                 190
```

```
Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg
        195                 200                 205

Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His
    210                 215                 220

Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val Val
225                 230                 235                 240

Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu Met
                245                 250                 255

Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys Glu
            260                 265                 270

Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His Asn
        275                 280                 285

Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu Pro
    290                 295                 300

Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val Asn
305                 310                 315                 320

Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr Ser
                325                 330                 335

Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu
            340                 345                 350

Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg
        355                 360                 365

Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly
    370                 375                 380

Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp
385                 390                 395                 400

Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn Pro
                405                 410                 415

Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp
            420                 425                 430

Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile
        435                 440                 445

Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu
    450                 455                 460

Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser
465                 470                 475                 480

Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro
                485                 490                 495

Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys
            500                 505                 510

Glu
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<210> 643
<211> 238
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(238)
<223> FRXA00055

<400> 643
tcttattggt tcttcgtttt gtatcgataa atacaatcgg tttcctggct taataaggct 60

gttcctgtca acctgcaatg gaagaggaag tgtacctagc gtg gat gtc gtc gac 115
Val Asp Val Val Asp
1 5

atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt 163
Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe
10 15 20

gtc cca ctg acc att ggc tta gca ccg ctg gtc gcg atc atg caa acg 211
Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr
25 30 35

ttt tgg caa gtt acc ggc aaa gag cac 238
Phe Trp Gln Val Thr Gly Lys Glu His
40 45

<210> 644
<211> 46
<212> PRT
<213> Corynebacterium glutamicum

<400> 644
Val Asp Val Val Asp Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val
1 5 10 15

Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val
20 25 30

Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His
35 40 45

<210> 645
<211> 1325
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1302)
<223> FRXA01744

<400> 645
tgg tcg gaa tat tcg cgt ttc gtc ggt gat gtt ttc ggc gga ccg ctg 48

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Trp Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu
  1               5                  10                  15

gct ttg gag ggt ctt atc gcg ttc ttc ctt gag tct gta ttc ctg gga   96
Ala Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly
            20                  25                  30

ctg tgg att ttc gga tgg ggg aag att cct ggt tgg ttg cac act gca   144
Leu Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala
        35                  40                  45

tcc att tgg atc gtt gct att gcg acg aat att tct gcc tat ttc atc   192
Ser Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile
    50                  55                  60

atc gtg gcc aac tcg ttt atg cag cat ccg gtg ggt gct gag tat aac   240
Ile Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn
65                  70                  75                  80

cct gag act ggt cgt gcg gag ctt act gat ttt tgg gct ctt ctc aca   288
Pro Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr
                85                  90                  95

aac tcc acc gcg ctg gct gcg ttc ccg cat gct gtt gcc ggt ggt ttt   336
Asn Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe
            100                 105                 110

tta aca gct gga act ttc gtt ctc gga att tcg ggt tgg tgg att att   384
Leu Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile
        115                 120                 125

cgt gcg cac cgt cag gcc aag aag gct gag tcg gaa atc gag tcg aag   432
Arg Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys
    130                 135                 140

cat tcg atg cac agg ccc gcg ttg tgg gtt ggt tgg tgg acc aca gtt   480
His Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val
145                 150                 155                 160

gtc tct tcc gtg gcg ctg ttc atc act ggc gat atc cag gcg aag ctc   528
Val Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu
                165                 170                 175

atg ttc gtg caa cag cca atg aag atg gcg tcg gcg gaa tcc ttg tgt   576
Met Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys
            180                 185                 190

gaa acc gcc aca gat cca aac ttc tcc att ctg aca att ggt acg cac   624
Glu Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His
        195                 200                 205

aac aac tgc gat acg gta acc cac ctg atc gat gtt ccg ttt gtg ctt   672
Asn Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu
    210                 215                 220

cca ttc ttg gct gaa gga aaa ttc acc ggt gtg act ttg cag ggt gta   720
Pro Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val
225                 230                 235                 240

aac cag ctc caa gct gca gcg gag caa gca tac ggt cct ggc aac tac   768
Asn Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr
```

```
                245                 250                 255

tcc cct aac ttg ttt gtc acc tac tgg tca ttc cgc gca atg atc ggc   816
Ser Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly
            260                 265                 270

ctg atg ctt ggt tct ttg gct atc gct gcg att gcg tgg ctg ttg ctg   864
Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu
        275                 280                 285

cgt aag aag cgc aca cca act gga aag att gct cgt ctg ttc cag atc   912
Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile
    290                 295                 300

ggc agc ctc att gct atc ccg ttc cca ttc ttg gcc aac tct gct ggt   960
Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly
305                 310                 315                 320

tgg atc ttc acc gag atg ggc cgc cag cct tgg gtg gtg cac ccg aac   1008
Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn
                325                 330                 335

cct gaa tct gcc ggc gat gcc cga aca gag atg atc cgg atg act gtt   1056
Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val
            340                 345                 350

gat atg ggt gta tct gat cat gcg cca tgg caa gtc tgg ctg act ctc   1104
Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu
        355                 360                 365

att ggc ttc acg att ctc tat ctc att ttg ttc gtg gtg tgg gtg tgg   1152
Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp
    370                 375                 380

ctg att cgc cgc gca gtt ctg atc gga cca cca gag gaa ggc gct cca   1200
Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro
385                 390                 395                 400

tcc gtg gag gca aag act gga ccg gca acc ccg att ggt tca gat atg   1248
Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met
                405                 410                 415

ccc atg aca ccg ctg caa ttt act gcc gct gcc cca acc aca ggt gaa   1296
Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu
            420                 425                 430

aag gaa taaccatgga tctcaatacc ttt                                1325
Lys Glu
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<210> 646
<211> 434
<212> PRT
<213> Corynebacterium glutamicum

<400> 646

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Trp Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu
  1               5                  10                  15

Ala Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly
```

```
                20                  25                  30

Leu Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala
          35                  40                  45

Ser Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile
     50                  55                  60

Ile Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn
 65                  70                  75                  80

Pro Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr
                85                  90                  95

Asn Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe
           100                 105                 110

Leu Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile
      115                 120                 125

Arg Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys
 130                 135                 140

His Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val
145                 150                 155                 160

Val Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu
                165                 170                 175

Met Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys
           180                 185                 190

Glu Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His
      195                 200                 205

Asn Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu
 210                 215                 220

Pro Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val
225                 230                 235                 240

Asn Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr
                245                 250                 255

Ser Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly
           260                 265                 270

Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu
      275                 280                 285

Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile
 290                 295                 300

Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly
305                 310                 315                 320

Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn
                325                 330                 335

Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val
           340                 345                 350
```

```
Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu
        355                 360                 365

Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp
    370                 375                 380

Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro
385                 390                 395                 400

Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met
                405                 410                 415

Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu
            420                 425                 430

Lys Glu
```

09825140.1

<210> 647
<211> 307
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(307)
<223> RXA00379

<400> 647
cgtgctggat aaacagcacc gccccgcagc agtgttcttg cgcgaagtca cctccaaaga 60

tgtgttggat gttgcgttgc cattggtaga tgaggcctaa atg tct gag att gtg 115
                                        Met Ser Glu Ile Val
                                          1   5

gta gcc caa agc atc ggc cag cag ttt gct gac gtc gca gct tcc ggg 163
Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp Val Ala Ala Ser Gly
                10   15   20

cca ctg ttc ctt ggc atc ctt gcc gca gcg ctc gca ggt ctg gtg tct 211
Pro Leu Phe Leu Gly Ile Leu Ala Ala Ala Leu Ala Gly Leu Val Ser
            25   30   35

ttt gcc agc ccg tgt gtt gtg ccg ttg gtg cca gga tat att tcc tac 259
Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro Gly Tyr Ile Ser Tyr
        40   45   50

ctc gcc ggc gtg gtc ggt ggg gaa gtg gaa tac agc gct cat gcc acc 307
Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr Ser Ala His Ala Thr
    55   60   65

<210> 648
<211> 69
<212> PRT
<213> Corynebacterium glutamicum

<400> 648
Met Ser Glu Ile Val Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp
```
```

```
  1               5                  10                  15

Val Ala Ala Ser Gly Pro Leu Phe Leu Gly Ile Leu Ala Ala Ala Leu
             20                  25                  30

Ala Gly Leu Val Ser Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro
         35                  40                  45

Gly Tyr Ile Ser Tyr Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr
     50                  55                  60

Ser Ala His Ala Thr
 65
```

<210> 649
<211> 362
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(339)
<223> RXA00385

<400> 649

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ctt ggc gga gtg ttc gct ctc ggt tgg acc cct tgt ttg ggc ccc acc   48
Leu Gly Gly Val Phe Ala Leu Gly Trp Thr Pro Cys Leu Gly Pro Thr
  1               5                  10                  15

ctg gct gcg atc atc tcc att tct gca ggt act gaa ggc atg acc gct   96
Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala
             20                  25                  30

gcg cgt ggc gtg atc tta att gtg ggt tac tgc ctc gga ctg ggg ctg   144
Ala Arg Gly Val Ile Leu Ile Val Gly Tyr Cys Leu Gly Leu Gly Leu
         35                  40                  45

ccg ttc ctg ctg atc gcg ttg ggc tcc agc aag gca ctc acc gga gtc   192
Pro Phe Leu Leu Ile Ala Leu Gly Ser Ser Lys Ala Leu Thr Gly Val
     50                  55                  60

gag tgg ttg cgc aag cat tcc cgc acc ctg caa att atc ggc ggt gtg   240
Glu Trp Leu Arg Lys His Ser Arg Thr Leu Gln Ile Ile Gly Gly Val
 65                  70                  75                  80

ttt ttg atc ttg gtc gga gta gcg ttg ctc tct ggc tca tgg gca att   288
Phe Leu Ile Leu Val Gly Val Ala Leu Leu Ser Gly Ser Trp Ala Ile
                 85                  90                  95

ttt atc aac tgg gtc cgt cag tgg acc gtt gaa tac ggc gca aca ctg   336
Phe Ile Asn Trp Val Arg Gln Trp Thr Val Glu Tyr Gly Ala Thr Leu
            100                 105                 110

ctc tagaaaaaga cttttagtag gaa                                    362
Leu
```

<210> 650
<211> 113

<212> PRT
<213> Corynebacterium glutamicum

<400> 650

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Leu Gly Gly Val Phe Ala Leu Gly Trp Thr Pro Cys Leu Gly Pro Thr
  1               5                  10                  15

Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala
             20                  25                  30

Ala Arg Gly Val Ile Leu Ile Val Gly Tyr Cys Leu Gly Leu Gly Leu
         35                  40                  45

Pro Phe Leu Leu Ile Ala Leu Gly Ser Ser Lys Ala Leu Thr Gly Val
     50                  55                  60

Glu Trp Leu Arg Lys His Ser Arg Thr Leu Gln Ile Ile Gly Gly Val
 65                  70                  75                  80

Phe Leu Ile Leu Val Gly Val Ala Leu Leu Ser Gly Ser Trp Ala Ile
                 85                  90                  95

Phe Ile Asn Trp Val Arg Gln Trp Thr Val Glu Tyr Gly Ala Thr Leu
            100                 105                 110

Leu
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<210> 651
<211> 901
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(901)
<223> RXA01743

<400> 651

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aggcaaagac tggaccggca accccgattg gttcagatat gcccatgaca ccgctgcaat 60

ttactgccgc tgccccaacc acaggtgaaa aggaataacc atg gat ctc aat acc   115
                                            Met Asp Leu Asn Thr
                                              1               5

ttt tgg ttt att ctc atc gca ttt ttg ttt gcg gga tac ttt ctc ctc   163
Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala Gly Tyr Phe Leu Leu
                 10                  15                  20

gaa gga ttc gac ttc ggc gtc gga att ttg gca ccc atc atc ggt aaa   211
Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala Pro Ile Ile Gly Lys
             25                  30                  35

gat tca gcg gct agg aac aca gtg atc cgt acg att ggc cct gtc tgg   259
Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr Ile Gly Pro Val Trp
         40                  45                  50

gac gga aat gaa gtg tgg ctg atc gtg gca ggt ggc gct ttg ttt gct   307
Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly Gly Ala Leu Phe Ala
     55                  60                  65
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gcc ttc cct gag tgg tac gca acg atg ttc tcc gga atg tat ctg ccg   355
Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser Gly Met Tyr Leu Pro
 70                  75                  80                  85

ctg ttc ctc gtg ctt gtg tcg ttg atc atg cgc gtg gtg ggc ctt gaa   403
Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg Val Val Gly Leu Glu
                90                  95                 100

tgg cgc aag aaa gtc gat gat cct cgt tgg caa aag tgg tct gac cgg   451
Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln Lys Trp Ser Asp Arg
            105                 110                 115

gcc atc ttt att ggt tct tgg act cca ccg ctg atg tgg gga ttc atc   499
Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu Met Trp Gly Phe Ile
        120                 125                 130

ttc gcc aat att ttg cgt ggc atg ccc ctc aag gcg gat cac acc atc   547
Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys Ala Asp His Thr Ile
    135                 140                 145

gat gct gcg gca gcc ctt cct ggc atg gtc aac gtc ttc gcc att ctg   595
Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn Val Phe Ala Ile Leu
150                 155                 160                 165

ggt gca ctt gcg ttc acc gca ctg ttc gcc ctt cat ggt ctc gca ttc   643
Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu His Gly Leu Ala Phe
                170                 175                 180

atc cgc ctg aaa act gct ggt cgg gtg cgc acc gat gcg gcg aag gca   691
Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr Asp Ala Ala Lys Ala
            185                 190                 195

gct cca gta gtc gca ctt ctt gct gcg gtg act ggt gga cct ttc gtg   739
Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr Gly Gly Pro Phe Val
        200                 205                 210

ttg tgg gct gcc atc gca tac ggc cgt tcc tgg tcc tgg atc ctc gca   787
Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp Ser Trp Ile Leu Ala
    215                 220                 225

gtg ctg atc atc gca gcg gtt ctc ggt gga gct ttc gca ctg atc aaa   835
Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala Phe Ala Leu Ile Lys
230                 235                 240                 245

gac cgc gat gga tta agc ttc ctg tcc act tcc gtc gct gtc atc ggt   883
Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser Val Ala Val Ile Gly
                250                 255                 260

gtc gtt gca ctg ctg ttt                                          901
Val Val Ala Leu Leu Phe
            265
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<210> 652
<211> 267
<212> PRT
<213> Corynebacterium glutamicum

<400> 652
Met Asp Leu Asn Thr Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala

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  1               5                  10                  15

Gly Tyr Phe Leu Leu Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala
            20                  25                  30

Pro Ile Ile Gly Lys Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr
        35                  40                  45

Ile Gly Pro Val Trp Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly
    50                  55                  60

Gly Ala Leu Phe Ala Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser
65                  70                  75                  80

Gly Met Tyr Leu Pro Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg
                85                  90                  95

Val Val Gly Leu Glu Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln
            100                 105                 110

Lys Trp Ser Asp Arg Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu
        115                 120                 125

Met Trp Gly Phe Ile Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys
    130                 135                 140

Ala Asp His Thr Ile Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn
145                 150                 155                 160

Val Phe Ala Ile Leu Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu
                165                 170                 175

His Gly Leu Ala Phe Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr
            180                 185                 190

Asp Ala Ala Lys Ala Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr
        195                 200                 205

Gly Gly Pro Phe Val Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp
    210                 215                 220

Ser Trp Ile Leu Ala Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala
225                 230                 235                 240

Phe Ala Leu Ile Lys Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser
                245                 250                 255

Val Ala Val Ile Gly Val Val Ala Leu Leu Phe
            260                 265
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<210> 653
<211> 1779
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1756)
<223> RXN02480

<400> 653
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gacaggccat gcacgcaagg gcagcaaagc atggttaatg atg acc acc acc gac 115
Met Thr Thr Thr Asp
1 5

cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttc 163
His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe
10 15 20

ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc 211
Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr
25 30 35

cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc 259
Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr
40 45 50

atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg 307
Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp
55 60 65

ggt ttt gct aac tac gtc ctg cca ctt cag atc ggt gcg cct gac gta 355
Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile Gly Ala Pro Asp Val
70 75 80 85

gct ttc cca cgt ttg aat gct ttc ggc ttc tgg atc acc acc gtc ggt 403
Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp Ile Thr Thr Val Gly
90 95 100

ggt gtc gcg atg ctg acc ggc ttc ctg acc ccg ggt ggt gct gcc gac 451
Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro Gly Gly Ala Ala Asp
105 110 115

ttc ggt tgg acc atg tac tcc cca ctg tct gac gca att cac tcc cca 499
Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp Ala Ile His Ser Pro
120 125 130

ggc ctt ggc tct gac atg tgg att gtc ggt gtc ggt gca act ggt att 547
Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val Gly Ala Thr Gly Ile
135 140 145

ggc tcc gtt gct tcc gca att aac atg ctc acc acc atc ctc tgc ctc 595
Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr Thr Ile Leu Cys Leu
150 155 160 165

cgc gca cct ggt atg acc atg ttc cgt atg cct att ttc acc tgg aat 643
Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn
170 175 180

atc ttc gtt gtt tcc gtt ctt gct ctg ctg atc ttc cca ctg ctg ctc 691
Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu
185 190 195

gct gct gca ctg ggt gtt ctg tat gac cgc aag ctt ggt gga cac ctg 739
Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu
200 205 210

tac gat cca gct aac ggc ggc tcc ctc ctg tgg cag cac ctg ttc tgg 787
Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp

<400> 653
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gacaggccat gcacgcaagg gcagcaaagc atggttaatg atg acc acc acc gac 115
Met Thr Thr Thr Asp
1 5

cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttc 163
His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe
10 15 20

ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc 211
Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr
25 30 35

cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc 259
Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr
40 45 50

atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg 307
Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp
55 60 65

ggt ttt gct aac tac gtc ctg cca ctt cag atc ggt gcg cct gac gta 355
Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile Gly Ala Pro Asp Val
70 75 80 85

gct ttc cca cgt ttg aat gct ttc ggc ttc tgg atc acc acc gtc ggt 403
Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp Ile Thr Thr Val Gly
90 95 100

ggt gtc gcg atg ctg acc ggc ttc ctg acc ccg ggt ggt gct gcc gac 451
Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro Gly Gly Ala Ala Asp
105 110 115

ttc ggt tgg acc atg tac tcc cca ctg tct gac gca att cac tcc cca 499
Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp Ala Ile His Ser Pro
120 125 130

ggc ctt ggc tct gac atg tgg att gtc ggt gtc ggt gca act ggt att 547
Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val Gly Ala Thr Gly Ile
135 140 145

ggc tcc gtt gct tcc gca att aac atg ctc acc acc atc ctc tgc ctc 595
Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr Thr Ile Leu Cys Leu
150 155 160 165

cgc gca cct ggt atg acc atg ttc cgt atg cct att ttc acc tgg aat 643
Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn
170 175 180

atc ttc gtt gtt tcc gtt ctt gct ctg ctg atc ttc cca ctg ctg ctc 691
Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu
185 190 195

gct gct gca ctg ggt gtt ctg tat gac cgc aag ctt ggt gga cac ctg 739
Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu
200 205 210

tac gat cca gct aac ggc ggc tcc ctc ctg tgg cag cac ctg ttc tgg 787
Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp

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    215                 220                 225

ttc ttc gga cac cct gag gtt tac gtt ctg gcg ctg ccg ttc ttc ggc   835
Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly
230                 235                 240                 245

att gtt tct gag atc att cct gtg ttc tcc cgt aag cca atg ttc ggt   883
Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly
                250                 255                 260

tac gtc ggc ctg atc ttc gca acc ttg tcc att ggt gca ctg tcc atg   931
Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile Gly Ala Leu Ser Met
            265                 270                 275

gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt ttg ctt ccg   979
Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val Leu Leu Pro
        280                 285                 290

ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc ggc gtt aag   1027
Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr Gly Val Lys
    295                 300                 305

ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc act tgg gaa   1075
Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile Thr Trp Glu
310                 315                 320                 325

acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc ctc ttc ggt   1123
Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe Leu Phe Gly
                330                 335                 340

ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac ttc cac ttg   1171
Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp Phe His Leu
            345                 350                 355

gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc ctc ttc ggt   1219
Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr Leu Phe Gly
        360                 365                 370

acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg ttc ccg aag   1267
Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp Phe Pro Lys
    375                 380                 385

atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc cac ttc tgg   1315
Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile His Phe Trp
390                 395                 400                 405

ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag cac tgg gtg   1363
Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln His Trp Val
                410                 415                 420

ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg gat tct gat   1411
Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu Asp Ser Asp
            425                 430                 435

ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac ttc ctg ctt   1459
Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr Phe Leu Leu
        440                 445                 450

ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag tcc tgg cgc   1507
Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys Ser Trp Arg
    455                 460                 465
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tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac ggc aac tcc   1555
Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr Gly Asn Ser
470                 475                 480                 485

ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac ttc gca tcc   1603
Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn Phe Ala Ser
                490                 495                 500

ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg cac tac ccg   1651
Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu His Tyr Pro
            505                 510                 515

cac atg att gaa cgc atg cgc gca gag gca cac act gga cat cac gat   1699
His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly His His Asp
        520                 525                 530

gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt gca tct gac   1747
Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu Ala Ser Asp
    535                 540                 545

tcc agc cgc taaaagcgtc tgatttaagt cgg                            1779
Ser Ser Arg
550
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<210> 654
<211> 552
<212> PRT
<213> Corynebacterium glutamicum

<400> 654

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Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met
  1               5                  10                  15

Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg
            20                  25                  30

Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe
        35                  40                  45

Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly
    50                  55                  60

Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile
65                  70                  75                  80

Gly Ala Pro Asp Val Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp
                85                  90                  95

Ile Thr Thr Val Gly Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro
            100                 105                 110

Gly Gly Ala Ala Asp Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp
        115                 120                 125

Ala Ile His Ser Pro Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val
    130                 135                 140

Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr
145                 150                 155                 160
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Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro
165 170 175

Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile
180 185 190

Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys
195 200 205

Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp
210 215 220

Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala
225 230 235 240

Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg
245 250 255

Lys Pro Met Phe Gly Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile
260 265 270

Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly
275 280 285

Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val
290 295 300

Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly
305 310 315 320

His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala
325 330 335

Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro
340 345 350

Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His
355 360 365

Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr
370 375 380

Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly
385 390 395 400

Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu
405 410 415

Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp
420 425 430

Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val
435 440 445

Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val
450 455 460

Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp
465 470 475 480

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Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg
                485                 490                 495

His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe
            500                 505                 510

Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His
        515                 520                 525

Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro
    530                 535                 540

Ala Leu Ala Ser Asp Ser Ser Arg
545                 550
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<210> 655
<211> 385
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA01919

<400> 655
acctatgacc gctgtggcgc ctagggtcga cgggcacgtc gcccctcaga ggcccgagcc 60

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gacaggccat gcacgcaagg gcagcaaagc atggttaatg atg acc acc acc gac   115
                                            Met Thr Thr Thr Asp
                                              1               5

cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttt   163
His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe
                10                  15                  20

ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc   211
Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr
            25                  30                  35

cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc   259
Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr
        40                  45                  50

atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg   307
Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp
    55                  60                  65

ggt ttt gct aac tac gtc ctg cca ctt cca acc acc ang caa gcc ttc   355
Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr Thr Xaa Gln Ala Phe
70                  75                  80                  85

tct aaa acc cgg gtg aac tct ccc agg gag                          385
Ser Lys Thr Arg Val Asn Ser Pro Arg Glu
                90                  95
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<210> 656
<211> 95
<212> PRT

<213> Corynebacterium glutamicum

<400> 656
Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met
1 5 10 15

Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg
20 25 30

Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe
35 40 45

Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly
50 55 60

Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr
65 70 75 80

Thr Xaa Gln Ala Phe Ser Lys Thr Arg Val Asn Ser Pro Arg Glu
85 90 95

<210> 657
<211> 972
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(949)
<223> FRXA02480

<400> 657
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aagccaatgt tcgggttacg tcggcctgat cttcgcaacc ttg tcc att ggt gca 115
Leu Ser Ile Gly Ala
1 5

ctg tcc atg gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt 163
Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val
10 15 20

ttg ctt ccg ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc 211
Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr
25 30 35

ggc gtt aag ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc 259
Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile
40 45 50

act tgg gaa acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc 307
Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe
55 60 65

ctc ttc ggt ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac 355
Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp
70 75 80 85

ttc cac ttg gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc 403
Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr

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                90                  95                 100

ctc ttc ggt acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg   451
Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp
            105                 110                 115

ttc ccg aag atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc   499
Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile
        120                 125                 130

cac ttc tgg ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag   547
His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln
    135                 140                 145

cac tgg gtg ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg   595
His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu
150                 155                 160                 165

gat tct gat ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac   643
Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr
                170                 175                 180

ttc ctg ctt ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag   691
Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys
            185                 190                 195

tcc tgg cgc tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac   739
Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr
        200                 205                 210

ggc aac tcc ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac   787
Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn
    215                 220                 225

ttc gca tcc ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg   835
Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu
230                 235                 240                 245

cac tac ccg cac atg att gaa cgc atg cgc gca gag gca cac act gga   883
His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly
                250                 255                 260

cat cac gat gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt   931
His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu
            265                 270                 275

gca tct gac tcc agc cgc taaaagcgtc tgatttaagt cgg                 972
Ala Ser Asp Ser Ser Arg
        280
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<210> 658
<211> 283
<212> PRT
<213> Corynebacterium glutamicum

<400> 658

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Leu Ser Ile Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe
  1               5                  10                  15

Val Thr Gly Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu
```

```
            20                  25                  30

Ile Ser Val Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met
        35                  40                  45

Trp Lys Gly His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly
    50                  55                  60

Phe Met Ala Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala
65                  70                  75                  80

Ser Pro Pro Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala
                85                  90                  95

His Phe His Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala
            100                 105                 110

Gly Val Tyr Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu
        115                 120                 125

Arg Leu Gly Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly
    130                 135                 140

Thr Phe Leu Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg
145                 150                 155                 160

Tyr Ala Asp Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile
                165                 170                 175

Ser Thr Val Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile
            180                 185                 190

Trp Asn Val Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp
        195                 200                 205

Asp Pro Trp Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro
    210                 215                 220

Pro Pro Arg His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg
225                 230                 235                 240

Pro Ala Phe Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala
                245                 250                 255

Glu Ala His Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly
            260                 265                 270

Thr Ala Pro Ala Leu Ala Ser Asp Ser Ser Arg
        275                 280
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<210> 659
<211> 735
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(712)
<223> FRXA02481

<400> 659
tgctaactac gtcctgccac ttcagatcgg tgcgcctgac gtagctttcc cacgttgaaa 60

tgctttcggc ttctgaatca ccaccgtcgg tggtgtcgcg atg ctg acc ggc ttc 115
Met Leu Thr Gly Phe
1 5

cta acc ccg ggt ggt gct gcc gac ttg ggt gga cca tgt act ccc cac 163
Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly Pro Cys Thr Pro His
10 15 20

tgt ctg acg caa ttc act ccc cag gcc ttg gtt cta aca tgt gga ttg 211
Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val Leu Thr Cys Gly Leu
25 30 35

tcg ggt gtc ggt gca act ggt att ggc tcc gtt gct tcc gca att aac 259
Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn
40 45 50

atg ctc acc acc atc ctc tgc ctc cgc gca cct ggt atg acc atg ttc 307
Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe
55 60 65

cgt atg cct att ttc acc tgg aat atc ttc gtt gtt tcc gtt ctt gct 355
Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala
70 75 80 85

ctg ctg atc ttc cca ctg ctg ctc gct gct gca ctg ggt gtt ctg tat 403
Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr
90 95 100

gac cgc aag ctt ggt gga cac ctg tac gat cca gct aac ggc ggc tcc 451
Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser
105 110 115

ctc ctg tgg cag cac ctg ttc tgg ttc ttc gga cac cct gag gtt tac 499
Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr
120 125 130

gtt ctg gcg ctg ccg ttc ttc ggc att gtt tct gag atc att cct gtg 547
Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val
135 140 145

ttc tcc cgt aag cca atg ttc ggg tta cgt cgg cct gat ctt cgc aac 595
Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg Pro Asp Leu Arg Asn
150 155 160 165

ctt gtc cat tgg tgc act gtc cat ggc tgt gtg ggc tca cca cat gtt 643
Leu Val His Trp Cys Thr Val His Gly Cys Val Gly Ser Pro His Val
170 175 180

cgt tac tgg cgc agt ttt gct tcc gtt ctt ctc ctt cat gac gtt cct 691
Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu Leu His Asp Val Pro
185 190 195

gat ttc ggt tcc tac cgg cgt taagttcttc aactgggttg gaa 735
Asp Phe Gly Ser Tyr Arg Arg
200

<210> 660

<211> 204
<212> PRT
<213> Corynebacterium glutamicum

<400> 660
Met Leu Thr Gly Phe Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly
1 5 10 15

Pro Cys Thr Pro His Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val
20 25 30

Leu Thr Cys Gly Leu Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val
35 40 45

Ala Ser Ala Ile Asn Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro
50 55 60

Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val
65 70 75 80

Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala
85 90 95

Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro
100 105 110

Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly
115 120 125

His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser
130 135 140

Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg
145 150 155 160

Pro Asp Leu Arg Asn Leu Val His Trp Cys Thr Val His Gly Cys Val
165 170 175

Gly Ser Pro His Val Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu
180 185 190

Leu His Asp Val Pro Asp Phe Gly Ser Tyr Arg Arg
195 200

<210> 661
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1177)
<223> RXA02140

<400> 661
aacacaagat atggaatcgg ctggcaaata ggctattctg cgaagataga aatgaccgta 60

aggtctctgg tttttgtgtg gacaggaagg cagaacacac gtg gaa cag caa aat 115
Val Glu Gln Gln Asn
1 5

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aag cgt ggt tta aag cgc aag gcc ctg ctt ggc ggt gtc ttg ggc tta   163
Lys Arg Gly Leu Lys Arg Lys Ala Leu Leu Gly Gly Val Leu Gly Leu
                10                  15                  20

ggt ggc ctc gcc atg gca ggc tgt gaa gtc gcc cct cct ggc ggt gtg   211
Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala Pro Pro Gly Gly Val
            25                  30                  35

ctt gga gat ttc cta cgt atg ggt tgg cct gat ggc att acc cct gaa   259
Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp Gly Ile Thr Pro Glu
        40                  45                  50

gca gtg gcc atg ggt aac ttc tgg tca tgg gtc tgg gtt gct gcc tgg   307
Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val Trp Val Ala Ala Trp
    55                  60                  65

atc atc ggc atc atc atg tgg ggt cta ttc ctc acc gcc atc ttt gcc   355
Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu Thr Ala Ile Phe Ala
70                  75                  80                  85

tgg ggc gca aag agg gct gaa aag cgc ggc gag ggt gaa ttc cct aag   403
Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu Gly Glu Phe Pro Lys
                90                  95                  100

cag ctc cag tac aac gtt cca ctt gag ctc gtt ctg acg atc gtt ccg   451
Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val Leu Thr Ile Val Pro
            105                 110                 115

atc atc att gtt atg gtg ctg ttc ttc ttc acc gtt caa act cag gac   499
Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr Val Gln Thr Gln Asp
        120                 125                 130

aag gtc acc gct ctg gat aag aac cca gag gtt acc gtg gac gtc acc   547
Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val Thr Val Asp Val Thr
    135                 140                 145

gct tac cag tgg aac tgg aag ttc gga tac tcc gaa att gat ggc tca   595
Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser Glu Ile Asp Gly Ser
150                 155                 160                 165

ctg gca cct ggt gga cag gat tac caa gga agc gac ccg gag cgt cag   643
Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser Asp Pro Glu Arg Gln
                170                 175                 180

gca gct gcc gag gct tcc aag aag gat cct tct gga gat aac cca att   691
Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser Gly Asp Asn Pro Ile
            185                 190                 195

cac ggc aac tca aag tct gac gtt tct tac ctt gag ttc aac cga att   739
His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu Glu Phe Asn Arg Ile
        200                 205                 210

gaa acc ctc gga acc act gat gaa atc cca gtg atg gtt ctt cct gtg   787
Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val Met Val Leu Pro Val
    215                 220                 225

aac acc cca atc gag ttc aac ctc gca tct gct gac gtt gca cac tcc   835
Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala Asp Val Ala His Ser
230                 235                 240                 245
```

```
ttc tgg gtt cca gag ttc ctc ttc aag cga gat gct tac gca cac cct   883
Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp Ala Tyr Ala His Pro
                250                 255                 260

gag gca aac aag tcc cag cgt gtc ttc cag att gaa gag atc act gag   931
Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile Glu Glu Ile Thr Glu
            265                 270                 275

gaa ggc gca ttc gtt ggt cgc tgt gca gaa atg tgc ggt act tac cac   979
Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met Cys Gly Thr Tyr His
        280                 285                 290

gca atg atg aac ttc gag ctt cgt gtc gtc gat cgc gat tcc ttc gct   1027
Ala Met Met Asn Phe Glu Leu Arg Val Val Asp Arg Asp Ser Phe Ala
    295                 300                 305

gag tac atc agc ttc cgt gac tcc aac cca gac gca acc aac gct cag   1075
Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp Ala Thr Asn Ala Gln
310                 315                 320                 325

gca ctt gag cac att ggt caa gct cct tac gct act tcc act agc cca   1123
Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala Thr Ser Thr Ser Pro
                330                 335                 340

ttc gtt tcc gat cgc acc gca acc cgc gac ggc gaa aac act cag agc   1171
Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly Glu Asn Thr Gln Ser
            345                 350                 355

aac gct taagaaggag tggcgaaaaa atg                                1200
Asn Ala
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<210> 662
<211> 359
<212> PRT
<213> Corynebacterium glutamicum

<400> 662

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Val Glu Gln Gln Asn Lys Arg Gly Leu Lys Arg Lys Ala Leu Leu Gly
  1               5                  10                  15

Gly Val Leu Gly Leu Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala
             20                  25                  30

Pro Pro Gly Gly Val Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp
         35                  40                  45

Gly Ile Thr Pro Glu Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val
     50                  55                  60

Trp Val Ala Ala Trp Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu
 65                  70                  75                  80

Thr Ala Ile Phe Ala Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu
                 85                  90                  95

Gly Glu Phe Pro Lys Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val
            100                 105                 110

Leu Thr Ile Val Pro Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr
```

```
        115                 120                 125

Val Gln Thr Gln Asp Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val
    130                 135                 140

Thr Val Asp Val Thr Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser
145                 150                 155                 160

Glu Ile Asp Gly Ser Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser
                165                 170                 175

Asp Pro Glu Arg Gln Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser
            180                 185                 190

Gly Asp Asn Pro Ile His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu
        195                 200                 205

Glu Phe Asn Arg Ile Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val
    210                 215                 220

Met Val Leu Pro Val Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala
225                 230                 235                 240

Asp Val Ala His Ser Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp
                245                 250                 255

Ala Tyr Ala His Pro Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile
            260                 265                 270

Glu Glu Ile Thr Glu Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met
        275                 280                 285

Cys Gly Thr Tyr His Ala Met Met Asn Phe Glu Leu Arg Val Val Asp
    290                 295                 300

Arg Asp Ser Phe Ala Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp
305                 310                 315                 320

Ala Thr Asn Ala Gln Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala
                325                 330                 335

Thr Ser Thr Ser Pro Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly
            340                 345                 350

Glu Asn Thr Gln Ser Asn Ala
        355


<210> 663
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXA02142

<400> 663
acgaaaagtt cccggaaggt cgattgaaaa gtttgcgaat tgggggaaaa ttcgcatcaa 60
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aagccgagtt caaactttca attgaaacgg ggggcttgaa gtg act ttg gcc aac   115
                                            Val Thr Leu Ala Asn
                                              1               5

caa aca gcc ata cta gat agc gtg acg agc gca gtt gga aat aca ggt   163
Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala Val Gly Asn Thr Gly
                 10                  15                  20

atg gca gca cca caa cgt gtt gcg gca ctg aac cgt ccg aat atg gtc   211
Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn Arg Pro Asn Met Val
             25                  30                  35

agt gtc ggc acc att gtg ttc ctg tct cag gaa tta atg ttc ttc gcc   259
Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu Leu Met Phe Phe Ala
         40                  45                  50

ggg cta ttc gcg atg tac ttc gtg tcc cgt gcg aac gga ctg gca aat   307
Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala Asn Gly Leu Ala Asn
     55                  60                  65

gga tca tgg gga gag cag aca gat cac ctc aac gtg ccc tac gca ctg   355
Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn Val Pro Tyr Ala Leu
 70                  75                  80                  85

ttg att acg gtc att ctg gtg tct tcc tca gtg act tgc cag ttc gga   403
Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val Thr Cys Gln Phe Gly
                 90                  95                 100

gtt ttt gcg gct gaa agg ggt gac gtt tac ggc ctc cgc aag tgg ttc   451
Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly Leu Arg Lys Trp Phe
             105                 110                 115

ttg gtc acg att atc ctc gga tca atc ttc gtg atc gga cag ggc tac   499
Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val Ile Gly Gln Gly Tyr
         120                 125                 130

gag tac atc act ctc gta ggt cac gga ctt aca atc cag agc agt gtc   547
Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr Ile Gln Ser Ser Val
     135                 140                 145

tac gga tcg gca ttc ttt att aca acc ggt ttc cac gca ctg cac gtg   595
Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe His Ala Leu His Val
150                 155                 160                 165

atc gcg ggt gtt atg gcc ttc gtt gtg gtt ctt atg aga atc cat aag   643
Ile Ala Gly Val Met Ala Phe Val Val Val Leu Met Arg Ile His Lys
                170                 175                 180

tcg aag ttc act ccg gca cag gca acc gca gca atg gtt gtg tct tat   691
Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala Met Val Val Ser Tyr
            185                 190                 195

tac tgg cac ttc gtt gac gtg gtc tgg atc ggc ctc ttc atc act att   739
Tyr Trp His Phe Val Asp Val Val Trp Ile Gly Leu Phe Ile Thr Ile
        200                 205                 210

tac ttc att cag taggcagtaa ggaatcctca acg                        774
Tyr Phe Ile Gln
    215
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<210> 664
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 664
Val Thr Leu Ala Asn Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala
1 5 10 15

Val Gly Asn Thr Gly Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn
20 25 30

Arg Pro Asn Met Val Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu
35 40 45

Leu Met Phe Phe Ala Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala
50 55 60

Asn Gly Leu Ala Asn Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn
65 70 75 80

Val Pro Tyr Ala Leu Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val
85 90 95

Thr Cys Gln Phe Gly Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly
100 105 110

Leu Arg Lys Trp Phe Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val
115 120 125

Ile Gly Gln Gly Tyr Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr
130 135 140

Ile Gln Ser Ser Val Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe
145 150 155 160

His Ala Leu His Val Ile Ala Gly Val Met Ala Phe Val Val Val Leu
165 170 175

Met Arg Ile His Lys Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala
180 185 190

Met Val Val Ser Tyr Tyr Trp His Phe Val Asp Val Val Trp Ile Gly
195 200 205

Leu Phe Ile Thr Ile Tyr Phe Ile Gln
210 215

<210> 665
<211> 1347
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1324)
<223> RXA02144

<400> 665
actcactcgg tagcttgggc ccagtggctg agggtctgtt catgtgggta ttcggcatct 60

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tggtcctcgt ggccgccgct atgtggattg gatcacgttc atg agt aac aac aac   115
                                            Met Ser Asn Asn Asn
                                              1               5

gac aaa cag tac aca acc caa gaa ctc aac gcg atg agc aat gag gat   163
Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala Met Ser Asn Glu Asp
                 10                  15                  20

ctt gca cga ctt ggt aca gag ctg gac gac gtt acc att gca tac cgc   211
Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val Thr Ile Ala Tyr Arg
             25                  30                  35

aag gaa cgt ttc cca atc gct aat gac cca gct gag aag cgc gct gca   259
Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala Glu Lys Arg Ala Ala
         40                  45                  50

cgt gca gtt act ttc tgg cta gtc ctc ggc atc att ggt gga ctt ggg   307
Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile Ile Gly Gly Leu Gly
     55                  60                  65

ttc ctg gct acc tac att ttc tgg cct tgg gag tac aag gca cac gga   355
Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu Tyr Lys Ala His Gly
 70                  75                  80                  85

gat gaa ggt ctc ctg gcg tac acc ttg tac acc cca atg ctg ggt att   403
Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr Pro Met Leu Gly Ile
                 90                  95                 100

act tcc ggt ctt tgc atc ctg tcc ctg gga ttt gca gtt gtc ctt tat   451
Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe Ala Val Val Leu Tyr
            105                 110                 115

gtc aag aag ttc att cca gag gaa atc gca gta cag cgt cgc cac gac   499
Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val Gln Arg Arg His Asp
        120                 125                 130

ggt cct tct gaa gaa gtt gac cgc cgc acc atc gtt gca ctt ctc aat   547
Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile Val Ala Leu Leu Asn
    135                 140                 145

gac tct tgg cag acc tct act ctt ggt cgt cgc aag ctg atc atg gga   595
Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg Lys Leu Ile Met Gly
150                 155                 160                 165

ctt gca ggt ggc gga gca gta ctg gcc ggc ctg acc atc atc gct cca   643
Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu Thr Ile Ile Ala Pro
                170                 175                 180

atg ggc ggt atg atc aag aac cct tgg aat cct aag gaa ggc cca atg   691
Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro Lys Glu Gly Pro Met
            185                 190                 195

gac gtt cag ggt gac ggc acc ctg tgg act tcc ggt tgg act ctc gtt   739
Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser Gly Trp Thr Leu Val
        200                 205                 210

gag aac gac gtc aag gtt tac ctc ggc cgc gac act gca gca att gcg   787
Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp Thr Ala Ala Ile Ala
    215                 220                 225
```

```
gag tcc cac acc gat gca acc ggt gag cac tgg tca acc act ggt gtt   835
Glu Ser His Thr Asp Ala Thr Gly Glu His Trp Ser Thr Thr Gly Val
230                 235                 240                 245

tcc cgc ctg gtt cgt atg cgc cca gaa gat ctg gca gca gca tcc atg   883
Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu Ala Ala Ala Ser Met
                250                 255                 260

gaa act gtc ttc cca ctt cca gct gaa atg gtg aac gac ggt gct gaa   931
Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val Asn Asp Gly Ala Glu
            265                 270                 275

tac gat cct gcg aag gac gtc tac gag cac caa atg cac tcg gtg cac   979
Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln Met His Ser Val His
        280                 285                 290

ggc cca cgc aac gca gtt atg ttg atc cgt ctc cgt acc gct gac gct   1027
Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu Arg Thr Ala Asp Ala
    295                 300                 305

gaa aag gtt atc gaa cgc gaa ggc cag gag tcc ttc cac tac ggt gac   1075
Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser Phe His Tyr Gly Asp
310                 315                 320                 325

tac tac gct tac tcc aag att tgt aca cac att ggt tgc cca acc tca   1123
Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile Gly Cys Pro Thr Ser
                330                 335                 340

ctg tac gag gct cag acc aat cgt att ctg tgc cca tgt cac cag tcg   1171
Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys Pro Cys His Gln Ser
            345                 350                 355

cag ttt gac gca ttg cac tac gga aag cca gtc ttt gga cct gct gcc   1219
Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val Phe Gly Pro Ala Ala
        360                 365                 370

cgt gca ctg cca cag ctg cca att acc gtt gat gaa gag ggc tac ctc   1267
Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp Glu Glu Gly Tyr Leu
    375                 380                 385

atc gcc gct ggt aac ttc att gag cca ctc ggc cct gca ttc tgg gag   1315
Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly Pro Ala Phe Trp Glu
390                 395                 400                 405

cgt aag tca tgagtctagc taccgtggga aac                            1347
Arg Lys Ser
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<210> 666
<211> 408
<212> PRT
<213> Corynebacterium glutamicum

<400> 666

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Met Ser Asn Asn Asn Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala
  1               5                  10                  15

Met Ser Asn Glu Asp Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val
             20                  25                  30
```

```
Thr Ile Ala Tyr Arg Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala
        35                  40                  45

Glu Lys Arg Ala Ala Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile
    50                  55                  60

Ile Gly Gly Leu Gly Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu
65                  70                  75                  80

Tyr Lys Ala His Gly Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr
                85                  90                  95

Pro Met Leu Gly Ile Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe
            100                 105                 110

Ala Val Val Leu Tyr Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val
        115                 120                 125

Gln Arg Arg His Asp Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile
    130                 135                 140

Val Ala Leu Leu Asn Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg
145                 150                 155                 160

Lys Leu Ile Met Gly Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu
                165                 170                 175

Thr Ile Ile Ala Pro Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro
            180                 185                 190

Lys Glu Gly Pro Met Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser
        195                 200                 205

Gly Trp Thr Leu Val Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp
    210                 215                 220

Thr Ala Ala Ile Ala Glu Ser His Thr Asp Ala Thr Gly Glu His Trp
225                 230                 235                 240

Ser Thr Thr Gly Val Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu
                245                 250                 255

Ala Ala Ala Ser Met Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val
            260                 265                 270

Asn Asp Gly Ala Glu Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln
        275                 280                 285

Met His Ser Val His Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu
    290                 295                 300

Arg Thr Ala Asp Ala Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser
305                 310                 315                 320

Phe His Tyr Gly Asp Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile
                325                 330                 335

Gly Cys Pro Thr Ser Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys
            340                 345                 350

Pro Cys His Gln Ser Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val
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09605760.090605

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        355                 360                 365

Phe Gly Pro Ala Ala Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp
    370                 375                 380

Glu Glu Gly Tyr Leu Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly
385                 390                 395                 400

Pro Ala Phe Trp Glu Arg Lys Ser
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<210> 667
<211> 1053
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1030)
<223> RXA02740

<400> 667

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tatgagtgat ttgaaaatgc aacgttctgg aggagaaccc ttg gac acg atc aag   115
                                            Leu Asp Thr Ile Lys
                                              1               5

gcc tat att gcg cta acg aag ccc agg gtt att gaa ctc ctc ctt gtc   163
Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile Glu Leu Leu Leu Val
                10                  15                  20

gcc aca atc ccc aca atg ctt cag gct gaa cgc ggt gag aac aac att   211
Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg Gly Glu Asn Asn Ile
            25                  30                  35

gtg ctc atc ttg ctg act gtg ttc ggt ggc tgg atg ggt gcg gcc gcc   259
Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp Met Gly Ala Ala Ala
        40                  45                  50

gcc aac acc ttc aac atg gtg gca gac tcc gat att gat cag cgc atg   307
Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp Ile Asp Gln Arg Met
    55                  60                  65

gga cgc act agg gct cgc cct ttg gtg cgc cac acc gtg agt aat cgc   355
Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His Thr Val Ser Asn Arg
70                  75                  80                  85

gac gcc tcc att ttt gcg tgg gtc ctg aca gtg gcc agc ttc ttg tgg   403
Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val Ala Ser Phe Leu Trp
                90                  95                  100

ctg tgg ctg ctg tgc gat tcg atg ctc gcc ggc atc ttc gtg ttg atc   451
Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly Ile Phe Val Leu Ile
            105                 110                 115

acg att ttc ttc tac att ttt gtc tac acc aag tgg ctg aag cgc cgc   499
Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys Trp Leu Lys Arg Arg
        120                 125                 130
```

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acg cac atg aat atc gtg tgg ggc gga gcc gca ggt tgt atg cca gtg   547
Thr His Met Asn Ile Val Trp Gly Gly Ala Ala Gly Cys Met Pro Val
    135                 140                 145

ctc gtc ggc tgg gca gtg atc gtt gat cag ttt gag cca ggc gtt cca   595
Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe Glu Pro Gly Val Pro
150                 155                 160                 165

cag cag tgg tgg cag gca att gtc ctg ttc atg gtg att ttc ttc tgg   643
Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met Val Ile Phe Phe Trp
                170                 175                 180

acc cca cct cac acc tgg gct ctg gcc atg aag tac cgc gaa gac tac   691
Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys Tyr Arg Glu Asp Tyr
            185                 190                 195

aag gcg gct ggc gtc cca atg ctt cct gtc gtg cgc acc cca gtc cag   739
Lys Ala Ala Gly Val Pro Met Leu Pro Val Val Arg Thr Pro Val Gln
        200                 205                 210

gtc acc gca caa atc gtg tgg tac tcc gtg gca act gtg ctg acc acc   787
Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala Thr Val Leu Thr Thr
    215                 220                 225

ttc ttg ctc atc cca gca act ggt tgg atc tac gca gcg atc gcc gtc   835
Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr Ala Ala Ile Ala Val
230                 235                 240                 245

att tcc ggc gtc acc ttc ttg ttc atg gcc atc aag ctg cac ctc ggc   883
Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile Lys Leu His Leu Gly
                250                 255                 260

atc aaa aac ggt ggc aag gtc aag cct ctg aag ctg ttt att ttg tcc   931
Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys Leu Phe Ile Leu Ser
            265                 270                 275

aac aac tac ttg gca gtc ctc ttc gtg gca ttg tcc gtc gac gcg gtc   979
Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu Ser Val Asp Ala Val
        280                 285                 290

ctc ggc ctt gag acc atc ggc gag atg ctc ggc tgg acc acc acc ttc  1027
Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly Trp Thr Thr Thr Phe
    295                 300                 305

ttc taaaagcttg cttttcgacg aaa                                    1053
Phe
310
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<210> 668
<211> 310
<212> PRT
<213> Corynebacterium glutamicum

<400> 668

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Leu Asp Thr Ile Lys Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile
  1               5                  10                  15

Glu Leu Leu Leu Val Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg
             20                  25                  30
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09092910.3600

Gly Glu Asn Asn Ile Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp
35 40 45

Met Gly Ala Ala Ala Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp
50 55 60

Ile Asp Gln Arg Met Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His
65 70 75 80

Thr Val Ser Asn Arg Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val
85 90 95

Ala Ser Phe Leu Trp Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly
100 105 110

Ile Phe Val Leu Ile Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys
115 120 125

Trp Leu Lys Arg Arg Thr His Met Asn Ile Val Trp Gly Gly Ala Ala
130 135 140

Gly Cys Met Pro Val Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe
145 150 155 160

Glu Pro Gly Val Pro Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met
165 170 175

Val Ile Phe Phe Trp Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys
180 185 190

Tyr Arg Glu Asp Tyr Lys Ala Ala Gly Val Pro Met Leu Pro Val Val
195 200 205

Arg Thr Pro Val Gln Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala
210 215 220

Thr Val Leu Thr Thr Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr
225 230 235 240

Ala Ala Ile Ala Val Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile
245 250 255

Lys Leu His Leu Gly Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys
260 265 270

Leu Phe Ile Leu Ser Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu
275 280 285

Ser Val Asp Ala Val Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly
290 295 300

Trp Thr Thr Thr Phe Phe
305 310

<210> 669
<211> 1161
<212> DNA
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<220>

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<223> RXA02743

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aattgtataa aactagccat gacctgctag gatcagcgac gtg tct act tca gat 115
Val Ser Thr Ser Asp
1 5

gct ccc tca aat aat cca gtt gag ttg aag ccc att act ttc tgg gca 163
Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro Ile Thr Phe Trp Ala
10 15 20

ccg acc atc aaa gtg cag cgc att ctc gcg ctc cta ctg ttg att ttc 211
Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu Leu Leu Leu Ile Phe
25 30 35

cag gga ggc atc acc gtt acg ggc tct atc gtc cgt gtc aca ggc tcc 259
Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val Arg Val Thr Gly Ser
40 45 50

ggc ctc ggt tgt gat acc tgg cca cta tgc cac gaa ggt tca cta gtc 307
Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His Glu Gly Ser Leu Val
55 60 65

cca gtc gca ggc gca gca cca tgg atc cac cag gca gtg gaa ttt ggt 355
Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln Ala Val Glu Phe Gly
70 75 80 85

aac cgc atg ctc act ttc gtg ctt gct gcc gca gcg ctt gcg ttg ttc 403
Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala Ala Leu Ala Leu Phe
90 95 100

att gca gtt ctt ggc gca aaa cgc cgc cgc gag atc ctg gtc cat tcc 451
Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu Ile Leu Val His Ser
105 110 115

ttc atc cag ggt ttg ggc atc atc ttg cag gct gtc atc ggt ggc atc 499
Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala Val Ile Gly Gly Ile
120 125 130

acc gtg ctg gtt gat ttg cac tgg tac gcc gtt gct ttg cac ttc ctg 547
Thr Val Leu Val Asp Leu His Trp Tyr Ala Val Ala Leu His Phe Leu
135 140 145

cca tcc atg atc ctt gtt ttc atg gcc gcg att ttg tac acc cgc atc 595
Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile Leu Tyr Thr Arg Ile
150 155 160 165

ggc gag ccc gat gac ggc gag att acc acc aca ttc ccc acg tgg atc 643
Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr Phe Pro Thr Trp Ile
170 175 180

cgc aat gta gct gtc att ggt gca gta gcg ctc tcc gta gta ctg atc 691
Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu Ser Val Val Leu Ile
185 190 195

acc ggc acc atg acc acc ggc gct ggc gtt cac tct ggc gat gca tca 739
Thr Gly Thr Met Thr Thr Gly Ala Gly Val His Ser Gly Asp Ala Ser

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        200                 205                 210

atc acc atg gat gat cgc ctc gat gtc agc atc gac ttg atg gcc cac   787
Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile Asp Leu Met Ala His
    215                 220                 225

atc cac ggc tac agc atg tac atc tac ctc ttc ttc acc ctc atc gtg   835
Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe Phe Thr Leu Ile Val
230                 235                 240                 245

gtc gcc ggt ctg tac aag gca aaa acc acc aag cac aac aag cag ctt   883
Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys His Asn Lys Gln Leu
                250                 255                 260

ggc ctc atg ctg att ctg ttc att ctg att cag gca ggt atc ggc atc   931
Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln Ala Gly Ile Gly Ile
            265                 270                 275

ttg cag tac cgc atg ggt gtg cca cgc tgg agc atc cca ttc cac atc   979
Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser Ile Pro Phe His Ile
        280                 285                 290

gca atg tct tct gtc gtt gtt gcc ttc act tcc ctt ctg tgg gcg cag   1027
Ala Met Ser Ser Val Val Val Ala Phe Thr Ser Leu Leu Trp Ala Gln
    295                 300                 305

ggt cgt ata cgc gtc ggc ggt aaa gcc acc gtt act ggt tct gtt gat   1075
Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val Thr Gly Ser Val Asp
310                 315                 320                 325

ggc gat att aag aac gag atc att acg aac ccc ttt gag aag aaa tca   1123
Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro Phe Glu Lys Lys Ser
                330                 335                 340

aag cag cct gtt aaa taacacgcaa ctgtatcggt aaa                     1161
Lys Gln Pro Val Lys
            345
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<210> 670
<211> 346
<212> PRT
<213> Corynebacterium glutamicum

<400> 670

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Ile Thr Phe Trp Ala Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu
             20                  25                  30

Leu Leu Leu Ile Phe Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val
         35                  40                  45

Arg Val Thr Gly Ser Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His
     50                  55                  60

Glu Gly Ser Leu Val Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln
 65                  70                  75                  80

Ala Val Glu Phe Gly Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala
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                85                  90                  95

Ala Leu Ala Leu Phe Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu
            100                 105                 110

Ile Leu Val His Ser Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala
        115                 120                 125

Val Ile Gly Gly Ile Thr Val Leu Val Asp Leu His Trp Tyr Ala Val
    130                 135                 140

Ala Leu His Phe Leu Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile
145                 150                 155                 160

Leu Tyr Thr Arg Ile Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr
                165                 170                 175

Phe Pro Thr Trp Ile Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu
            180                 185                 190

Ser Val Val Leu Ile Thr Gly Thr Met Thr Thr Gly Ala Gly Val His
        195                 200                 205

Ser Gly Asp Ala Ser Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile
    210                 215                 220

Asp Leu Met Ala His Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe
225                 230                 235                 240

Phe Thr Leu Ile Val Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys
                245                 250                 255

His Asn Lys Gln Leu Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln
            260                 265                 270

Ala Gly Ile Gly Ile Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser
        275                 280                 285

Ile Pro Phe His Ile Ala Met Ser Ser Val Val Val Ala Phe Thr Ser
    290                 295                 300

Leu Leu Trp Ala Gln Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val
305                 310                 315                 320

Thr Gly Ser Val Asp Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro
                325                 330                 335

Phe Glu Lys Lys Ser Lys Gln Pro Val Lys
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<210> 671
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(421)
<223> RXA01227

<400> 671
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Met Thr Tyr Thr Ile
1 5

gcc cag ccc tgc gtt gat gtc ctg gat cga gcc tgc gtc gag gaa tgt 163
Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys
10 15 20

ccc gtg gac tgc atc tac gag ggc aaa cgg atg ctc tac atc cac ccc 211
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro
25 30 35

gat gag tgc gtc gac tgc ggt gcc tgc gag ccc gtc tgc ccg gtt gaa 259
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Val Cys Pro Val Glu
40 45 50

gcc atc ttc tac gaa gat gat gtt ccc cac gaa tgg tgg gac tac acc 307
Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu Trp Trp Asp Tyr Thr
55 60 65

ggc gct aac gcc gcc ttt ttc gac gac ctc ggt tcg cca ggc ggt gcc 355
Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala
70 75 80 85

gcc agc ctg ggt ccg cag gac ttc gac gcc cag ctc gtc gcg gtg ctg 403
Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln Leu Val Ala Val Leu
90 95 100

ccg cca cag aac cag aac taggacctga tatcggccct aaa 444
Pro Pro Gln Asn Gln Asn
105

<210> 672
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 672
Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala
1 5 10 15

Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met
20 25 30

Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro
35 40 45

Val Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu
50 55 60

Trp Trp Asp Tyr Thr Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly
65 70 75 80

Ser Pro Gly Gly Ala Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln
85 90 95

Leu Val Ala Val Leu Pro Pro Gln Asn Gln Asn

100 105

<210> 673
<211> 438
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(415)
<223> RXA01865

<400> 673
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ttattagcct cttagagttc tcaggagaaa acgaaatccc atg aca tac aca atc 115
Met Thr Tyr Thr Ile
1 5

gca cag ccc tgc gtt gac gtc ttg gat cgt gcc tgc gtt gaa gaa tgc 163
Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys
10 15 20

cca gta gat tgc atc tac gaa ggt aag cgc atg ctg tac atc cac ccg 211
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro
25 30 35

gat gag tgc gtt gac tgt ggt gca tgt gag cct gct tgc cca gtt gag 259
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Ala Cys Pro Val Glu
40 45 50

gca atc ttc tac gag gac gat gtc cca gac gaa tgg ctt gac tac aac 307
Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu Trp Leu Asp Tyr Asn
55 60 65

gat gcc aac gct gca ttc ttc gat gat ctg ggc tcc cca ggt ggt gcg 355
Asp Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala
70 75 80 85

gct aag ctt gga cca caa gat ttt gat cac cca atg atc gct gcg ctg 403
Ala Lys Leu Gly Pro Gln Asp Phe Asp His Pro Met Ile Ala Ala Leu
90 95 100

ccg cct cag gca taatctaacg catgacctct cgc 438
Pro Pro Gln Ala
105

<210> 674
<211> 105
<212> PRT
<213> Corynebacterium glutamicum

<400> 674
Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala
1 5 10 15

Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met
20 25 30

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Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro
         35                  40                  45

Ala Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu
     50                  55                  60

Trp Leu Asp Tyr Asn Asp Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly
 65                  70                  75                  80

Ser Pro Gly Gly Ala Ala Lys Leu Gly Pro Gln Asp Phe Asp His Pro
                 85                  90                  95

Met Ile Ala Ala Leu Pro Pro Gln Ala
            100                 105


<210> 675
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXA00680

<400> 675
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gacagttcat ctaagtacta aaagttctaa ggagaagatc atg tct act att cat   115
                                            Met Ser Thr Ile His
                                              1               5

ttc att gat cat gct ggc aaa acc cgc acc atc gag gcg act gtt ggt   163
Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile Glu Ala Thr Val Gly
                 10                  15                  20

gat tca gta atg gag acc gca gtc cga aac gga gtg cct gga att gtt   211
Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly Val Pro Gly Ile Val
             25                  30                  35

gct gaa tgc ggc ggt tcc tta tcg tgt gca acc tgc cat gtg ttt gtt   259
Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr Cys His Val Phe Val
         40                  45                  50

gac cct gca cag tat gat gcg ctt ccc cca atg gag gag atg gaa gat   307
Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met Glu Glu Met Glu Asp
     55                  60                  65

gaa atg ctg tgg ggt gct gcc gtg gac cgt gag gat tgc tcc cgt ttg   355
Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu Asp Cys Ser Arg Leu
 70                  75                  80                  85

tct tgc caa atc aag gtc acc gaa ggc atg gat ctt tcg ttg acc acg   403
Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp Leu Ser Leu Thr Thr
                 90                  95                 100

cca gaa acg caa gtg tgaggttgaa tcatgaatac ttc                    441
Pro Glu Thr Gln Val
            105
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<210> 676
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<212> PRT
<213> Corynebacterium glutamicum

<400> 676
Met Ser Thr Ile His Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile
1 5 10 15

Glu Ala Thr Val Gly Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly
20 25 30

Val Pro Gly Ile Val Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr
35 40 45

Cys His Val Phe Val Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met
50 55 60

Glu Glu Met Glu Asp Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu
65 70 75 80

Asp Cys Ser Arg Leu Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp
85 90 95

Leu Ser Leu Thr Thr Pro Glu Thr Gln Val
100 105

<210> 677
<211> 1389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1366)
<223> RXA00679

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ggaccgtgag gattgctccc gtttgtcttg ccaaatcaag gtcaccgaag gcatggatct 60

ttcgttgacc acgccagaaa cgcaagtgtg aggttgaatc atg aat act tca gct 115
Met Asn Thr Ser Ala
1 5

gaa act gga atc ttg atc atc ggt gca aac caa tcg ggt gtg cag ctg 163
Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln Ser Gly Val Gln Leu
10 15 20

gcg att tcc ctg cgg gcc acg ggt ttc acc gaa tcg atc acg ctt cta 211
Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu Ser Ile Thr Leu Leu
25 30 35

ggc gag gag gat cac cgc ccc tac cag cgt ccc gcc ttg tcc aag gag 259
Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro Ala Leu Ser Lys Glu
40 45 50

ttc ctc cag gac aag atc gac aaa gag cgt ctg att ttc cgt tcc aat 307
Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu Ile Phe Arg Ser Asn
55 60 65

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gag tat tgg gaa gaa aat aat att cgc ctg gtc aag ggc gtg cgc atc   355
Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val Lys Gly Val Arg Ile
 70                  75                  80                  85

gaa cgc att gaa aag aac gac gac gga tca ggg gtc gcc tac ggc gcc   403
Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly Val Ala Tyr Gly Ala
                 90                  95                 100

gga caa gaa ttc gct ttt cga cgt ctc gct cta gcg gtt ggt gcc cgc   451
Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu Ala Val Gly Ala Arg
            105                 110                 115

cct cgc cac ctc gac ctc ccg ggc gcc acc ttg gag ggt gtc acc tac   499
Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu Glu Gly Val Thr Tyr
        120                 125                 130

ctg cgc aac gcg gac gac gcc ttg gcg ctc aaa gcg atg att ggt tct   547
Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys Ala Met Ile Gly Ser
    135                 140                 145

gtc acc gat gcc gtt gta gtc ggt ggt ggg ttc atc gga ttg gaa gct   595
Val Thr Asp Ala Val Val Val Gly Gly Gly Phe Ile Gly Leu Glu Ala
150                 155                 160                 165

gcg tgt tcg ctt cat gac ctc ggc aaa aat gtc acc gtc ctg gaa tat   643
Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val Thr Val Leu Glu Tyr
                170                 175                 180

ggt ccg cgt ctg att ggc cga gcg gtg ggt gaa gaa acc gca gca ttc   691
Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu Glu Thr Ala Ala Phe
            185                 190                 195

ttc ctc gaa caa cac cgt tcc cgt ggc gta aat atc gtg ctt gat gcc   739
Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn Ile Val Leu Asp Ala
        200                 205                 210

cgc atg aaa cag ttt gtg ggc aag gat gga aag ctc agc ggc att gag   787
Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys Leu Ser Gly Ile Glu
    215                 220                 225

cta gaa gat ggc aca gta att cct gcc caa cta gtc att gtg ggc atc   835
Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu Val Ile Val Gly Ile
230                 235                 240                 245

ggt gtc att ccg aac aca gaa ctt gcc gct gtt ctg ggc tta gac atc   883
Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val Leu Gly Leu Asp Ile
                250                 255                 260

aac aac ggc atc gtg gtg gat aaa cat gcc gtc gcg tca gat ggc acc   931
Asn Asn Gly Ile Val Val Asp Lys His Ala Val Ala Ser Asp Gly Thr
            265                 270                 275

acc att gcg att ggc gat gtc gcc aac att ccc aat cca atc cct ggt   979
Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro Asn Pro Ile Pro Gly
        280                 285                 290

tcc ccc gct gat gaa cgc atc cga cta gaa agc gtc aat aac gcc atc   1027
Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser Val Asn Asn Ala Ile
    295                 300                 305
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gag cac gca aag atc gct gca tac tca ctc gtc ggc cag ccc gaa gcc   1075
Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val Gly Gln Pro Glu Ala
310                 315                 320                 325

tac gcc gga atc ccc tgg ttc tgg tcc aac caa ggc gat ctc aaa cta   1123
Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln Gly Asp Leu Lys Leu
                330                 335                 340

caa att gca gga ctt acc ctt ggt tat gac agc aca gta atc cga cag   1171
Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser Thr Val Ile Arg Gln
            345                 350                 355

gat ccc gag aaa aag aag ttc tct gtc ctt tat tac cgt ggc gac aac   1219
Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr Tyr Arg Gly Asp Asn
        360                 365                 370

atc atc gcc gcc gat tgt gtc aac gct cca ctg gat ttc atg gct gtg   1267
Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu Asp Phe Met Ala Val
    375                 380                 385

cgc agt gca ctt tcc agg aac caa aat atc ccc gcc gac ctt gct gca   1315
Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro Ala Asp Leu Ala Ala
390                 395                 400                 405

gat att tcg cag ccg ctg aaa aaa cta gcc gtt gac ctg gag gtt acc   1363
Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val Asp Leu Glu Val Thr
                410                 415                 420

cga tgactcgcag taatttaccc gct                                    1389
Arg
```

09839200.1

<210> 678
<211> 422
<212> PRT
<213> Corynebacterium glutamicum

<400> 678

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Met Asn Thr Ser Ala Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln
  1               5                  10                  15

Ser Gly Val Gln Leu Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu
             20                  25                  30

Ser Ile Thr Leu Leu Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro
         35                  40                  45

Ala Leu Ser Lys Glu Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu
     50                  55                  60

Ile Phe Arg Ser Asn Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val
 65                  70                  75                  80

Lys Gly Val Arg Ile Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly
                 85                  90                  95

Val Ala Tyr Gly Ala Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu
            100                 105                 110

Ala Val Gly Ala Arg Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu
```

```
        115                 120                 125

Glu Gly Val Thr Tyr Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys
    130                 135                 140

Ala Met Ile Gly Ser Val Thr Asp Ala Val Val Val Gly Gly Gly Phe
145                 150                 155                 160

Ile Gly Leu Glu Ala Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val
                165                 170                 175

Thr Val Leu Glu Tyr Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu
            180                 185                 190

Glu Thr Ala Ala Phe Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn
        195                 200                 205

Ile Val Leu Asp Ala Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys
    210                 215                 220

Leu Ser Gly Ile Glu Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu
225                 230                 235                 240

Val Ile Val Gly Ile Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val
                245                 250                 255

Leu Gly Leu Asp Ile Asn Asn Gly Ile Val Val Asp Lys His Ala Val
            260                 265                 270

Ala Ser Asp Gly Thr Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro
        275                 280                 285

Asn Pro Ile Pro Gly Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser
    290                 295                 300

Val Asn Asn Ala Ile Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val
305                 310                 315                 320

Gly Gln Pro Glu Ala Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln
                325                 330                 335

Gly Asp Leu Lys Leu Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser
            340                 345                 350

Thr Val Ile Arg Gln Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr
        355                 360                 365

Tyr Arg Gly Asp Asn Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu
    370                 375                 380

Asp Phe Met Ala Val Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro
385                 390                 395                 400

Ala Asp Leu Ala Ala Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val
                405                 410                 415

Asp Leu Glu Val Thr Arg
            420
```

<210> 679

<211> 1074
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1051)
<223> RXA00224

<400> 679
gtgatgtcat tggtgcatcg ggtgctgctg aaaagattgc tgagtacctc gcttcagaga 60

acctcatcta gccactatct tcacaaagga gaacatttaa atg tct att tct tat 115
Met Ser Ile Ser Tyr
1 5

gtg ctg gtt gag cag cta gat ggc cgc cca gaa cca gtt acc ctt gaa 163
Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu Pro Val Thr Leu Glu
10 15 20

ttg atc act gct gct cgc gca ctc ggt gac gtc gtt gcc gtt gtc gtt 211
Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val Val Ala Val Val Val
25 30 35

ggc gag cca ggt gcc ggc gta aac ctt gct gct gag ctc ggc aat tgg 259
Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala Glu Leu Gly Asn Trp
40 45 50

ggt gca gca cag gtt gtt tcc gct gaa atc tct ggc gct tcc aac cgt 307
Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser Gly Ala Ser Asn Arg
55 60 65

ttg atc ttg cct gct gtt gat gcg ctg cac att ttg gct gcg aac aac 355
Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile Leu Ala Ala Asn Asn
70 75 80 85

cca ggt cca att gtt atc gct gca act gca agc ggt aat gag atc gct 403
Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser Gly Asn Glu Ile Ala
90 95 100

ggt cgt ttg gct gcc cgt ttg gct tct ggt gtg ctc acc gat gtc gtc 451
Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val Leu Thr Asp Val Val
105 110 115

gga atc aat gcc gac cgc acc gca cag cag tcc att ttc ggc gac acc 499
Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser Ile Phe Gly Asp Thr
120 125 130

att cag gtg tcc gct gca gtt ggt ggc gct tca ccg ctg tac acc ctg 547
Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser Pro Leu Tyr Thr Leu
135 140 145

cgt cca ggt gcc ctt gat ggc gtg gcc gtt cct gca acc ggt gaa ttg 595
Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro Ala Thr Gly Glu Leu
150 155 160 165

gca acc att gag atc cca ggc gca acc gcc aag gat gtc acc atc acc 643
Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys Asp Val Thr Ile Thr
170 175 180

tcc ttc acg cca agc acc cag agc gat cgc cct gag ctg cca cag gca 691

```
Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro Glu Leu Pro Gln Ala
            185                 190                 195

aag gtc gtt atc gca ggt gga cgt ggt gtc gga agc gaa gaa aac ttc   739
Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly Ser Glu Glu Asn Phe
        200                 205                 210

cgc agc atc gtt gaa cca ctg gca gat gca ttg ggc ggt gcc gtt ggc   787
Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu Gly Gly Ala Val Gly
    215                 220                 225

gca acc cgc gac gcc gtt gat ctg ggc tac tac cca ggc gag tac cag   835
Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr Pro Gly Glu Tyr Gln
230                 235                 240                 245

gtt ggt cag acc ggt gtc acc gtg tcc cca gac ctc tac atc ggc ctc   883
Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp Leu Tyr Ile Gly Leu
                250                 255                 260

ggc att tcc ggt gca att cag cac act tct ggt atg cag acc gca aag   931
Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly Met Gln Thr Ala Lys
            265                 270                 275

aag gtt att gtg atc aac aac gat gag gac gcg ccg atc ttc cag att   979
Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala Pro Ile Phe Gln Ile
        280                 285                 290

gcg gac ctc ggt gtc gtt ggc gac ctc ttt gac atc gcc cct gcg ctc   1027
Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp Ile Ala Pro Ala Leu
    295                 300                 305

atc gaa gag atc aac aag cgc aag taggagtttt gaacactttt tat         1074
Ile Glu Glu Ile Asn Lys Arg Lys
310                 315
```

<210> 680
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 680

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Met Ser Ile Ser Tyr Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu
  1               5                  10                  15

Pro Val Thr Leu Glu Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val
             20                  25                  30

Val Ala Val Val Val Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala
         35                  40                  45

Glu Leu Gly Asn Trp Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser
     50                  55                  60

Gly Ala Ser Asn Arg Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile
 65                  70                  75                  80

Leu Ala Ala Asn Asn Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser
                 85                  90                  95

Gly Asn Glu Ile Ala Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val
```

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            100                 105                 110

Leu Thr Asp Val Val Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser
        115                 120                 125

Ile Phe Gly Asp Thr Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser
    130                 135                 140

Pro Leu Tyr Thr Leu Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro
145                 150                 155                 160

Ala Thr Gly Glu Leu Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys
                165                 170                 175

Asp Val Thr Ile Thr Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro
            180                 185                 190

Glu Leu Pro Gln Ala Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly
        195                 200                 205

Ser Glu Glu Asn Phe Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu
    210                 215                 220

Gly Gly Ala Val Gly Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr
225                 230                 235                 240

Pro Gly Glu Tyr Gln Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp
                245                 250                 255

Leu Tyr Ile Gly Leu Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly
            260                 265                 270

Met Gln Thr Ala Lys Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala
        275                 280                 285

Pro Ile Phe Gln Ile Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp
    290                 295                 300

Ile Ala Pro Ala Leu Ile Glu Glu Ile Asn Lys Arg Lys
305                 310                 315


<210> 681
<211> 909
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(886)
<223> RXA00225

<400> 681
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ccaaaaacgc caaaaatcgt gaattgaaag gtgagtgtgg atg tcc aca atc gtg   115
                                              Met Ser Thr Ile Val
                                                1               5

gtt ctg gtt aaa aat gtt cca gac acc tgg tct aag agg act ctg gaa   163
Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser Lys Arg Thr Leu Glu
```

```
                  10                  15                  20

gct gat ttc acc ctt gac cgt gag ggt gta gat cga gtc ttg gat gag   211
Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp Arg Val Leu Asp Glu
            25                  30                  35

atc aat gag ttt gct ctg gag cag gca ctg cgc ttg cgg gag tcc aac   259
Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg Leu Arg Glu Ser Asn
        40                  45                  50

ccg gat gct ggt tac cgc gtt gtt gcg ctg agc gcc ggc cct gcc ggt   307
Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser Ala Gly Pro Ala Gly
    55                  60                  65

ggg gaa gag gcg ctg cgt aag gcg ctg tcc atg ggt gct gat gaa gca   355
Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met Gly Ala Asp Glu Ala
70                  75                  80                  85

atc cag ctc agt gat gat gcc ttg gct ggt tct gat ctt ttg gga acc   403
Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser Asp Leu Leu Gly Thr
                90                  95                  100

gct tgg gcg ctg aac aac gct atc aac acc atc gcg ggt gtt gct ctc   451
Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile Ala Gly Val Ala Leu
            105                 110                 115

atc gtg acg ggt tcg gct tct tcc gat ggt tcc atg ggt gcg ctt cct   499
Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser Met Gly Ala Leu Pro
        120                 125                 130

ggc gtg tta gct gag tac cgc cag gtc cca gcg ttg act aac ttg tct   547
Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala Leu Thr Asn Leu Ser
    135                 140                 145

gcg ctg aag gtc gag ggt gca tct att act gcc act cgc att gat aac   595
Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala Thr Arg Ile Asp Asn
150                 155                 160                 165

cac ggc acc tat gag ttg cag gct gca ctt cct gcg gtt gtg tcg att   643
His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro Ala Val Val Ser Ile
                170                 175                 180

tcc gat aag gct gac aag cca cgt ttc cct aac ttc aag ggc atc atg   691
Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn Phe Lys Gly Ile Met
            185                 190                 195

gct gct aag aag gct gag atc aag aag ctt tcc ttg gct gaa atc ggc   739
Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser Leu Ala Glu Ile Gly
        200                 205                 210

gtg gct cca gag cag gtt ggt ctg tct cac gcg gca act gct gtt act   787
Val Ala Pro Glu Gln Val Gly Leu Ser His Ala Ala Thr Ala Val Thr
    215                 220                 225

gct gca gct gat cgt cct gag cgc tcc caa ggt gat gtc att ggt gca   835
Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly Asp Val Ile Gly Ala
230                 235                 240                 245

tcg ggt gct gct gaa aag att gct gag tac ctc gct tca gag aac ctc   883
Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu Ala Ser Glu Asn Leu
                250                 255                 260
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atc tagccactat cttcacaaag gag 909
Ile

<210> 682
<211> 262
<212> PRT
<213> Corynebacterium glutamicum

<400> 682
Met Ser Thr Ile Val Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser
1 5 10 15

Lys Arg Thr Leu Glu Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp
20 25 30

Arg Val Leu Asp Glu Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg
35 40 45

Leu Arg Glu Ser Asn Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser
50 55 60

Ala Gly Pro Ala Gly Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met
65 70 75 80

Gly Ala Asp Glu Ala Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser
85 90 95

Asp Leu Leu Gly Thr Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile
100 105 110

Ala Gly Val Ala Leu Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser
115 120 125

Met Gly Ala Leu Pro Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala
130 135 140

Leu Thr Asn Leu Ser Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala
145 150 155 160

Thr Arg Ile Asp Asn His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro
165 170 175

Ala Val Val Ser Ile Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn
180 185 190

Phe Lys Gly Ile Met Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser
195 200 205

Leu Ala Glu Ile Gly Val Ala Pro Glu Gln Val Gly Leu Ser His Ala
210 215 220

Ala Thr Ala Val Thr Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly
225 230 235 240

Asp Val Ile Gly Ala Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu
245 250 255

Ala Ser Glu Asn Leu Ile

260

<210> 683
<211> 2378
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (82)..(2355)
<223> RXN00606

<400> 683
tgcggtggcg attgctgcga cccaagctgg caccaccagc ctcgatggta ttttgcactc 60

tgatttctgg cggagaagcc agtg ctc acg ggt gtt att gcg gtg ctg att 111
Val Leu Thr Gly Val Ile Ala Val Leu Ile
1 5 10

gca atg tcc gcg ttc act aag tcc gca cag ttc ccg ttc cac ttc tgg 159
Ala Met Ser Ala Phe Thr Lys Ser Ala Gln Phe Pro Phe His Phe Trp
15 20 25

ctg cct gag gcg atg gct gcg gcc acc cca gtg tcg gcg ttc ctg cac 207
Leu Pro Glu Ala Met Ala Ala Ala Thr Pro Val Ser Ala Phe Leu His
30 35 40

gct gcg gcc gtg gtc aag gcg ggt att tac ctg ttg ctg cgc ttt agc 255
Ala Ala Ala Val Val Lys Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser
45 50 55

att gtg ttc cat gat gtt gcg gtc tgg aat tgg ttg ctg att atc gtc 303
Ile Val Phe His Asp Val Ala Val Trp Asn Trp Leu Leu Ile Ile Val
60 65 70

ggc atg ggt acg gcc atc atg tcg gcg tat ttc gcg gtg cag aag acc 351
Gly Met Gly Thr Ala Ile Met Ser Ala Tyr Phe Ala Val Gln Lys Thr
75 80 85 90

gat ctg aag aag ctc acg gca tat tcc acg gtg tcg cat ttg ggt tgg 399
Asp Leu Lys Lys Leu Thr Ala Tyr Ser Thr Val Ser His Leu Gly Trp
95 100 105

atc gta gcg acc atc ggc gtg ggc act cct ttc gcg ctc ggc gct gcc 447
Ile Val Ala Thr Ile Gly Val Gly Thr Pro Phe Ala Leu Gly Ala Ala
110 115 120

att gtg cac acg ctc agc cac gcg ctg ttt aag tcc tcg ttg ttc atg 495
Ile Val His Thr Leu Ser His Ala Leu Phe Lys Ser Ser Leu Phe Met
125 130 135

ctc att ggc gtg att gat cac cag act ggc acg cgc gat att cgt cgc 543
Leu Ile Gly Val Ile Asp His Gln Thr Gly Thr Arg Asp Ile Arg Arg
140 145 150

ctc ggt ttc ctg gtc aag aag atg ccg ttc acg ttt gtg tct gta tta 591
Leu Gly Phe Leu Val Lys Lys Met Pro Phe Thr Phe Val Ser Val Leu
155 160 165 170

ata ggt gcg ttg tcg atg gca tcg gtt ccg ccg ttg ctc ggc ttc gtg 639

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Ile Gly Ala Leu Ser Met Ala Ser Val Pro Pro Leu Leu Gly Phe Val
                175                 180                 185

tcc aaa gaa ggc atg atc aca gcg ttc atg gac gcc ccc atc ggc aac   687
Ser Lys Glu Gly Met Ile Thr Ala Phe Met Asp Ala Pro Ile Gly Asn
            190                 195                 200

tcc tat gtt gta tta ctg ctg gtc ggc gca gca atc ggc gcg gtc cta   735
Ser Tyr Val Val Leu Leu Leu Val Gly Ala Ala Ile Gly Ala Val Leu
        205                 210                 215

acc ttc aca tac tcc gcg aaa ctc gtg ctc ggc gca ttc gtc gac ggc   783
Thr Phe Thr Tyr Ser Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly
    220                 225                 230

cca cgc gac atg tca cac gtc aag gaa gcc ccc gtc tcc ctc tgg ctt   831
Pro Arg Asp Met Ser His Val Lys Glu Ala Pro Val Ser Leu Trp Leu
235                 240                 245                 250

ccg gcc gcc ctg cct gga ctt atg tct ctg cca cta gtc cta gta ctt   879
Pro Ala Ala Leu Pro Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu
                255                 260                 265

tcg ctt ttc gac gcc ccc gtc tcc gcc gca gcc acc tcc gcc gcg ggg   927
Ser Leu Phe Asp Ala Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly
            270                 275                 280

gaa gcg gcg cac atg cac ctg gca ttg tgg cac ggc atc aac acc cca   975
Glu Ala Ala His Met His Leu Ala Leu Trp His Gly Ile Asn Thr Pro
        285                 290                 295

ctg ttg att tcc ttg ggt gtg ctg gtg gcc gga atc ctt ggt gtg ctg   1023
Leu Leu Ile Ser Leu Gly Val Leu Val Ala Gly Ile Leu Gly Val Leu
    300                 305                 310

ttc cgc aaa gag ctg tgg aaa atc gcc gag acc agc cct ttc ccc atc   1071
Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile
315                 320                 325                 330

gcc aca ggc aac gac atc cta tcg atg ctg gtt tac cga gcc aac ttg   1119
Ala Thr Gly Asn Asp Ile Leu Ser Met Leu Val Tyr Arg Ala Asn Leu
                335                 340                 345

ctg ggt aaa ttc ttc ggt cgc atg gct gat tcg atg agc cca cgc agg   1167
Leu Gly Lys Phe Phe Gly Arg Met Ala Asp Ser Met Ser Pro Arg Arg
            350                 355                 360

cac ttg gtc agc ctc atc gtg ctg ctc tgg gcg ctg gct gct ttt gcc   1215
His Leu Val Ser Leu Ile Val Leu Leu Trp Ala Leu Ala Ala Phe Ala
        365                 370                 375

acc att cac ccc tcg gtt cag ctt gca cca aag caa ccg gga att gat   1263
Thr Ile His Pro Ser Val Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp
    380                 385                 390

cgt tgg atc gac ctc att ccg ctt gcc atc atc gcg cta tct gtc ttc   1311
Arg Trp Ile Asp Leu Ile Pro Leu Ala Ile Ile Ala Leu Ser Val Phe
395                 400                 405                 410

ggc ctg ctc acc acc cga aac cgc ctc agc gca gcc gtg ctt gtg ggt   1359
Gly Leu Leu Thr Thr Arg Asn Arg Leu Ser Ala Ala Val Leu Val Gly
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                415                 420                 425

acc gtt ggt gtg ggt gtt tcc ttc cag atg cta ctt ctg ggc gct ccc   1407
Thr Val Gly Val Gly Val Ser Phe Gln Met Leu Leu Leu Gly Ala Pro
            430                 435                 440

gat gtt gca ctt acc cag ttc ctg gta gaa ggc ctc gtc gtg gta atc   1455
Asp Val Ala Leu Thr Gln Phe Leu Val Glu Gly Leu Val Val Val Ile
        445                 450                 455

atc atg atg gtt gtc cgg cac cag cct gcc aac ttc aag cgc atc aag   1503
Ile Met Met Val Val Arg His Gln Pro Ala Asn Phe Lys Arg Ile Lys
    460                 465                 470

ccc agc aga agg cgc agc acc gtt ctt gtc gcc gtc ctt gct gcc ttc   1551
Pro Ser Arg Arg Arg Ser Thr Val Leu Val Ala Val Leu Ala Ala Phe
475                 480                 485                 490

gcc gca ttc atg gcg gtg tgg gga ttg ctt ggc cgt cac gaa cgt tct   1599
Ala Ala Phe Met Ala Val Trp Gly Leu Leu Gly Arg His Glu Arg Ser
                495                 500                 505

gag ctg gcc atg tgg tac ctc aac caa ggt cca gag atc acc tct ggc   1647
Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly
            510                 515                 520

gcc aac gtg gtg aac acc atc ctc gtg gaa ttc cgt gca ctg gat acg   1695
Ala Asn Val Val Asn Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr
        525                 530                 535

ttg ggc gag ctc tcc gtg ctt ggc atg gca gct gtc gtc atc ggt gcg   1743
Leu Gly Glu Leu Ser Val Leu Gly Met Ala Ala Val Val Ile Gly Ala
    540                 545                 550

atg gtg gct tcc atg cct cgt cat ccg ttt gcc aag ggc acc cac cct   1791
Met Val Ala Ser Met Pro Arg His Pro Phe Ala Lys Gly Thr His Pro
555                 560                 565                 570

cgc ccc ttt ggc caa tca cag ttg aac tcc att ccg ctg cgc atg ctg   1839
Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser Ile Pro Leu Arg Met Leu
                575                 580                 585

ctt aag gtg ctg gtt cca gcg cta tgc ttc ttg agc ttc atg gtg ttc   1887
Leu Lys Val Leu Val Pro Ala Leu Cys Phe Leu Ser Phe Met Val Phe
            590                 595                 600

atg cgt gga cac aat gat ccg gga ggc ggt ttc atc gca gcc cta att   1935
Met Arg Gly His Asn Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile
        605                 610                 615

gcc ggt ggc gcg ctg atg ctc ctg tac ctg tcc aag gcc aaa gat ggc   1983
Ala Gly Gly Ala Leu Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly
    620                 625                 630

cgc att ttc cgc ccg aat gtt cct ttc att ctc act ggt gcg ggc atc   2031
Arg Ile Phe Arg Pro Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile
635                 640                 645                 650

ttg atg gca gtg ttc tcg ggc gta ctg gga ctc acc cac ggt tct ttc   2079
Leu Met Ala Val Phe Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe
                655                 660                 665
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09592160.030502

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ctg tac gcc atc cac ttc aac ttc gta ggc cag cac tgg acc acc tcg   2127
Leu Tyr Ala Ile His Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser
            670                 675                 680

atg atc ttc gac ctc ggc gtg tac ctg gcc gtg ttg ggc atg gtg tcc   2175
Met Ile Phe Asp Leu Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser
        685                 690                 695

atg gca atc aac ggc ctg ggc gga tac ctg cgc cca ggt acc gac aat   2223
Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn
    700                 705                 710

gca gat ctg gac tac gcc cgc cga agt ggc cca ctg cca gca acg cca   2271
Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro
715                 720                 725                 730

acg gtt gaa ccc gaa cca gaa ggc gat gaa gac tgg ccc gaa ccc atc   2319
Thr Val Glu Pro Glu Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile
                735                 740                 745

aac ccc gca ggc gat aac aaa gag gag gca aac cga tgattctcgc        2365
Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala Asn Arg
            750                 755

actgacagtc gcg                                                   2378
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<210> 684
<211> 758
<212> PRT
<213> Corynebacterium glutamicum

<400> 684

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Val Leu Thr Gly Val Ile Ala Val Leu Ile Ala Met Ser Ala Phe Thr
  1               5                  10                  15

Lys Ser Ala Gln Phe Pro Phe His Phe Trp Leu Pro Glu Ala Met Ala
             20                  25                  30

Ala Ala Thr Pro Val Ser Ala Phe Leu His Ala Ala Ala Val Val Lys
         35                  40                  45

Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser Ile Val Phe His Asp Val
     50                  55                  60

Ala Val Trp Asn Trp Leu Leu Ile Ile Val Gly Met Gly Thr Ala Ile
 65                  70                  75                  80

Met Ser Ala Tyr Phe Ala Val Gln Lys Thr Asp Leu Lys Lys Leu Thr
                 85                  90                  95

Ala Tyr Ser Thr Val Ser His Leu Gly Trp Ile Val Ala Thr Ile Gly
            100                 105                 110

Val Gly Thr Pro Phe Ala Leu Gly Ala Ala Ile Val His Thr Leu Ser
        115                 120                 125

His Ala Leu Phe Lys Ser Ser Leu Phe Met Leu Ile Gly Val Ile Asp
    130                 135                 140
```

09852760.1

His Gln Thr Gly Thr Arg Asp Ile Arg Arg Leu Gly Phe Leu Val Lys
145 150 155 160

Lys Met Pro Phe Thr Phe Val Ser Val Leu Ile Gly Ala Leu Ser Met
165 170 175

Ala Ser Val Pro Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile
180 185 190

Thr Ala Phe Met Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu
195 200 205

Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala
210 215 220

Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His
225 230 235 240

Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly
245 250 255

Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro
260 265 270

Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His
275 280 285

Leu Ala Leu Trp His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly
290 295 300

Val Leu Val Ala Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp
305 310 315 320

Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile
325 330 335

Leu Ser Met Leu Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly
340 345 350

Arg Met Ala Asp Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile
355 360 365

Val Leu Leu Trp Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val
370 375 380

Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu Ile
385 390 395 400

Pro Leu Ala Ile Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr Arg
405 410 415

Asn Arg Leu Ser Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val
420 425 430

Ser Phe Gln Met Leu Leu Leu Gly Ala Pro Asp Val Ala Leu Thr Gln
435 440 445

Phe Leu Val Glu Gly Leu Val Val Val Ile Ile Met Met Val Val Arg
450 455 460

His Gln Pro Ala Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg Ser

```
465                 470                 475                 480

Thr Val Leu Val Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val
                485                 490                 495

Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr
            500                 505                 510

Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr
        515                 520                 525

Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val
    530                 535                 540

Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro
545                 550                 555                 560

Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser
                565                 570                 575

Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro
            580                 585                 590

Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp
        595                 600                 605

Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met
    610                 615                 620

Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn
625                 630                 635                 640

Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser
                645                 650                 655

Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe
            660                 665                 670

Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly
        675                 680                 685

Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu
    690                 695                 700

Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala
705                 710                 715                 720

Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro
                725                 730                 735

Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn
            740                 745                 750

Lys Glu Glu Ala Asn Arg
        755
```

<210> 685
<211> 1872
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1849)
<223> FRXA00606

<400> 685
atggataacc agactggcac gcgcgatatt cgtcgcctcg gtttcctggt caagaaaaat 60

gccgttcacg tttgtgtctg tattaatagg tgcgttgtcg atg gca tcg gtt ccg 115
Met Ala Ser Val Pro
1 5

ccg ttg ctc ggc ttc gtg tcc aaa gaa ggc atg atc aca gcg ttc atg 163
Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile Thr Ala Phe Met
10 15 20

gac gcc ccc atc ggc aac tcc tat gtt gta tta ctg ctg gtc ggc gca 211
Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu Leu Val Gly Ala
25 30 35

gca atc ggc gcg gtc cta acc ttc aca tac tcc gcg aaa ctc gtg ctc 259
Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala Lys Leu Val Leu
40 45 50

ggc gca ttc gtc gac ggc cca cgc gac atg tca cac gtc aag gaa gcc 307
Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His Val Lys Glu Ala
55 60 65

ccc gtc tcc ctc tgg ctt ccg gcc gcc ctg cct gga ctt atg tct ctg 355
Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly Leu Met Ser Leu
70 75 80 85

cca cta gtc cta gta ctt tcg ctt ttc gac gcc ccc gtc tcc gcc gca 403
Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro Val Ser Ala Ala
90 95 100

gcc acc tcc gcc gcg ggg gaa gcg gcg cac atg cac ctg gca ttg tgg 451
Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His Leu Ala Leu Trp
105 110 115

cac ggc atc aac acc cca ctg ttg att tcc ttg ggt gtg ctg gtg gcc 499
His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly Val Leu Val Ala
120 125 130

gga atc ctt ggt gtg ctg ttc cgc aaa gag ctg tgg aaa atc gcc gag 547
Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu
135 140 145

acc agc cct ttc ccc atc gcc aca ggc aac gac atc cta tcg atg ctg 595
Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu
150 155 160 165

gtt tac cga gcc aac ttg ctg ggt aaa ttc ttc ggt cgc atg gct gat 643
Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly Arg Met Ala Asp
170 175 180

tcg atg agc cca cgc agg cac ttg gtc agc ctc atc gtg ctg ctc tgg 691
Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile Val Leu Leu Trp
185 190 195

```
gcg ctg gct gct ttt gcc acc att cac ccc tcg gtt cag ctt gca cca   739
Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val Gln Leu Ala Pro
        200                 205                 210

aag caa ccg gga att gat cgt tgg atc gac ctc att ccg ctt gcc atc   787
Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu Ile Pro Leu Ala Ile
    215                 220                 225

atc gcg cta tct gtc ttc ggc ctg ctc acc acc cga aac cgc ctc agc   835
Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr Arg Asn Arg Leu Ser
230                 235                 240                 245

gca gcc gtg ctt gtg ggt acc gtt ggt gtg ggt gtt tcc ttc cag atg   883
Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val Ser Phe Gln Met
                250                 255                 260

cta ctt ctg ggc gct ccc gat gtt gca ctt acc cag ttc ctg gta gaa   931
Leu Leu Leu Gly Ala Pro Asp Val Ala Leu Thr Gln Phe Leu Val Glu
            265                 270                 275

ggc ctc gtc gtg gta atc atc atg atg gtt gtc cgg cac cag cct gcc   979
Gly Leu Val Val Val Ile Ile Met Met Val Val Arg His Gln Pro Ala
        280                 285                 290

aac ttc aag cgc atc aag ccc agc aga agg cgc agc acc gtt ctt gtc   1027
Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg Ser Thr Val Leu Val
    295                 300                 305

gcc gtc ctt gct gcc ttc gcc gca ttc atg gcg gtg tgg gga ttg ctt   1075
Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val Trp Gly Leu Leu
310                 315                 320                 325

ggc cgt cac gaa cgt tct gag ctg gcc atg tgg tac ctc aac caa ggt   1123
Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly
                330                 335                 340

cca gag atc acc tct ggc gcc aac gtg gtg aac acc atc ctc gtg gaa   1171
Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr Ile Leu Val Glu
            345                 350                 355

ttc cgt gca ctg gat acg ttg ggc gag ctc tcc gtg ctt ggc atg gca   1219
Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val Leu Gly Met Ala
        360                 365                 370

gct gtc gtc atc ggt gcg atg gtg gct tcc atg cct cgt cat ccg ttt   1267
Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro Arg His Pro Phe
    375                 380                 385

gcc aag ggc acc cac cct cgc ccc ttt ggc caa tca cag ttg aac tcc   1315
Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser
390                 395                 400                 405

att ccg ctg cgc atg ctg ctt aag gtg ctg gtt cca gcg cta tgc ttc   1363
Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro Ala Leu Cys Phe
                410                 415                 420

ttg agc ttc atg gtg ttc atg cgt gga cac aat gat ccg gga ggc ggt   1411
Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp Pro Gly Gly Gly
            425                 430                 435

ttc atc gca gcc cta att gcc ggt ggc gcg ctg atg ctc ctg tac ctg   1459
```

```
Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met Leu Leu Tyr Leu
        440                 445                 450

tcc aag gcc aaa gat ggc cgc att ttc cgc ccg aat gtt cct ttc att   1507
Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn Val Pro Phe Ile
    455                 460                 465

ctc act ggt gcg ggc atc ttg atg gca gtg ttc tcg ggc gta ctg gga   1555
Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser Gly Val Leu Gly
470                 475                 480                 485

ctc acc cac ggt tct ttc ctg tac gcc atc cac ttc aac ttc gta ggc   1603
Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe Asn Phe Val Gly
                490                 495                 500

cag cac tgg acc acc tcg atg atc ttc gac ctc ggc gtg tac ctg gcc   1651
Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly Val Tyr Leu Ala
            505                 510                 515

gtg ttg ggc atg gtg tcc atg gca atc aac ggc ctg ggc gga tac ctg   1699
Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu
        520                 525                 530

cgc cca ggt acc gac aat gca gat ctg gac tac gcc cgc cga agt ggc   1747
Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly
    535                 540                 545

cca ctg cca gca acg cca acg gtt gaa ccc gaa cca gaa ggc gat gaa   1795
Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro Glu Gly Asp Glu
550                 555                 560                 565

gac tgg ccc gaa ccc atc aac ccc gca ggc gat aac aaa gag gag gca   1843
Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala
                570                 575                 580

aac cga tgattctcgc actgacagtc gcg                                1872
Asn Arg
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<210> 686
<211> 583
<212> PRT
<213> Corynebacterium glutamicum

<400> 686

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Met Ala Ser Val Pro Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met
  1               5                  10                  15

Ile Thr Ala Phe Met Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu
             20                  25                  30

Leu Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser
         35                  40                  45

Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser
     50                  55                  60

His Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro
 65                  70                  75                  80
```

Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala
85 90 95

Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met
100 105 110

His Leu Ala Leu Trp His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu
115 120 125

Gly Val Leu Val Ala Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu
130 135 140

Trp Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp
145 150 155 160

Ile Leu Ser Met Leu Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe
165 170 175

Gly Arg Met Ala Asp Ser Met Ser Pro Arg Arg His Leu Val Ser Leu
180 185 190

Ile Val Leu Leu Trp Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser
195 200 205

Val Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu
210 215 220

Ile Pro Leu Ala Ile Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr
225 230 235 240

Arg Asn Arg Leu Ser Ala Ala Val Leu Val Gly Thr Val Gly Val Gly
245 250 255

Val Ser Phe Gln Met Leu Leu Leu Gly Ala Pro Asp Val Ala Leu Thr
260 265 270

Gln Phe Leu Val Glu Gly Leu Val Val Val Ile Ile Met Met Val Val
275 280 285

Arg His Gln Pro Ala Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg
290 295 300

Ser Thr Val Leu Val Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala
305 310 315 320

Val Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp
325 330 335

Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn
340 345 350

Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser
355 360 365

Val Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met
370 375 380

Pro Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln
385 390 395 400

Ser Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val

```
                405                 410                 415

Pro Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn
            420                 425                 430

Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu
        435                 440                 445

Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro
    450                 455                 460

Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe
465                 470                 475                 480

Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His
                485                 490                 495

Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu
            500                 505                 510

Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly
        515                 520                 525

Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr
    530                 535                 540

Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu
545                 550                 555                 560

Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp
                565                 570                 575

Asn Lys Glu Glu Ala Asn Arg
            580
```

US 2003/0175950 A1

<210> 687
<211> 1653
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1630)
<223> RXN00595

<400> 687
cgacgacacc cggtccatcg aaccagatga cgatcaatcg cctttgacta ctagcgctcg 60

ttcagtcacc aacccaacag atcaggagga taaagcttaa atg gcc atg gat gtt 115
                                                Met Ala Met Asp Val
                                                  1   5

ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg 163
Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala
                10   15   20

gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg 211
Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val
            25   30   35
```
```

```
cct ttc gcg ggt att ttt gct ggc atc tgg ttg ttt gca cac acc gct   259
Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala
         40                  45                  50

gaa cac ggc ccg att gct cac aac gtg ggc ctt tat gtc ggt ggc gtg   307
Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val
     55                  60                  65

gca atc ccc ttt gct gcc gat acg ttc agc gcc atc atg ttg atc acc   355
Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala Ile Met Leu Ile Thr
 70                  75                  80                  85

acc tcg atc gtt gcg gtg gct gcc aac tgg ttt gcc acc atc gtc ggt   403
Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe Ala Thr Ile Val Gly
                 90                  95                 100

gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg   451
Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr Leu Met Leu Ile Thr
            105                 110                 115

ggc gtc aac ggt gct ctg ctg act gcc gat ctg ttc aac ttc ttt gtg   499
Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu Phe Asn Phe Phe Val
        120                 125                 130

ttc atc gaa gtg atg ctg ctg cct tcc tat ggt ttg atc gcc atg acc   547
Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly Leu Ile Ala Met Thr
    135                 140                 145

gga acg tgg gcg cgc cta gcc tct gga cga atc ttc gta cta gtc aat   595
Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile Phe Val Leu Val Asn
150                 155                 160                 165

ctc tct gcc tcc aca ttg ctg gtt gca ggt gtg gga atc gtc tac ggt   643
Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val Gly Ile Val Tyr Gly
                170                 175                 180

gtc ata ggc tca gtc aac atc gca gct ctg caa gat gtc gta gag ggc   691
Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln Asp Val Val Glu Gly
            185                 190                 195

aac ccc ctg gtt gcc agc gca atg ggc atc gtg gtt att gcc atc gcg   739
Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val Val Ile Ala Ile Ala
        200                 205                 210

gtt aaa gcc ggt gta ttc cca gtg cac aca tgg ctg cca cgc acc tat   787
Val Lys Ala Gly Val Phe Pro Val His Thr Trp Leu Pro Arg Thr Tyr
    215                 220                 225

cct ggt aca tca gca gct gtg atg ggg ttg ttc tcc ggt ttg cac acc   835
Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe Ser Gly Leu His Thr
230                 235                 240                 245

aaa gtc gcg gta tac atg ctc tat cgc att tgg gtc cac att ttt aac   883
Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp Val His Ile Phe Asn
                250                 255                 260

atg gat ccc acg tgg aat tgg ctg att gtc gca ttc atg gtg ata tcc   931
Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala Phe Met Val Ile Ser
            265                 270                 275

atg ctg gtc ggt ggc ttc gct gga ctt gct gaa aac tcc atc cgt cgc   979
```

```
Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu Asn Ser Ile Arg Arg
        280                 285                 290

gtc ctt gcc tac caa atg gtc aac ggc atg cca ttt att ctc atc atg   1027
Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro Phe Ile Leu Ile Met
    295                 300                 305

atg gcg ttt acc tct gac gat cca cag cgc gca ctt gcc gct ggt ctg   1075
Met Ala Phe Thr Ser Asp Asp Pro Gln Arg Ala Leu Ala Ala Gly Leu
310                 315                 320                 325

ttg tac acc ctg cac cac atg atc acc atc gcc gca ttg gtg ctc act   1123
Leu Tyr Thr Leu His His Met Ile Thr Ile Ala Ala Leu Val Leu Thr
                330                 335                 340

tcc ggc gca atc gaa gaa acc tac ggc acc ggt atg ttg tcc aag ctg   1171
Ser Gly Ala Ile Glu Glu Thr Tyr Gly Thr Gly Met Leu Ser Lys Leu
            345                 350                 355

tct ggc ctt gca cgc cgc gaa ccc gtc gtc gca gca gtg ttc gct gca   1219
Ser Gly Leu Ala Arg Arg Glu Pro Val Val Ala Ala Val Phe Ala Ala
        360                 365                 370

ggt gcc ttc tct gtt gtc ggt ttc cca ccg ttt tcc ggt atg tgg ggc   1267
Gly Ala Phe Ser Val Val Gly Phe Pro Pro Phe Ser Gly Met Trp Gly
    375                 380                 385

aaa gcg ctc atc ctg ctc gag atc gcc cgc gtc ggc aat att gca gca   1315
Lys Ala Leu Ile Leu Leu Glu Ile Ala Arg Val Gly Asn Ile Ala Ala
390                 395                 400                 405

tgg atc gca atc gcc gcc atc atc atc gcc agc ctg ggc gca ctg ctc   1363
Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser Leu Gly Ala Leu Leu
                410                 415                 420

tcg atg atc cgc gtg tgg cgt gaa gtc ttc tgg ggt ggc gca atg cac   1411
Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp Gly Gly Ala Met His
            425                 430                 435

cag cgc ggc gtc tcg ccg cag ctg cgc atc agc cca gca aaa atc gcc   1459
Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser Pro Ala Lys Ile Ala
        440                 445                 450

cca gcg ctc agc ctg atc att tta tcg gta ggc atg ttc atc ttc gcg   1507
Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly Met Phe Ile Phe Ala
    455                 460                 465

ggc ccg ctt atc gac gcg acc ctc acc gcc acc gac ggc ctc ttg aac   1555
Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr Asp Gly Leu Leu Asn
470                 475                 480                 485

acc gat gca tac caa cag gct gtg ctc ggt gaa aat gcc atc gga gtg   1603
Thr Asp Ala Tyr Gln Gln Ala Val Leu Gly Glu Asn Ala Ile Gly Val
                490                 495                 500

cca agc cct agc tac cag gga gga aac taatgcttaa cgccctgaaa         1650
Pro Ser Pro Ser Tyr Gln Gly Gly Asn
            505                 510

ttc                                                              1653
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PCT/US2003/030693

<210> 688
<211> 510
<212> PRT
<213> Corynebacterium glutamicum

<400> 688

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Met Ala Met Asp Val Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala
 1               5                  10                  15

Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile
            20                  25                  30

Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
        35                  40                  45

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
    50                  55                  60

Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
65                  70                  75                  80

Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
                85                  90                  95

Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
            100                 105                 110

Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
        115                 120                 125

Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
    130                 135                 140

Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
145                 150                 155                 160

Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
                165                 170                 175

Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
            180                 185                 190

Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
        195                 200                 205

Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
    210                 215                 220

Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
225                 230                 235                 240

Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp
                245                 250                 255

Val His Ile Phe Asn Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala
            260                 265                 270

Phe Met Val Ile Ser Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu
        275                 280                 285
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9950340.960509

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Asn Ser Ile Arg Arg Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro
    290                 295                 300

Phe Ile Leu Ile Met Met Ala Phe Thr Ser Asp Asp Pro Gln Arg Ala
305                 310                 315                 320

Leu Ala Ala Gly Leu Leu Tyr Thr Leu His His Met Ile Thr Ile Ala
                325                 330                 335

Ala Leu Val Leu Thr Ser Gly Ala Ile Glu Glu Thr Tyr Gly Thr Gly
            340                 345                 350

Met Leu Ser Lys Leu Ser Gly Leu Ala Arg Arg Glu Pro Val Val Ala
        355                 360                 365

Ala Val Phe Ala Ala Gly Ala Phe Ser Val Val Gly Phe Pro Pro Phe
    370                 375                 380

Ser Gly Met Trp Gly Lys Ala Leu Ile Leu Leu Glu Ile Ala Arg Val
385                 390                 395                 400

Gly Asn Ile Ala Ala Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser
                405                 410                 415

Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp
            420                 425                 430

Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser
        435                 440                 445

Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly
    450                 455                 460

Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr
465                 470                 475                 480

Asp Gly Leu Leu Asn Thr Asp Ala Tyr Gln Gln Ala Val Leu Gly Glu
                485                 490                 495

Asn Ala Ile Gly Val Pro Ser Pro Ser Tyr Gln Gly Gly Asn
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<213> Corynebacterium glutamicum

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<223> FRXA00608

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ttcagtcacc aacccaacag atcaggagga taaagcttaa atg gcc atg gat gtt   115
                                              Met Ala Met Asp Val
                                                1               5

ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg   163
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Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala
                10                  15                  20

gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg   211
Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val
            25                  30                  35

cct ttc gcg ggt att ttt gct ggc atc tgg ttg ttt gca cac acc gct   259
Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala
        40                  45                  50

gaa cac ggc ccg att gct cac aac gtg ggc ctt tat gtc ggt ggc gtg   307
Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val
    55                  60                  65

gca atc ccc ttt gct gcc gat acg ttc agc gcc atc atg ttg atc acc   355
Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala Ile Met Leu Ile Thr
70                  75                  80                  85

acc tcg atc gtt gcg gtg gct gcc aac tgg ttt gcc acc atc gtc ggt   403
Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe Ala Thr Ile Val Gly
                90                  95                  100

gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg   451
Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr Leu Met Leu Ile Thr
            105                 110                 115

ggc gtc aac ggt gct ctg ctg act gcc gat ctg ttc aac ttc ttt gtg   499
Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu Phe Asn Phe Phe Val
        120                 125                 130

ttc atc gaa gtg atg ctg ctg cct tcc tat ggt ttg atc gcc atg acc   547
Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly Leu Ile Ala Met Thr
    135                 140                 145

gga acg tgg gcg cgc cta gcc tct gga cga atc ttc gta cta gtc aat   595
Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile Phe Val Leu Val Asn
150                 155                 160                 165

ctc tct gcc tcc aca ttg ctg gtt gca ggt gtg gga atc gtc tac ggt   643
Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val Gly Ile Val Tyr Gly
                170                 175                 180

gtc ata ggc tca gtc aac atc gca gct ctg caa gat gtc gta gag ggc   691
Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln Asp Val Val Glu Gly
            185                 190                 195

aac ccc ctg gtt gcc agc gca atg ggc atc gtg gtt att gcc atc gcg   739
Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val Val Ile Ala Ile Ala
        200                 205                 210

gtt aaa gcc ggt gta ttc cca gtg cac aca tgg ctg cca cgc acc tat   787
Val Lys Ala Gly Val Phe Pro Val His Thr Trp Leu Pro Arg Thr Tyr
    215                 220                 225

cct ggt aca tca gca gct gtg atg ggg ttg ttc tcc ggt ttg cac acc   835
Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe Ser Gly Leu His Thr
230                 235                 240                 245

aaa gtc gcg gta tac atg ctc tat cgc att                          865
Lys Val Ala Val Tyr Met Leu Tyr Arg Ile
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250 255

<210> 690
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<213> Corynebacterium glutamicum

<400> 690

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Met Ala Met Asp Val Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala
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Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile
            20                  25                  30

Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
        35                  40                  45

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
    50                  55                  60

Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
65                  70                  75                  80

Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
                85                  90                  95

Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
            100                 105                 110

Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
        115                 120                 125

Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
    130                 135                 140

Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
145                 150                 155                 160

Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
                165                 170                 175

Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
            180                 185                 190

Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
        195                 200                 205

Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
    210                 215                 220

Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
225                 230                 235                 240

Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile
                245                 250                 255
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<213> Corynebacterium glutamicum

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<223> RXA00913

<400> 691

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  1               5                  10                  15

ctt gca ctg acc gtt gcg cac tcc ttg ttt aag gca aca ttg ttc atg   96
Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met
            20                  25                  30

aca gtt ggt gcc att gac cac acc acc gga act cgt gat att cgt aaa   144
Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys
        35                  40                  45

ctc tcc ggt ctg tgg cgt aaa caa ccg atc ctg ttc gcc gtt gct gct   192
Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala
    50                  55                  60

gtt tcg gcg gcg tcc atg gct ggt att ccg cca ctg ttt ggt ttt atc   240
Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile
65                  70                  75                  80

gcc aag gaa aca gcg ctg gat acc gtg ttg aat gag cag atg ttg cat   288
Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His
                85                  90                  95

ggc atg cca ggt cga ttg atg ctg gct ggc atc gtt ttg ggt tcc atc   336
Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile
            100                 105                 110

ttc acc atg gca tat tcc tgc tac ttc ctg tac gaa gcc ttt gcc acg   384
Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr
        115                 120                 125

aag cac tcc aaa ttc cca gag gcc aac ggt gtc tca cct gca gtg gag   432
Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu
    130                 135                 140

gca atg cat ccg gtg aag ttt aag ctg tgg atc gca cct gtc atc ctg   480
Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu
145                 150                 155                 160

gct att ttg acc gta gtg ttt ggt gtt ttc ccc aag cca gtg tcg gaa   528
Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu
                165                 170                 175

gca att gtc acg cat ctt gat aac gtc acg cca tcg ctt gat gat gtc   576
Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val
            180                 185                 190

cac acc aaa ctg gcc ttg tgg cat ggt ctg aat cta ccg ctg ctg ctg   624
His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu
        195                 200                 205

tct gtg gtg atc atc att tcc gga ttc atc atc ttc tgg gag cga gac   672
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Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp
    210                 215                 220

acc gtc gaa cgt ttg cgc cct aac acc gca gcg ttt ggc agt gcc gat   720
Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp
225                 230                 235                 240

acc gcc tac gac gcc att ctt gat gca ctg cgt gtg ctc tcc cac cgc   768
Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg
                245                 250                 255

ctg act gca tcc acc cag cgt ggt tct ttg acc ctg aac gtc ggt gtg   816
Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val
            260                 265                 270

atc ttc ttc gtc ctc acg att gtt ccg ctg atc gct ttg atc act ggc   864
Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly
        275                 280                 285

gaa caa agc gat gtc cgc atg gag ctg tgg gat agc cct att cag ggc   912
Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly
    290                 295                 300

ttc atc gcg gcc atc att atc gtc gtt gcg att gtg gca acc acc atg   960
Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met
305                 310                 315                 320

gat aac cgt ttg tct gcg ctg att ttg gtg ggt gtg aca ggt tat ggc  1008
Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly
                325                 330                 335

att gcc gtt atc ttc gcg cta cat ggc gca ccg gac ttg gcg cta acc  1056
Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr
            340                 345                 350

cag gtg ctg gtg gag acc atc gtc atg gtg gta ttc atg ctg gtg ctg  1104
Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu
        355                 360                 365

cgt aaa atg ccg aca gaa gtt gcg tgg aag gca gaa cct aaa cag tct  1152
Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser
    370                 375                 380

cgc gtg cga gcg tgg ctt gct ggc gcc acc gga ttg tcc gtt gtt att  1200
Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile
385                 390                 395                 400

gtc acc att ttt gcc atg aat gct cgc acc act gaa ccg atc tct gta  1248
Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val
                405                 410                 415

tac atg cag gat ctg gcc tat gag atc gga cat ggc gca aac acc gtc  1296
Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val
            420                 425                 430

aac gta ctg ctc gta gac ctg cgt ggt ttt gat acc ttc ggt gaa att  1344
Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile
        435                 440                 445

tcc gtc ctt gtg atc gcg gca acc ggt atc gcc tcc ctg gtc tac cga  1392
Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg
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    450                 455                 460

aac cgc agc ttc cgc aag gat tct cgc aga cca acc ctg gct acc act   1440
Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr
465                 470                 475                 480

ggt cgc cgt tgg ttg gct gct gct gtt gat acc gaa agg gcg cag aac   1488
Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn
                485                 490                 495

cgc tcg ctg atg gtt gat gtg gca acg cgc atc ctc ttc cct gcc atg   1536
Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met
            500                 505                 510

atc atg ttg tct gtg tac ttc ttc ttc gcc gga cac aac gcg ccg ggc   1584
Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly
        515                 520                 525

ggc gga ttc gcc ggc ggc ctt gtt gcc tcc ttg gcg ttc gcc ttg cgc   1632
Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg
    530                 535                 540

tac ctt gcc ggt gga cgt gaa gaa ctt gaa gaa gcg ttg cct atc gac   1680
Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp
545                 550                 555                 560

gcc ggc cgt atc ttg gga act gga cta ttt gtt tct gca act gca gtg   1728
Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val
                565                 570                 575

ctg tgg ccc atg gtt ctt ctt ggt gaa cca ccg ctg acc tcc cat att   1776
Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile
            580                 585                 590

tgg gat ctc aca ctg cca ctt atc ggt gag att cac att gca tcc gcg   1824
Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala
        595                 600                 605

ctg ctc ttt gac ctt ggt gtc tac ctg atc gtc atc ggt ttg acc atg   1872
Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met
    610                 615                 620

cac att ctc aac agt ttg ggc ggc cag ctc gac cgc gat gag gaa atg   1920
His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met
625                 630                 635                 640

cgt aag cag cgt gcg cgc gac cga gct cga cgc ttg gcg cgc aac cag   1968
Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln
                645                 650                 655

cgt cga gaa gca gca acc gtc ggc gca cgc agg tcg aac gag aaa tcg   2016
Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser
            660                 665                 670

aca cgc caa atg ccg acg att cgg cct cca ggg gca gac aca gaa tcg   2064
Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser
        675                 680                 685

gtg gag cag aac ggt gag aac cag acg tcg ata agc aca aag cgt tta   2112
Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu
    690                 695                 700
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aag cag 2118
Lys Gln
705

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<213> Corynebacterium glutamicum

<400> 692
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1 5 10 15

Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met
20 25 30

Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys
35 40 45

Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala
50 55 60

Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile
65 70 75 80

Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His
85 90 95

Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile
100 105 110

Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr
115 120 125

Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu
130 135 140

Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu
145 150 155 160

Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu
165 170 175

Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val
180 185 190

His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu
195 200 205

Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp
210 215 220

Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp
225 230 235 240

Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg
245 250 255

Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val

260 265 270

Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly
275 280 285

Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly
290 295 300

Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met
305 310 315 320

Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly
325 330 335

Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr
340 345 350

Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu
355 360 365

Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser
370 375 380

Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile
385 390 395 400

Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val
405 410 415

Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val
420 425 430

Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile
435 440 445

Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg
450 455 460

Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr
465 470 475 480

Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn
485 490 495

Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met
500 505 510

Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly
515 520 525

Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg
530 535 540

Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp
545 550 555 560

Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val
565 570 575

Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile
580 585 590

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Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala
        595                 600                 605

Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met
    610                 615                 620

His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met
625                 630                 635                 640

Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln
                645                 650                 655

Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser
            660                 665                 670

Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser
        675                 680                 685

Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu
    690                 695                 700

Lys Gln
705
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09292010

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<223> RXA00909

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cagagtaatc cacaacgcgc aaaggggaac tggagaacac gtg ctc att ctt ttt   115
                                            Val Leu Ile Leu Phe
                                              1               5

ctc gcg ctc act gca gcc gca gta gtc gcc ccc atc ctg atc cga act   163
Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr
                  10                  15                  20

ctc ggt cga cca gct ttt ggt ctg ctg gcg ctt gta cct ggc att ggt   211
Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly
              25                  30                  35

ttt ttc tgg gtg ctt tcg gag ttc atc aaa ggc act ttc aag gat gga   259
Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly
          40                  45                  50

ggt gaa ctc ctc ctc cac tat gcc tgg atg cct tcg gct cac ctc aat   307
Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn
      55                  60                  65

atc gat ttc cgt atg gat tcc ctc gcg gcg ctg ttc tca ctc atc gtc   355
Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val
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70                  75                  80                  85

tta ggc gtg ggc gcc cta gtg ctg ctg tac tgc tgg gga tat ttt gat   403
Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys Trp Gly Tyr Phe Asp
                90                  95                 100

tcc aac gcg ggt cgc ctc agt gcc ttt ggt gct gaa ctg gtg gcc ttc   451
Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala Glu Leu Val Ala Phe
            105                 110                 115

gcc atg gcg atg ttt ggt ctt gtc att tca gac aac atc ctg ctg atg   499
Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp Asn Ile Leu Leu Met
        120                 125                 130

tac gtc ttc tgg gaa atc acc tcc gtt tta tcc ttc ctc ctg gtt ggt   547
Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser Phe Leu Leu Val Gly
    135                 140                 145

tat tac ggc gaa cgc gca tct tca cgt cgc tct gca ggt caa gcc ttg   595
Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser Ala Gly Gln Ala Leu
150                 155                 160                 165

atg gtg acc acc ctg ggt gga ttg gcc atg ctg gtg ggc atc att ttg   643
Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu Val Gly Ile Ile Leu
                170                 175                 180

atg ggt acc caa act ggc gtg tgg cga ttc tct gag atc cct gcc tac   691
Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser Glu Ile Pro Ala Tyr
            185                 190                 195

tca agc tcc tgg gca gat gtg ccg tat att tcc gct gct gct gcc ctt   739
Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser Ala Ala Ala Ala Leu
        200                 205                 210

atc ttg gct ggc gca cta tcc aaa tcg gct atc gca cca acc cac ttc   787
Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile Ala Pro Thr His Phe
    215                 220                 225

tgg ctt ccc ggc gcg atg gcc gca cca acg ccg gtg tct gct tac ctg   835
Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro Val Ser Ala Tyr Leu
230                 235                 240                 245

cac tcc gca gcg atg gtg aag gcg ggt att tac ctt gtg gct cgc ctc   883
His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr Leu Val Ala Arg Leu
                250                 255                 260

tct cca gac ctc aac gta gtt ggt tcg tgg tac ctg atc atc atc ccg   931
Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr Leu Ile Ile Ile Pro
            265                 270                 275

ttg ggc atg ttg acc atg ctc atg                                  955
Leu Gly Met Leu Thr Met Leu Met
        280                 285
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<210> 694
<211> 285
<212> PRT
<213> Corynebacterium glutamicum

<400> 694

```
Val Leu Ile Leu Phe Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro
 1               5                  10                  15

Ile Leu Ile Arg Thr Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu
            20                  25                  30

Val Pro Gly Ile Gly Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly
        35                  40                  45

Thr Phe Lys Asp Gly Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro
    50                  55                  60

Ser Ala His Leu Asn Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu
65                  70                  75                  80

Phe Ser Leu Ile Val Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys
                85                  90                  95

Trp Gly Tyr Phe Asp Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala
            100                 105                 110

Glu Leu Val Ala Phe Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp
        115                 120                 125

Asn Ile Leu Leu Met Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser
    130                 135                 140

Phe Leu Leu Val Gly Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser
145                 150                 155                 160

Ala Gly Gln Ala Leu Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu
                165                 170                 175

Val Gly Ile Ile Leu Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser
            180                 185                 190

Glu Ile Pro Ala Tyr Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser
        195                 200                 205

Ala Ala Ala Ala Leu Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile
    210                 215                 220

Ala Pro Thr His Phe Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro
225                 230                 235                 240

Val Ser Ala Tyr Leu His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr
                245                 250                 255

Leu Val Ala Arg Leu Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr
            260                 265                 270

Leu Ile Ile Ile Pro Leu Gly Met Leu Thr Met Leu Met
        275                 280                 285
```

<210> 695
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(904)
<223> RXA00700

<400> 695
acgccccaca agtcgcaaaa atcaccgccg gcatccaaga ggaatcacac tggctcacag 60

tctcggccgt gaaagctgcg ctagggcatg gtgaaatctc atg atc aac gcc atc 115
Met Ile Asn Ala Ile
1 5

aca ctc aag ccc aaa acc ttc ctc acc tta agc ttc ctt gcg gtt ttg 163
Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser Phe Leu Ala Val Leu
10 15 20

agc atc gtg att ttc ttc tgg ccg ctg atc gtc aac ccg gaa tcc ttc 211
Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val Asn Pro Glu Ser Phe
25 30 35

ctg tcc gac aaa gcc caa gcg ccc ctc tac atc gcg atc gtc att ccc 259
Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile Ala Ile Val Ile Pro
40 45 50

ctc gtg ctg gcc gct gtc atc gcc gaa atc agt gaa aac gga ttc gac 307
Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser Glu Asn Gly Phe Asp
55 60 65

gtt aaa gcc gta gcc atg ctc ggc gtc ctc acc gcc atg gtt gcc gta 355
Val Lys Ala Val Ala Met Leu Gly Val Leu Thr Ala Met Val Ala Val
70 75 80 85

gtc cga cca ttc ggt gcc ggc gca gca ggc ttt gaa gca gtc ttc ttt 403
Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe Glu Ala Val Phe Phe
90 95 100

gtc ctc atc ctc ggc gga cga gcc ttc gga ccc ggc ttc gga ttc atc 451
Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro Gly Phe Gly Phe Ile
105 110 115

ctc ggc aac acc gga ctg ttc gca tcc gcg ctg ctc acc gca gga atc 499
Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu Leu Thr Ala Gly Ile
120 125 130

gga ccg tgg ctc ccc tac caa atg ctc gca gcc gcc tgg gtc agc ttc 547
Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala Ala Trp Val Ser Phe
135 140 145

ggc gcc ggc cta ctc ccc caa gta cgc ggc aaa aag gaa atg ctc atc 595
Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys Lys Glu Met Leu Ile
150 155 160 165

atc gtc cta tac gcc atc gtc tct tca ctc ggc tac gga acc atg atg 643
Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly Tyr Gly Thr Met Met
170 175 180

aac atg agc ttc tgg ccc tac gcc atc ggt gtc acc agc ggg ctt tcc 691
Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val Thr Ser Gly Leu Ser
185 190 195

ttc aca ccc ggc gcg ccc gtc ctg gaa aac ctc cac acc ttc atg ctg 739
Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu His Thr Phe Met Leu

```
        200                 205                 210

ttc tgc ctc acc aca tcc atg ggt tgg gat ctc ggc cgc gcc ttc ttc   787
Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu Gly Arg Ala Phe Phe
    215                 220                 225

acc tca gtg cta tta ctg ctc aca gcc aaa ccc gtt tta ggt gct tta   835
Thr Ser Val Leu Leu Leu Leu Thr Ala Lys Pro Val Leu Gly Ala Leu
230                 235                 240                 245

cga cgc gcc agc cgc cgc gcc gct ttc ggc gtc gag cgt gac ttc ggg   883
Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val Glu Arg Asp Phe Gly
                250                 255                 260

gag gcc ggg gtg cct cgg gtc taaagatttt gttggcttgc ttc             927
Glu Ala Gly Val Pro Arg Val
            265
```

<210> 696
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 696

```
Met Ile Asn Ala Ile Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser
  1               5                  10                  15

Phe Leu Ala Val Leu Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val
            20                  25                  30

Asn Pro Glu Ser Phe Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile
        35                  40                  45

Ala Ile Val Ile Pro Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser
    50                  55                  60

Glu Asn Gly Phe Asp Val Lys Ala Val Ala Met Leu Gly Val Leu Thr
65                  70                  75                  80

Ala Met Val Ala Val Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe
                85                  90                  95

Glu Ala Val Phe Phe Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro
            100                 105                 110

Gly Phe Gly Phe Ile Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu
        115                 120                 125

Leu Thr Ala Gly Ile Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala
    130                 135                 140

Ala Trp Val Ser Phe Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys
145                 150                 155                 160

Lys Glu Met Leu Ile Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly
                165                 170                 175

Tyr Gly Thr Met Met Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val
            180                 185                 190
```

```
Thr Ser Gly Leu Ser Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu
        195                 200                 205

His Thr Phe Met Leu Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu
    210                 215                 220

Gly Arg Ala Phe Phe Thr Ser Val Leu Leu Leu Leu Thr Ala Lys Pro
225                 230                 235                 240

Val Leu Gly Ala Leu Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val
                245                 250                 255

Glu Arg Asp Phe Gly Glu Ala Gly Val Pro Arg Val
            260                 265


<210> 697
<211> 1587
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1564)
<223> RXN00483

<400> 697
agacccaaga gtaaaatccc aggatttgct tatacttgcg ctcatggata atcaacttcg 60

tcccactttg cattatcaag ctcaaaaccc gcaccggcga gtg ctg gtc acc ggt   115
                                            Val Leu Val Thr Gly
                                              1               5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc   163
Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala
                  10                  15                  20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc   211
Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg
              25                  30                  35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac   259
Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp
          40                  45                  50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat   307
Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr
      55                  60                  65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag   355
Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu
  70                  75                  80                  85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata   403
Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile
                  90                  95                 100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata   451
Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile
              105                 110                 115
```

```
gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att   499
Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile
        120                 125                 130

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att   547
Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile
    135                 140                 145

att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag   595
Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu
150                 155                 160                 165

cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag   643
Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu
                170                 175                 180

cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat   691
Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp
            185                 190                 195

tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg   739
Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser
        200                 205                 210

tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg   787
Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu
    215                 220                 225

aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta   835
Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu
230                 235                 240                 245

tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct   883
Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser
                250                 255                 260

ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac   931
Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His
            265                 270                 275

agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat   979
Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr
        280                 285                 290

cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt   1027
Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val
    295                 300                 305

cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc   1075
Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly
310                 315                 320                 325

cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc   1123
Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val
                330                 335                 340

cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att   1171
Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile
            345                 350                 355

gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg   1219
```

```
Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp
        360                 365                 370

cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc   1267
Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly
    375                 380                 385

gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg   1315
Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp
390                 395                 400                 405

tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca   1363
Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala
                410                 415                 420

gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac   1411
Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp
            425                 430                 435

aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg   1459
Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro
        440                 445                 450

aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat   1507
Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His
    455                 460                 465

gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt   1555
Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg
470                 475                 480                 485

aaa ctc act taatcgcaga gtaggcgtct aaa                            1587
Lys Leu Thr
```

EP 1 108 790 A2

<210> 698
<211> 488
<212> PRT
<213> Corynebacterium glutamicum

<400> 698

```
Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr
  1               5                  10                  15

Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys
            20                  25                  30

Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
        35                  40                  45

Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
    50                  55                  60

Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
65                  70                  75                  80

Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
                85                  90                  95

Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
```

```
            100                 105                 110

Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
        115                 120                 125

Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu
    130                 135                 140

Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile
145                 150                 155                 160

Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile
                165                 170                 175

Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu
            180                 185                 190

Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile
        195                 200                 205

Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala
    210                 215                 220

Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu
225                 230                 235                 240

Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val
                245                 250                 255

Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala
            260                 265                 270

Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp
        275                 280                 285

Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu
    290                 295                 300

Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln
305                 310                 315                 320

Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala
                325                 330                 335

Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln
            340                 345                 350

Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser
        355                 360                 365

Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly
    370                 375                 380

Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly
385                 390                 395                 400

Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg
                405                 410                 415

Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile
            420                 425                 430
```

09892120.030902

```
Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg
        435                 440                 445

Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val
    450                 455                 460

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
465                 470                 475                 480

Leu Lys Ala Ala Arg Lys Leu Thr
                485
```

<210> 699
<211> 1587
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1564)
<223> FRXA00483

<400> 699

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agacccaaga gtaaaatccc aggatttgct tatacttgcg ctcatggata atcaacttcg 60

tcccactttg cattatcaag ctcaaaaccc gcaccggcga gtg ctg gtc acc ggt   115
                                            Val Leu Val Thr Gly
                                              1               5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc   163
Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala
                10                  15                  20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc   211
Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg
            25                  30                  35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac   259
Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp
        40                  45                  50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat   307
Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr
    55                  60                  65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag   355
Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu
70                  75                  80                  85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata   403
Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile
                90                  95                  100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata   451
Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile
            105                 110                 115

gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att   499
Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile
```

```
        120                 125                 130

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att   547
Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile
    135                 140                 145

att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag   595
Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu
150                 155                 160                 165

cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag   643
Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu
                170                 175                 180

cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat   691
Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp
            185                 190                 195

tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg   739
Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser
        200                 205                 210

tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg   787
Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu
    215                 220                 225

aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta   835
Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu
230                 235                 240                 245

tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct   883
Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser
                250                 255                 260

ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac   931
Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His
            265                 270                 275

agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat   979
Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr
        280                 285                 290

cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt   1027
Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val
    295                 300                 305

cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc   1075
Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly
310                 315                 320                 325

cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc   1123
Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val
                330                 335                 340

cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att   1171
Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile
            345                 350                 355

gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg   1219
Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp
        360                 365                 370
```

09609260.1050302

```
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc   1267
Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly
    375                 380                 385

gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg   1315
Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp
390                 395                 400                 405

tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca   1363
Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala
                410                 415                 420

gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac   1411
Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp
            425                 430                 435

aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg   1459
Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro
        440                 445                 450

aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat   1507
Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His
    455                 460                 465

gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt   1555
Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg
470                 475                 480                 485

aaa ctc act taatcgcaga gtaggcgtct aaa                            1587
Lys Leu Thr
```

<210> 700
<211> 488
<212> PRT
<213> Corynebacterium glutamicum

<400> 700

```
Val Leu Val Thr Gly Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr
  1               5                  10                  15

Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys
            20                  25                  30

Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
        35                  40                  45

Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
    50                  55                  60

Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
65                  70                  75                  80

Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
                85                  90                  95

Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
            100                 105                 110
```

```
Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
        115                 120                 125

Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu
    130                 135                 140

Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile
145                 150                 155                 160

Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile
                165                 170                 175

Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu
            180                 185                 190

Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile
        195                 200                 205

Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala
    210                 215                 220

Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu
225                 230                 235                 240

Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val
                245                 250                 255

Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala
            260                 265                 270

Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp
        275                 280                 285

Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu
    290                 295                 300

Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln
305                 310                 315                 320

Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala
                325                 330                 335

Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln
            340                 345                 350

Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser
        355                 360                 365

Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly
    370                 375                 380

Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly
385                 390                 395                 400

Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg
                405                 410                 415

Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile
            420                 425                 430

Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg
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```
        435                 440                 445

Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val
    450                 455                 460

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
465                 470                 475                 480

Leu Lys Ala Ala Arg Lys Leu Thr
                485
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<210> 701
<211> 612
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(589)
<223> RXA01534

<400> 701

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attgctctca tcggttcgat atagactgaa ttgtctaggt taatatccaa tatggaagaa 60

aaactagaca gttaagtaga ctgaatggcc tactaggtgc atg act tca gca atc   115
                                            Met Thr Ser Ala Ile
                                              1               5

acc acc gca act gat ctt cgc tcc gta ctg cga aac gta cca acc cca   163
Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg Asn Val Pro Thr Pro
                 10                  15                  20

att agc ttc att gca acc cac acc gat cag cct ctg ggc atg atc gtt   211
Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro Leu Gly Met Ile Val
             25                  30                  35

ggt tca ttc gtc agc att agc gcc gaa cca cca ttg gta ggc atc ttc   259
Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro Leu Val Gly Ile Phe
         40                  45                  50

ttg cag aag agc tct tct tca tgg cca gct atc gag cag gca tta gtt   307
Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile Glu Gln Ala Leu Val
     55                  60                  65

acc ggc caa gag cta ggc att tct atc ctc ggc ggg gca cac gca gac   355
Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly Gly Ala His Ala Asp
 70                  75                  80                  85

cat gtg cgt aag ctt tct ggc cca tcc gac cag cgc ttt gaa aac ctt   403
His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln Arg Phe Glu Asn Leu
                 90                  95                 100

ggg tgg gca tcc acc gaa aac ggt gcg att cac ctt gaa ggc gct gat   451
Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His Leu Glu Gly Ala Asp
            105                 110                 115

gca caa cta acc acg aaa ctt cat gat ctc cag gaa atc ggc gat cac   499
Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln Glu Ile Gly Asp His
        120                 125                 130
```

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ttc ttt gca gtt cta gaa gtt att gac gct tcc gct gac caa gac ttc   547
Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser Ala Asp Gln Asp Phe
    135                 140                 145

agc tca gcg ctg gtg tac cac cgc tca cag gtg tcc tcg ctg          589
Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val Ser Ser Leu
150                 155                 160

taggacacta aattttaaga ggg                                       612


<210> 702
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 702
Met Thr Ser Ala Ile Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg
  1               5                  10                  15

Asn Val Pro Thr Pro Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro
            20                  25                  30

Leu Gly Met Ile Val Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro
        35                  40                  45

Leu Val Gly Ile Phe Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile
    50                  55                  60

Glu Gln Ala Leu Val Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly
65                  70                  75                  80

Gly Ala His Ala Asp His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln
                85                  90                  95

Arg Phe Glu Asn Leu Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His
            100                 105                 110

Leu Glu Gly Ala Asp Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln
        115                 120                 125

Glu Ile Gly Asp His Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser
    130                 135                 140

Ala Asp Gln Asp Phe Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val
145                 150                 155                 160

Ser Ser Leu


<210> 703
<211> 1134
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1111)
<223> RXA00288
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acacgggcat gaaacgtacc caagggctaa catcgggggc atg agc gcg caa atg 115
Met Ser Ala Gln Met
1 5

gat acc cct gat ccc act atg tct gct gtt gca atg tta gat tcc atc 163
Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala Met Leu Asp Ser Ile
10 15 20

cct tct gat caa cca gat ttc ctg atc gat gta gaa gta gat cga cca 211
Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val Glu Val Asp Arg Pro
25 30 35

act ccc gga cca cat gat ctg cta gtc cac att gag gcg gtc tca att 259
Thr Pro Gly Pro His Asp Leu Leu Val His Ile Glu Ala Val Ser Ile
40 45 50

aac cct gtt gat acc aag gta cgc atg cgg gcc ggg aag caa aag cat 307
Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala Gly Lys Gln Lys His
55 60 65

cct aaa att tta ggt ttt gat gct gca ggt gag gtg gtg gct gtt gga 355
Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu Val Val Ala Val Gly
70 75 80 85

tcg cag gtc acg ctc ttc aat gtt ggt gac aaa gtg ttc tac gca gga 403
Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys Val Phe Tyr Ala Gly
90 95 100

tcc aat cag cgt cca gga agt aac gca gag tac cag gtg gtg gat gaa 451
Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr Gln Val Val Asp Glu
105 110 115

cgg ctg gtg ggt cac gca cca caa agc ttg ggg gca cac gac gcc gct 499
Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly Ala His Asp Ala Ala
120 125 130

gct ctc cca ctt gtc gcg ctc act gca tgg gag tca ctt ttt gac cga 547
Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu Ser Leu Phe Asp Arg
135 140 145

ttg gga gta act cag tca act act gga aca ctg ttg gtc ttg ggc ggt 595
Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu Leu Val Leu Gly Gly
150 155 160 165

tca gga ggt gtg cct tca gct ctt att caa ctt gct cga gct ctc act 643
Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu Ala Arg Ala Leu Thr
170 175 180

ggt ctg aaa gta gtg gca aca gct tct cgc cct gaa tca caa gaa tgg 691
Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro Glu Ser Gln Glu Trp
185 190 195

gtg aca aag ctc ggt gct cat gag gtg att gat cac tcc aag gat ttg 739
Val Thr Lys Leu Gly Ala His Glu Val Ile Asp His Ser Lys Asp Leu
200 205 210

agt gag caa atc tcc gac gtg gat ttt gtt ttc agc tcg tgg act act 787
Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe Ser Ser Trp Thr Thr

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    215                 220                 225

ggg cgt gaa gta gag ctc gcc acg ttg atg aaa ccc cag tcc cac cta   835
Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys Pro Gln Ser His Leu
230                 235                 240                 245

gtg ctc atc gat gat cca gtg gat ccc aat ttg ggc gct ttt aag caa   883
Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu Gly Ala Phe Lys Gln
                250                 255                 260

aaa gcg atc gct ttg cac tgg gag ttc atg ttt acc cgc gct atg ttc   931
Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe Thr Arg Ala Met Phe
            265                 270                 275

aac act cct gat atg ggt gaa caa ggg aaa att ctg aat aag atc gcc   979
Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile Leu Asn Lys Ile Ala
        280                 285                 290

gac atg gtt gat cgg ggt cag ttt gag tcc gtg aca gca acg gtg ctg   1027
Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val Thr Ala Thr Val Leu
    295                 300                 305

gat ggg ctc aac gct gca aac atc atg gag ggg cac cgg ctc gtt gag   1075
Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly His Arg Leu Val Glu
310                 315                 320                 325

cag ggt aaa acc tca gga aaa att gtt gtg agg gta taaagaggac        1121
Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg Val
                330                 335

ttgaaaaatg cac                                                   1134


<210> 704
<211> 337
<212> PRT
<213> Corynebacterium glutamicum

<400> 704
Met Ser Ala Gln Met Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala
  1               5                  10                  15

Met Leu Asp Ser Ile Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val
             20                  25                  30

Glu Val Asp Arg Pro Thr Pro Gly Pro His Asp Leu Leu Val His Ile
         35                  40                  45

Glu Ala Val Ser Ile Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala
     50                  55                  60

Gly Lys Gln Lys His Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu
 65                  70                  75                  80

Val Val Ala Val Gly Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys
                 85                  90                  95

Val Phe Tyr Ala Gly Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr
            100                 105                 110

Gln Val Val Asp Glu Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly
```

```
        115                 120                 125

Ala His Asp Ala Ala Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu
    130                 135                 140

Ser Leu Phe Asp Arg Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu
145                 150                 155                 160

Leu Val Leu Gly Gly Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu
                165                 170                 175

Ala Arg Ala Leu Thr Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro
            180                 185                 190

Glu Ser Gln Glu Trp Val Thr Lys Leu Gly Ala His Glu Val Ile Asp
        195                 200                 205

His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe
    210                 215                 220

Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys
225                 230                 235                 240

Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu
                245                 250                 255

Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe
            260                 265                 270

Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile
        275                 280                 285

Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val
    290                 295                 300

Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly
305                 310                 315                 320

His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg
                325                 330                 335

Val
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<210> 705
<211> 1089
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1066)
<223> RXA02741

<400> 705
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ttcccaacct tgtctttcag tcatggttag tgtgggaacc atg aag gca atc tta 115
                                                Met Lys Ala Ile Leu
                                                  1   5

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gtt tcc cgc acc ggc gga cca gag gtg ttg gag ttc acc gac act gac   163
Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu Phe Thr Asp Thr Asp
                 10                  15                  20

gcc cca aag ccc act gat gat cag gtt tta gtt gaa gtt gat atg gct   211
Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val Glu Val Asp Met Ala
             25                  30                  35

ggc gtc aac ttt att gat act tac tat cgc cag ggt gaa tat cac gct   259
Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln Gly Glu Tyr His Ala
         40                  45                  50

cgc ctg ccg ttt atc cca ggt ttt gaa ggc act ggt cgg gtg ttg gag   307
Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr Gly Arg Val Leu Glu
     55                  60                  65

gat ccg cag ggg ttg att gcg gcg ggt acc aag gtg gcg tgg tgt gat   355
Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys Val Ala Trp Cys Asp
 70                  75                  80                  85

gcc atg ggt tcg tat gct cag cag gtg tgt gtg ccg cgg gat cgc ttg   403
Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val Pro Arg Asp Arg Leu
                 90                  95                 100

gtg gcg gtt ccc gag ggc gtg agt tcg gaa gtg gct gcg tcg atg ttg   451
Val Ala Val Pro Glu Gly Val Ser Ser Glu Val Ala Ala Ser Met Leu
             105                 110                 115

atg cag gga atc act gcg cat tat cta acc aat ggt gtg tat gag ctt   499
Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn Gly Val Tyr Glu Leu
         120                 125                 130

gaa gag ggc gat tct tgc ctc atc act gct ggc gcg ggt ggt gtt gga   547
Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly Ala Gly Gly Val Gly
     135                 140                 145

ttg ttg gct acg cag atg gcg gcg gcc aag gga gtg cgc gtg tac agc   595
Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly Val Arg Val Tyr Ser
150                 155                 160                 165

gtg gtg tcc acg gat gaa aaa gct gag ctt gct ttg gat gcc ggt gct   643
Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala Leu Asp Ala Gly Ala
                 170                 175                 180

tat gag gtg ttt cgt tat tcc gat aat ttg gcg gag cag gtt cgt cgg   691
Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala Glu Gln Val Arg Arg
             185                 190                 195

cac aac ggg ggt cgc gga gtt gat gtg gtg tat gac ggt gtc ggc cag   739
His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln
         200                 205                 210

tcc acg ttc aat gag tcc tta gag gct gtt cgt ccg cgc ggc act gtg   787
Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg Pro Arg Gly Thr Val
     215                 220                 225

tgt ttg ttt ggt gcg gcg tcg ggt cct gtg gag cct ttt gat ccg cag   835
Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Pro Phe Asp Pro Gln
230                 235                 240                 245
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ctg ttg aac act cac ggt tcg atc ttc ttg acc cgc cca agc att ggc   883
Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly
                250                 255                 260

gcg tgg acg tct gag gag ggc gaa ttt gcc aag cgt gca cag gcg gtc   931
Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys Arg Ala Gln Ala Val
            265                 270                 275

acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca   979
Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr
        280                 285                 290

tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt   1027
Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg
    295                 300                 305

agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca    1076
Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp
310                 315                 320

taaaaagatc ctg                                                   1089
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<210> 706
<211> 322
<212> PRT
<213> Corynebacterium glutamicum

<400> 706

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Met Lys Ala Ile Leu Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu
  1               5                  10                  15

Phe Thr Asp Thr Asp Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val
             20                  25                  30

Glu Val Asp Met Ala Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln
         35                  40                  45

Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr
     50                  55                  60

Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys
 65                  70                  75                  80

Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val
                 85                  90                  95

Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val
            100                 105                 110

Ala Ala Ser Met Leu Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn
        115                 120                 125

Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly
    130                 135                 140

Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly
145                 150                 155                 160

Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala
                165                 170                 175
```

```
Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala
            180                 185                 190

Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr
        195                 200                 205

Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg
    210                 215                 220

Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu
225                 230                 235                 240

Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr
                245                 250                 255

Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys
            260                 265                 270

Arg Ala Gln Ala Val Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val
        275                 280                 285

Arg Val Thr Gly Thr Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg
    290                 295                 300

Asp Leu Gln Ala Arg Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro
305                 310                 315                 320

Lys Asp
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09802NP2.SEQ.ST25

<210> 707
<211> 990
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(967)
<223> RXN02560

<400> 707
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ggaacttcta agagcagtgg aatgaaataa tccggtgctg atg cag ggc aac tcg 115
                                    Met Gln Gly Asn Ser
                                      1   5

ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
                  10   15   20

gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211
Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
              25   30   35

ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259
Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
          40   45   50

```
cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att   307
Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
     55                  60                  65

att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att   355
Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile
 70                  75                  80                  85

tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg   403
Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly
                 90                  95                 100

atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg   451
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu
            105                 110                 115

att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa   499
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
        120                 125                 130

gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg   547
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
    135                 140                 145

ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag   595
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu
150                 155                 160                 165

tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg   643
Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala
                170                 175                 180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc   691
Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
            185                 190                 195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att   739
Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
        200                 205                 210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc   787
Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
    215                 220                 225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act   835
Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
230                 235                 240                 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg   883
Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
                250                 255                 260

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt   931
His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
            265                 270                 275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg       977
Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
        280                 285

attatggacg cct                                                   990
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<210> 708
<211> 289
<212> PRT
<213> Corynebacterium glutamicum

<400> 708

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Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys
 1               5                  10                  15

Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
            20                  25                  30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
        35                  40                  45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
    50                  55                  60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
65                  70                  75                  80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
                85                  90                  95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
            100                 105                 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
        115                 120                 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
    130                 135                 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
145                 150                 155                 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
                165                 170                 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
            180                 185                 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
        195                 200                 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
    210                 215                 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
225                 230                 235                 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
                245                 250                 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr
            260                 265                 270

Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu
        275                 280                 285
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Arg

<210> 709
<211> 922
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(922)
<223> FRXA02560

<400> 709
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ggaacttcta agagcagtgg aatgaaataa tccggtgctg atg cag ggc aac tcg 115
Met Gln Gly Asn Ser
1 5

ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
10 15 20

gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211
Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
25 30 35

ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259
Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
40 45 50

cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307
Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
55 60 65

att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355
Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile
70 75 80 85

tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg 403
Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly
90 95 100

atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg 451
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu
105 110 115

att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa 499
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
120 125 130

gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
135 140 145

ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu
150 155 160 165

```
tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg   643
Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala
                170                 175                 180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc   691
Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
            185                 190                 195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att   739
Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
        200                 205                 210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc   787
Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
    215                 220                 225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act   835
Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
230                 235                 240                 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg   883
Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
                250                 255                 260

cat agg gcg gcg tct aaa cgc tgt tac aag aac caa gaa               922
His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn Gln Glu
            265                 270
```

<210> 710
<211> 274
<212> PRT
<213> Corynebacterium glutamicum

<400> 710

```
Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys
  1               5                  10                  15

Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
            20                  25                  30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
        35                  40                  45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
    50                  55                  60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
65                  70                  75                  80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
                85                  90                  95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
            100                 105                 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
        115                 120                 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
```

```
    130                 135                 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
145                 150                 155                 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
                165                 170                 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
            180                 185                 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
        195                 200                 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
    210                 215                 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
225                 230                 235                 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
                245                 250                 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn
            260                 265                 270

Gln Glu
```

US 9,969,969 B2

<210> 711
<211> 870
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(847)
<223> RXA01311

<400> 711
tcgtctccgc atgggaacca ggcgagaatg gaaccttcgt ctgccacgca gaaccactgt 60

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tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt   115
                                              Met Lys Leu Thr Leu
                                                1               5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc   163
Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
                10                  15                  20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt   211
Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
            25                  30                  35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg   259
Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
        40                  45                  50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc   307
Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
```

```
     55                  60                  65

gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg   355
Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala
 70                  75                  80                  85

cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca   403
Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro
                 90                  95                 100

ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc   451
Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg
            105                 110                 115

tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac   499
Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn
        120                 125                 130

gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc   547
Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr
    135                 140                 145

gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt   595
Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys
150                 155                 160                 165

gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag   643
Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys
                170                 175                 180

ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg   691
Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu
            185                 190                 195

cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc   739
Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys
        200                 205                 210

tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg   787
Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu
    215                 220                 225

acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga   835
Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg
230                 235                 240                 245

ggc aaa gac gac tagtctttaa tccaagtaag tac                        870
Gly Lys Asp Asp
```

Sequence Listing

<210> 712
<211> 249
<212> PRT
<213> Corynebacterium glutamicum

<400> 712

```
Met Lys Leu Thr Leu Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu
  1               5                  10                  15

Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser
```

```
            20                  25                  30

Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly
        35                  40                  45

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
    50                  55                  60

Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
65                  70                  75                  80

Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
                85                  90                  95

Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
            100                 105                 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
        115                 120                 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
    130                 135                 140

Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
145                 150                 155                 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
                165                 170                 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
            180                 185                 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
        195                 200                 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
    210                 215                 220

Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
225                 230                 235                 240

Arg Ala Ala Phe Arg Gly Lys Asp Asp
                245
```

US20050196848A1

<210> 713
<211> 929
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(906)
<223> RXN03014

<400> 713

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tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc   48
Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
  1               5                  10                  15

ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg   96
```

```
Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
            20                  25                  30

gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt   144
Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
        35                  40                  45

tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg   192
Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
    50                  55                  60

gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc   240
Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
65                  70                  75                  80

gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg   288
Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
                85                  90                  95

ccg gac tcc tac ccc acc gcg cca tcg ctg gtc acc gcg gtg ttc gca   336
Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
            100                 105                 110

ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tcg   384
Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
        115                 120                 125

att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gtg gca   432
Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
    130                 135                 140

ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat   480
Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
145                 150                 155                 160

atc aaa cgt ttg ttg tca ttt act ctg gtc agc cac atc ggc tac atg   528
Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
                165                 170                 175

atc ttc ggc gta gcc ctt gga tct gca cag ggt ttg tct ggt gcg atc   576
Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
            180                 185                 190

ttc tac gca atc cac cac att ctg gtt cag act tcc ctg ttc ctg gtg   624
Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
        195                 200                 205

gtc ggt ctg gtg gaa cgc caa gcc gga tcc tcc tcg ctg cga cgc ctt   672
Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
    210                 215                 220

gga tcc ctg gca tat atc tcc cca ctt ctt gcg att ttg tac ttc atc   720
Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
225                 230                 235                 240

ccc gcc atc aac ctg ggt ggt atc cca ccg ttc tcc ggc ttc ctg ggc   768
Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly
                245                 250                 255

aag atc atg ctc atc gaa gcc ggc gcc cga aga tgg cag ttg gct ggc   816
Lys Ile Met Leu Ile Glu Ala Gly Ala Arg Arg Trp Gln Leu Ala Gly
```

US 9,580,500 B2

```
            260                 265                 270

atg ggt cct tat cgc agg cgc cgt tgt cac ctc act gct cac ctt gta   864
Met Gly Pro Tyr Arg Arg Arg Arg Cys His Leu Thr Ala His Leu Val
        275                 280                 285

cac cat ggt tct ggt ctg gtc caa ggc ctt ctg gcg cga ccg           906
His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro
    290                 295                 300

taaagacgcc cccgatggag caa                                        929
```

<210> 714
<211> 302
<212> PRT
<213> Corynebacterium glutamicum

<400> 714

```
Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
  1               5                  10                  15

Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
             20                  25                  30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
         35                  40                  45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
     50                  55                  60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65                  70                  75                  80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
                 85                  90                  95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
            100                 105                 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
        115                 120                 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
    130                 135                 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
145                 150                 155                 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
                165                 170                 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
            180                 185                 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
        195                 200                 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
    210                 215                 220
```

```
Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
225                 230                 235                 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly
                245                 250                 255

Lys Ile Met Leu Ile Glu Ala Gly Ala Arg Arg Trp Gln Leu Ala Gly
            260                 265                 270

Met Gly Pro Tyr Arg Arg Arg Arg Cys His Leu Thr Ala His Leu Val
        275                 280                 285

His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro
    290                 295                 300
```

<210> 715
<211> 1280
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1257)
<223> FRXA00910

<400> 715

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tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc   48
Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
  1               5                  10                  15

ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg   96
Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
             20                  25                  30

gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt   144
Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
         35                  40                  45

tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg   192
Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
     50                  55                  60

gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc   240
Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65                  70                  75                  80

gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg   288
Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
                 85                  90                  95

ccg gac tcc tac ccc acc gcg cca tcg ctg gtc acc gcg gtg ttc gca   336
Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
            100                 105                 110

ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tcg   384
Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
        115                 120                 125

att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gtg gca   432
Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
```

```
    130                 135                 140

ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat   480
Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
145                 150                 155                 160

atc aaa cgt ttg ttg tca ttt act ctg gtc agc cac atc ggc tac atg   528
Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
                165                 170                 175

atc ttc ggc gta gcc ctt gga tct gca cag ggt ttg tct ggt gcg atc   576
Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
            180                 185                 190

ttc tac gca atc cac cac att ctg gtt cag act tcc ctg ttc ctg gtg   624
Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
        195                 200                 205

gtc ggt ctg gtg gaa cgc caa gcc gga tcc tcc tcg ctg cga cgc ctt   672
Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
    210                 215                 220

gga tcc ctg gca tat atc tcc cca ctt ctt gcg att ttg tac ttc atc   720
Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
225                 230                 235                 240

ccc gcc atc aac ctg ggt ggt atc cca ccg ttc tcc ggc ttc ctg ggc   768
Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly
                245                 250                 255

aag atc atg ctc atc gaa gcc ggc gcc gaa gat ggc agt tgg ctg gca   816
Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala
            260                 265                 270

tgg gtc ctt atc gca ggc gcc gtt gtc acc tca ctg ctc acc ttg tac   864
Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr
        275                 280                 285

acc atg gtt ctg gtc tgg tcc aag gcc ttc tgg cgc gac cgt aaa gac   912
Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp
    290                 295                 300

gcc ccc gat gga gca acc gca ctt gcg cga ccc gca cct ttg gta gat   960
Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp
305                 310                 315                 320

gtc caa gac gaa gtc gcc gtt aaa gac cgc aac gat gtc gga cgg atg  1008
Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met
                325                 330                 335

cct tgg ggc atg gtc ttc tcc act gct ctc ctg gtt tca gca tct ctt  1056
Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu
            340                 345                 350

gct gta tcc gtg ctc gca gga cca ctg tca tct att act gga cgc gcc  1104
Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala
        355                 360                 365

gcc gaa tcc gca caa gat gtc aac atc tac cgc gcc gca gta ctc ggc  1152
Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly
    370                 375                 380
```

```
ccc aac tac ctc gac cca tca cgc aca ctc gag atg gag cgt tac gac   1200
Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp
385                 390                 395                 400

gcc aac cgc gat gac atc aac cac cgc gtc gac acc aac gga acg gag   1248
Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu
                405                 410                 415

gac caa cca tgatcagtgg attcaaacga cga                             1280
Asp Gln Pro
```

<210> 716
<211> 419
<212> PRT
<213> Corynebacterium glutamicum

<400> 716

```
Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
 1               5                  10                  15

Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
            20                  25                  30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
        35                  40                  45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
    50                  55                  60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
65                  70                  75                  80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
                85                  90                  95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
            100                 105                 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
        115                 120                 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
    130                 135                 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
145                 150                 155                 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
                165                 170                 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
            180                 185                 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
        195                 200                 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
    210                 215                 220
```

```
Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
225                 230                 235                 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly
                245                 250                 255

Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala
            260                 265                 270

Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr
        275                 280                 285

Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp
    290                 295                 300

Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp
305                 310                 315                 320

Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met
                325                 330                 335

Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu
            340                 345                 350

Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala
        355                 360                 365

Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly
    370                 375                 380

Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp
385                 390                 395                 400

Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu
                405                 410                 415

Asp Gln Pro
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US 6,962,798 B2

<210> 717
<211> 1051
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1051)
<223> RXN01895

<400> 717
cgcgtacacg tgctcaacac gacaacgctt aaacggctgc acgcgtaaca cggcagaccg 60

cacaagcttt aagatccacg atcaggagac tttgacaaat atg tca gtt aac cca 115
Met Ser Val Asn Pro
1 5

acc cgc ccc gaa ggc ggc cgt cac cac gtc gtc gtc atc ggt tct ggt 163
Thr Arg Pro Glu Gly Gly Arg His His Val Val Val Ile Gly Ser Gly
10 15 20

```
ttt ggt ggc ctt ttt gct gcc aag aac ctg gcc aag gca gac gtc gat   211
Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala Lys Ala Asp Val Asp
            25                  30                  35

gtc act ctg att gac cgc acc aac cac cac ctc ttc cag cca ctg ctg   259
Val Thr Leu Ile Asp Arg Thr Asn His His Leu Phe Gln Pro Leu Leu
        40                  45                  50

tac caa gtg gca acc ggt atc ctc tcc tcc ggt gaa atc gca cct tcc   307
Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly Glu Ile Ala Pro Ser
    55                  60                  65

act cga cag atc ctg ggc tcc cag gaa aac gtc aac gtc atc aag ggc   355
Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val Asn Val Ile Lys Gly
70                  75                  80                  85

gaa gtc acc gac atc aac gtc gag tcc cag act gtg acc gcc tcc ctg   403
Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr Val Thr Ala Ser Leu
                90                  95                  100

ggc gag ttc acc cgc gtt ttt gag tac gat tcc ttg gtc gtt ggt gct   451
Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser Leu Val Val Gly Ala
            105                 110                 115

ggc gca ggt cag tcc tac ttc ggc aat gat cac ttc gct gag ttc gca   499
Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His Phe Ala Glu Phe Ala
        120                 125                 130

cct ggc atg aag tcc atc gac gat gca ctg gag att cgt gca cgc atc   547
Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu Ile Arg Ala Arg Ile
    135                 140                 145

atc ggt gct ttc gag cgc gct gag atc tgc gag gat cca gct gag cgc   595
Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu Asp Pro Ala Glu Arg
150                 155                 160                 165

gaa cgc ctg ctc acc ttc gtc gtt gtt ggc gct ggc cca acc ggt gtt   643
Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala Gly Pro Thr Gly Val
                170                 175                 180

gag ctt gct ggc cag ttg gct gag atg gct cac cgc acc ctt gct ggt   691
Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His Arg Thr Leu Ala Gly
            185                 190                 195

gag tac aag aac ttc aac acc aac tcc gca aag atc atc ctg ctt gat   739
Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys Ile Ile Leu Leu Asp
        200                 205                 210

ggt gct cca cag gtt ctt cct cca ttc ggt aag cgc cta ggc cgc aac   787
Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys Arg Leu Gly Arg Asn
    215                 220                 225

gca cag cgc acc ctg gaa aag atg ggt gtc aac gtt cgc ctg aac gct   835
Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn Val Arg Leu Asn Ala
230                 235                 240                 245

atg gtc acc aac gtt gac gct acc tcg gtc acc tac aag acc aag gac   883
Met Val Thr Asn Val Asp Ala Thr Ser Val Thr Tyr Lys Thr Lys Asp
                250                 255                 260
```

09609760.030502

```
ggc gaa gag cac acc atc gaa tct ttc tgc aag att tgg tcc gct ggt   931
Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys Ile Trp Ser Ala Gly
            265                 270                 275

gtt gcg gca tcc cca ctg ggc aag ctc gtc gca gag cag acc ggt gtt   979
Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala Glu Gln Thr Gly Val
        280                 285                 290

gag acc gac cgc gca ggc cgc gtc atg gtt aac gat gac ctg tct gtt   1027
Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn Asp Asp Leu Ser Val
    295                 300                 305

ggc gat cag aag aac gtc ttc gtt                                  1051
Gly Asp Gln Lys Asn Val Phe Val
310                 315
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<210> 718
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 718

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Met Ser Val Asn Pro Thr Arg Pro Glu Gly Gly Arg His His Val Val
  1               5                  10                  15

Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala
            20                  25                  30

Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu
        35                  40                  45

Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
    50                  55                  60

Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val
65                  70                  75                  80

Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr
                85                  90                  95

Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser
            100                 105                 110

Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His
        115                 120                 125

Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu
    130                 135                 140

Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu
145                 150                 155                 160

Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala
                165                 170                 175

Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His
            180                 185                 190

Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys
        195                 200                 205
```

```
Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys
    210                 215                 220

Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn
225                 230                 235                 240

Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr
                245                 250                 255

Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys
            260                 265                 270

Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala
        275                 280                 285

Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn
    290                 295                 300

Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
305                 310                 315
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US20050196809

<210> 719
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(816)
<223> FRXA01895

<400> 719

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cac cac ctc ttc cag cca ctg ctg tac caa gtg gca acc ggt atc ctc   48
His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu
  1               5                  10                  15

tcc tcc ggt gaa atc gca cct tcc act cga cag atc ctg ggc tcc cag   96
Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln
            20                  25                  30

gaa aac gtc aac gtc atc aag ggc gaa gtc acc gac atc aac gtc gag   144
Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu
        35                  40                  45

tcc cag act gtg acc gcc tcc ctg ggc gag ttc acc cgc gtt ttt gag   192
Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu
    50                  55                  60

tac gat tcc ttg gtc gtt ggt gct ggc gca ggt cag tcc tac ttc ggc   240
Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly
65                  70                  75                  80

aat gat cac ttc gct gag ttc gca cct ggc atg aag tcc atc gac gat   288
Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp
                85                  90                  95

gca ctg gag att cgt gca cgc atc atc ggt gct ttc gag cgc gct gag   336
Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu
            100                 105                 110
```

```
atc tgc gag gat cca gct gag cgc gaa cgc ctg ctc acc ttc gtc gtt   384
Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val
        115                 120                 125

gtt ggc gct ggc cca acc ggt gtt gag ctt gct ggc cag ttg gct gag   432
Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu
    130                 135                 140

atg gct cac cgc acc ctt gct ggt gag tac aag aac ttc aac acc aac   480
Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn
145                 150                 155                 160

tcc gca aag atc atc ctg ctt gat ggt gct cca cag gtt ctt cct cca   528
Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro
                165                 170                 175

ttc ggt aag cgc cta ggc cgc aac gca cag cgc acc ctg gaa aag atg   576
Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met
            180                 185                 190

ggt gtc aac gtt cgc ctg aac gct atg gtc acc aac gtt gac gct acc   624
Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr
        195                 200                 205

tcg gtc acc tac aag acc aag gac ggc gaa gag cac acc atc gaa tct   672
Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser
    210                 215                 220

ttc tgc aag att tgg tcc gct ggt gtt gcg gca tcc cca ctg ggc aag   720
Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys
225                 230                 235                 240

ctc gtc gca gag cag acc ggt gtt gag acc gac cgc gca ggc cgc gtc   768
Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val
                245                 250                 255

atg gtt aac gat gac ctg tct gtt ggc gat cag aag aac gtc ttc gtt   816
Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
            260                 265                 270
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<210> 720
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 720

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His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu
  1               5                  10                  15

Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln
            20                  25                  30

Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu
        35                  40                  45

Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu
    50                  55                  60

Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly
```

```
65                  70                  75                  80

Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp
                85                  90                  95

Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu
            100                 105                 110

Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val
        115                 120                 125

Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu
    130                 135                 140

Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn
145                 150                 155                 160

Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro
                165                 170                 175

Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met
            180                 185                 190

Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr
        195                 200                 205

Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser
    210                 215                 220

Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys
225                 230                 235                 240

Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val
                245                 250                 255

Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
            260                 265                 270
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09090704.090306

<210> 721
<211> 2409
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2386)
<223> RXA00703

<400> 721
ctgggagtcc tcttgatttt aggttttcca catacccca tatagattga agaattcatt 60

tttcggcatg ggttcaattg ccgggtctag actgtgacct atg aca acc cct cca 115
                                        Met Thr Thr Pro Pro
                                         1   5

act gag att tcg aac gtg aat ccc acc gcg aat gaa ttt gat gat ccg 163
Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn Glu Phe Asp Asp Pro

```
                  10                  15                  20

gat gtg gga cgg cgc att act tct gct gct ggt gtg cca ggc gtt ttg   211
Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly Val Pro Gly Val Leu
             25                  30                  35

cat gcg ctc cag cat gct gtt ccg aat cgt gcc ctg ctg ccg ttg ctc   259
His Ala Leu Gln His Ala Val Pro Asn Arg Ala Leu Leu Pro Leu Leu
         40                  45                  50

acc atg aat aaa cca ggc ggc atc gac tgt cct ggt tgt gct tgg cct   307
Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro Gly Cys Ala Trp Pro
     55                  60                  65

gag cct tcc act gcc aac ctt ggt gtg gtt gag ttc tgc gag aac ggt   355
Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu Phe Cys Glu Asn Gly
 70                  75                  80                  85

gcc aag gcg gtc gcc gag gaa aca aca cct gat cgt gcc ggc aaa gag   403
Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp Arg Ala Gly Lys Glu
                 90                  95                 100

ttc tgg gca gag cat tct att tat gat ctg cgg gaa aag acc gat cac   451
Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg Glu Lys Thr Asp His
            105                 110                 115

tgg ctg gga aag cgt ggc cga atc acc gag ccc atg ttt tat gat cgt   499
Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro Met Phe Tyr Asp Arg
        120                 125                 130

tct tct ggc gat gat cac tac cgc cct att tct tgg gat cgt gca ttt   547
Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser Trp Asp Arg Ala Phe
    135                 140                 145

gcg atc att gcg tcg aag ctc cgc gag atc gag cca gat gaa gcg gtg   595
Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu Pro Asp Glu Ala Val
150                 155                 160                 165

ttt tac acc tct ggt cga gca ccc aat gag ccg gct tat atg ctg cag   643
Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro Ala Tyr Met Leu Gln
                170                 175                 180

ctt cta gcc cgc cga ctt ggc aca aat aat ctt cca gac tgt gga aac   691
Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu Pro Asp Cys Gly Asn
            185                 190                 195

atg tgc cac gag tcc acc ggt act gcc ttg ggt gag acc ttg ggt ttg   739
Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly Glu Thr Leu Gly Leu
        200                 205                 210

ggc aag gga tcc gtg gtg atg gag gat ttc tac aac act gat ttg ttg   787
Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr Asn Thr Asp Leu Leu
    215                 220                 225

att tcc gtg gga caa aac ccg ggc acc aac cac cca cgt gcg ttg acg   835
Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His Pro Arg Ala Leu Thr
230                 235                 240                 245

gct ttc aaa gaa ttg aag gaa aac ggt ggc aag att ctg gcg ctg aac   883
Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys Ile Leu Ala Leu Asn
                250                 255                 260
```

US 2009/0192296 A1

```
ccc atg cca gag acc ggt ctg atg aaa ttc cgt gag ccc caa tca gtc   931
Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg Glu Pro Gln Ser Val
            265                 270                 275

aag ggc gcg ttg agc att tca gac aaa ctt gct gat gaa tac ttg cag   979
Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala Asp Glu Tyr Leu Gln
        280                 285                 290

atc cgt ctt gat gga gac cgc gca ttc ttc cag gcg ctc aac aag gaa   1027
Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln Ala Leu Asn Lys Glu
    295                 300                 305

ctc atc cgt aga gat gcc cta gat cat gca ttc ttg gat aaa ttc tgt   1075
Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe Leu Asp Lys Phe Cys
310                 315                 320                 325

tca ggt gtg gat gaa acc atc gag cac ctc aaa tca ctc gat gat gag   1123
Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys Ser Leu Asp Asp Glu
                330                 335                 340

gtt ctg ctc aag gga tgc ggt ctg acg gca gcg gag atc aac aag gcc   1171
Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala Glu Ile Asn Lys Ala
            345                 350                 355

gct gac atg gtg gaa aag tct gac acc gtg gtg gtg tca tgg act ctc   1219
Ala Asp Met Val Glu Lys Ser Asp Thr Val Val Val Ser Trp Thr Leu
        360                 365                 370

ggg gtc acc cag cat aag aac gct gtg tac acc atc cgt gaa atg gtg   1267
Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr Ile Arg Glu Met Val
    375                 380                 385

aac ttc ctg ctg ctt act gga aat att ggt aag cct ggc gca ggc act   1315
Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys Pro Gly Ala Gly Thr
390                 395                 400                 405

gcc ccg ctt cgt ggg cac tca aac gtc cag ggt gat cga acc atg ggt   1363
Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly Asp Arg Thr Met Gly
                410                 415                 420

att tgg gag aaa atg ccg gag gca ttc ctt gct gct ctt gaa aac gag   1411
Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala Ala Leu Glu Asn Glu
            425                 430                 435

ttt ggt ttc gat gtg ccc cgc aag cac ggc ttc gac acg gta aat tcc   1459
Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe Asp Thr Val Asn Ser
        440                 445                 450

ctg cga gcc atg cgc gaa ggc aag acc aag ttc ttt ctc tcc ctc ggt   1507
Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe Phe Leu Ser Leu Gly
    455                 460                 465

ggc aac ctt gtt cga gtg tcc tca gat acg tct gtt gtc gaa aag ggc   1555
Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser Val Val Glu Lys Gly
470                 475                 480                 485

atg gaa tcc aat gag ctg acg gtg cat ctg tcg acc aag ccc aat ggt   1603
Met Glu Ser Asn Glu Leu Thr Val His Leu Ser Thr Lys Pro Asn Gly
                490                 495                 500
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```
tca caa gca tgg cct ggt gag cag tca ctt atc ctt ccg gtg att gct   1651
Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile Leu Pro Val Ile Ala
            505                 510                 515

cga aca gat aag gat gtc caa aag tca ggc gtc cag cgt gtg aca gtt   1699
Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val Gln Arg Val Thr Val
        520                 525                 530

gag gat tct gcc ggc gct gtt cac gca tcc act ggt aaa cga acc gcc   1747
Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr Gly Lys Arg Thr Ala
    535                 540                 545

aac aag gat ctg aat ttg aag tcc gaa tgc gac atc att gga acc atc   1795
Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp Ile Ile Gly Thr Ile
550                 555                 560                 565

ggt aag cag acc ttc ggt gat gcc ttc tgg cag ccg atg att gat aac   1843
Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln Pro Met Ile Asp Asn
                570                 575                 580

tac gat gtg gtc cgc gat cac atc gag gcc acc att cct ggg ttc cac   1891
Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr Ile Pro Gly Phe His
            585                 590                 595

gat ttc aac cgt cgc atc gac aac ccc ggt gga ttc ctc ctc ccc aac   1939
Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly Phe Leu Leu Pro Asn
        600                 605                 610

gga cct cgt gag cgc atc ttc aac aca tcc aat ggc aag gcc caa ttg   1987
Gly Pro Arg Glu Arg Ile Phe Asn Thr Ser Asn Gly Lys Ala Gln Leu
    615                 620                 625

acg gtt aat gaa acc aat gtg att gag cta ccc aag gac tat ttg ctt   2035
Thr Val Asn Glu Thr Asn Val Ile Glu Leu Pro Lys Asp Tyr Leu Leu
630                 635                 640                 645

atg aac acg gta cgt tca cat gat caa tac aac tcc acg att tac ggt   2083
Met Asn Thr Val Arg Ser His Asp Gln Tyr Asn Ser Thr Ile Tyr Gly
                650                 655                 660

ctg gat gac cgc tac cgc ggt gtt cgc aat ggt cgc cgc gta gtg ttc   2131
Leu Asp Asp Arg Tyr Arg Gly Val Arg Asn Gly Arg Arg Val Val Phe
            665                 670                 675

gtc aat cct caa gat tgt aag caa cgt ggt ctc aag gat gga gac atc   2179
Val Asn Pro Gln Asp Cys Lys Gln Arg Gly Leu Lys Asp Gly Asp Ile
        680                 685                 690

gtc gat atc gtc tct gtc ttt gat gat ggc gaa cgc cga gca ccg aat   2227
Val Asp Ile Val Ser Val Phe Asp Asp Gly Glu Arg Arg Ala Pro Asn
    695                 700                 705

ttc cga gtg gtg gaa tat gac acc gcg agg gac tgc gtc acc acg tat   2275
Phe Arg Val Val Glu Tyr Asp Thr Ala Arg Asp Cys Val Thr Thr Tyr
710                 715                 720                 725

ttc cct gag gcc aac gta ttg gtt cca ttg gat tca gta gct gaa aaa   2323
Phe Pro Glu Ala Asn Val Leu Val Pro Leu Asp Ser Val Ala Glu Lys
                730                 735                 740

tcc aac act cca gtg tcc aag tca gtt gtg gtt cgc ctt gaa gca aca   2371
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US 2006/0160164 A1

```
Ser Asn Thr Pro Val Ser Lys Ser Val Val Val Arg Leu Glu Ala Thr
           745                 750                 755

gga cgt act gct tct tagaaaaaca ccagggaatt ttc                    2409
Gly Arg Thr Ala Ser
        760
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<210> 722
<211> 762
<212> PRT
<213> Corynebacterium glutamicum

<400> 722

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Met Thr Thr Pro Pro Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn
  1               5                  10                  15

Glu Phe Asp Asp Pro Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly
            20                  25                  30

Val Pro Gly Val Leu His Ala Leu Gln His Ala Val Pro Asn Arg Ala
        35                  40                  45

Leu Leu Pro Leu Leu Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro
    50                  55                  60

Gly Cys Ala Trp Pro Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu
65                  70                  75                  80

Phe Cys Glu Asn Gly Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp
                85                  90                  95

Arg Ala Gly Lys Glu Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg
            100                 105                 110

Glu Lys Thr Asp His Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro
        115                 120                 125

Met Phe Tyr Asp Arg Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser
    130                 135                 140

Trp Asp Arg Ala Phe Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu
145                 150                 155                 160

Pro Asp Glu Ala Val Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro
                165                 170                 175

Ala Tyr Met Leu Gln Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu
            180                 185                 190

Pro Asp Cys Gly Asn Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly
        195                 200                 205

Glu Thr Leu Gly Leu Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr
    210                 215                 220

Asn Thr Asp Leu Leu Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His
225                 230                 235                 240

Pro Arg Ala Leu Thr Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys
                245                 250                 255
```

```
Ile Leu Ala Leu Asn Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg
            260                 265                 270

Glu Pro Gln Ser Val Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala
        275                 280                 285

Asp Glu Tyr Leu Gln Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln
    290                 295                 300

Ala Leu Asn Lys Glu Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe
305                 310                 315                 320

Leu Asp Lys Phe Cys Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys
                325                 330                 335

Ser Leu Asp Asp Glu Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala
            340                 345                 350

Glu Ile Asn Lys Ala Ala Asp Met Val Glu Lys Ser Asp Thr Val Val
        355                 360                 365

Val Ser Trp Thr Leu Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr
    370                 375                 380

Ile Arg Glu Met Val Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys
385                 390                 395                 400

Pro Gly Ala Gly Thr Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly
                405                 410                 415

Asp Arg Thr Met Gly Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala
            420                 425                 430

Ala Leu Glu Asn Glu Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe
        435                 440                 445

Asp Thr Val Asn Ser Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe
    450                 455                 460

Phe Leu Ser Leu Gly Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser
465                 470                 475                 480

Val Val Glu Lys Gly Met Glu Ser Asn Glu Leu Thr Val His Leu Ser
                485                 490                 495

Thr Lys Pro Asn Gly Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile
            500                 505                 510

Leu Pro Val Ile Ala Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val
        515                 520                 525

Gln Arg Val Thr Val Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr
    530                 535                 540

Gly Lys Arg Thr Ala Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp
545                 550                 555                 560

Ile Ile Gly Thr Ile Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln
                565                 570                 575
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US 9,856,320 B2

```
Pro Met Ile Asp Asn Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr
            580                 585                 590

Ile Pro Gly Phe His Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly
        595                 600                 605

Phe Leu Leu Pro Asn Gly Pro Arg Glu Arg Ile Phe Asn Thr Ser Asn
    610                 615                 620

Gly Lys Ala Gln Leu Thr Val Asn Glu Thr Asn Val Ile Glu Leu Pro
625                 630                 635                 640

Lys Asp Tyr Leu Leu Met Asn Thr Val Arg Ser His Asp Gln Tyr Asn
                645                 650                 655

Ser Thr Ile Tyr Gly Leu Asp Asp Arg Tyr Arg Gly Val Arg Asn Gly
            660                 665                 670

Arg Arg Val Val Phe Val Asn Pro Gln Asp Cys Lys Gln Arg Gly Leu
        675                 680                 685

Lys Asp Gly Asp Ile Val Asp Ile Val Ser Val Phe Asp Asp Gly Glu
    690                 695                 700

Arg Arg Ala Pro Asn Phe Arg Val Val Glu Tyr Asp Thr Ala Arg Asp
705                 710                 715                 720

Cys Val Thr Thr Tyr Phe Pro Glu Ala Asn Val Leu Val Pro Leu Asp
                725                 730                 735

Ser Val Ala Glu Lys Ser Asn Thr Pro Val Ser Lys Ser Val Val Val
            740                 745                 750

Arg Leu Glu Ala Thr Gly Arg Thr Ala Ser
        755                 760


<210> 723
<211> 1038
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1015)
<223> RXN00705

<400> 723
gttctggaac aagcactgat gattgggccg agtccacgtt ggttaatgct ctgcatcttc 60

aagaaatcat cgctaaaaat tacccggagg ctaaataaaa atg ggt cgg att acc   115
                                               Met Gly Arg Ile Thr
                                                 1               5

caa aac ttg cag gtc cca cgc gtt gtg tcc act gac gag caa gtt ttt   163
Gln Asn Leu Gln Val Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe
                10                  15                  20

gtt aac act cgt ccg gat act gtt gcg gtg gag gag cct cta gaa att   211
Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile
            25                  30                  35
```

```
cgg gtt aat ggc act gcg ctt acc acc act atg cgc acg ccc ggc cat   259
Arg Val Asn Gly Thr Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His
         40                  45                  50

gat att gag ttg gtg cat ggc ctc ctc ttg tca gaa ggt ctg atc acg   307
Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr
     55                  60                  65

gat gct tct gag gtt ttt acc gcc cgc tat tgt gca gga gct gtt ggc   355
Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly
 70                  75                  80                  85

cca gat aat caa aat acg tac aac gtc tta gaa ctt gat gtc atc ccc   403
Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro
                 90                  95                 100

aaa gac aat ccg gcc cgg gat ccc gtc cag aat ccc tcc cat aat ccc   451
Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro
            105                 110                 115

gaa ggc agc caa cac gaa gca ctc cac atc cca act ttc caa ccg gta   499
Glu Gly Ser Gln His Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val
        120                 125                 130

cgc gaa cta aac ctc gtg gca gcc caa cgc aat gtg ctg act acg tct   547
Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser
    135                 140                 145

gct tgt ggt gtt tgt ggc acg acg tct att gag cag ttg atg aac aag   595
Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys
150                 155                 160                 165

aag ggc tgg ccc att acg ccg att aca ccg gat cct cgg atg att gtg   643
Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val
                170                 175                 180

tcg ttg cca gat aag ttg aag tcg aag cag aag att ttc gac aaa act   691
Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr
            185                 190                 195

ggt ggg gtt cat gct gct ggt ttg gcc acg ctt gat ggt gag atg ttg   739
Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu
        200                 205                 210

att att cga gag gat gtc ggt cgg cat aac gca gct gac aaa gtt ata   787
Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala Ala Asp Lys Val Ile
    215                 220                 225

gga aac atg ctg atg gcg gga aag ctc ccc ttg gaa aac act att ttg   835
Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu
230                 235                 240                 245

gtg atg agt tct agg gcg tct ttt gag ctt gtc caa aag gct gcc atg   883
Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met
                250                 255                 260

gct gga att tcg ggt gta atc gct gtt ggt gct gca aca tcg ctg gca   931
Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala
            265                 270                 275
```

```
atc gag gcg gcg cag gat tca ggt att ttc ctt gct ggt ttt gtt cgg   979
Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg
        280                 285                 290

ggc aac aag ttt aac cac tat gcg ggc gag ctc gga taatgccaga       1025
Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu Gly
    295                 300                 305

acaggtagaa cag                                                   1038
```

<210> 724
<211> 305
<212> PRT
<213> Corynebacterium glutamicum

<400> 724

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Met Gly Arg Ile Thr Gln Asn Leu Gln Val Pro Arg Val Val Ser Thr
  1               5                  10                  15

Asp Glu Gln Val Phe Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu
             20                  25                  30

Glu Pro Leu Glu Ile Arg Val Asn Gly Thr Ala Leu Thr Thr Thr Met
         35                  40                  45

Arg Thr Pro Gly His Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser
     50                  55                  60

Glu Gly Leu Ile Thr Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys
 65                  70                  75                  80

Ala Gly Ala Val Gly Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu
                 85                  90                  95

Leu Asp Val Ile Pro Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn
            100                 105                 110

Pro Ser His Asn Pro Glu Gly Ser Gln His Glu Ala Leu His Ile Pro
        115                 120                 125

Thr Phe Gln Pro Val Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn
    130                 135                 140

Val Leu Thr Thr Ser Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu
145                 150                 155                 160

Gln Leu Met Asn Lys Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp
                165                 170                 175

Pro Arg Met Ile Val Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys
            180                 185                 190

Ile Phe Asp Lys Thr Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu
        195                 200                 205

Asp Gly Glu Met Leu Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala
    210                 215                 220

Ala Asp Lys Val Ile Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu
225                 230                 235                 240
```

```
Glu Asn Thr Ile Leu Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val
                245                 250                 255

Gln Lys Ala Ala Met Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala
            260                 265                 270

Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu
        275                 280                 285

Ala Gly Phe Val Arg Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu
    290                 295                 300

Gly
305
```

<210> 725
<211> 908
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(885)
<223> FRXA00705

<400> 725

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cca cgc gtt gtg tcc act gac gag caa gtt ttt gtt aac act cgt ccg   48
Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe Val Asn Thr Arg Pro
  1               5                  10                  15

gat act gtt gcg gtg gag gag cct cta gaa att cgg gtt aat ggc act   96
Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr
            20                  25                  30

gcg ctt acc acc act atg cgc acg ccc ggc cat gat att gag ttg gtg   144
Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val
        35                  40                  45

cat ggc ctc ctc ttg tca gaa ggt ctg atc acg gat gct tct gag gtt   192
His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val
    50                  55                  60

ttt acc gcc cgc tat tgt gca gga gct gtt ggc cca gat aat caa aat   240
Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn
65                  70                  75                  80

acg tac aac gtc tta gaa ctt gat gtc atc ccc aaa gac aat ccg gcc   288
Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala
                85                  90                  95

cgg gat ccc gtc cag aat ccc tcc cat aat ccc gaa ggc agc caa cac   336
Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His
            100                 105                 110

gaa gca ctc cac atc cca act ttc caa ccg gta cgc gaa cta aac ctc   384
Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu
        115                 120                 125

gtg gca gcc caa cgc aat gtg ctg act acg tct gct tgt ggt gtt tgt   432
```

```
Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser Ala Cys Gly Val Cys
    130                 135                 140

ggc acg acg tct att gag cag ttg atg aac aag aag ggc tgg ccc att   480
Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys Lys Gly Trp Pro Ile
145                 150                 155                 160

acg ccg att aca ccg gat cct cgg atg att gtg tcg ttg cca gat aag   528
Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val Ser Leu Pro Asp Lys
                165                 170                 175

ttg aag tcg aag cag aag att ttc gac aaa act ggt ggg gtt cat gct   576
Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr Gly Gly Val His Ala
            180                 185                 190

gct ggt ttg gcc acg ctt gat ggt gag atg ttg att att cga gag gat   624
Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu Ile Ile Arg Glu Asp
        195                 200                 205

gtc ggt cgg cat aac gca gct gac aaa gtt ata gga aac atg ctg atg   672
Val Gly Arg His Asn Ala Ala Asp Lys Val Ile Gly Asn Met Leu Met
    210                 215                 220

gcg gga aag ctc ccc ttg gaa aac act att ttg gtg atg agt tct agg   720
Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu Val Met Ser Ser Arg
225                 230                 235                 240

gcg tct ttt gag ctt gtc caa aag gct gcc atg gct gga att tcg ggt   768
Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met Ala Gly Ile Ser Gly
                245                 250                 255

gta atc gct gtt ggt gct gca aca tcg ctg gca atc gag gcg gcg cag   816
Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln
            260                 265                 270

gat tca ggt att ttc ctt gct ggt ttt gtt cgg ggc aac aag ttt aac   864
Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg Gly Asn Lys Phe Asn
        275                 280                 285

cac tat gcg ggc gag ctc gga taatgccaga acaggtagaa cag            908
His Tyr Ala Gly Glu Leu Gly
    290                 295
```

<210> 726
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 726

```
Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe Val Asn Thr Arg Pro
  1               5                  10                  15

Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr
             20                  25                  30

Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val
         35                  40                  45

His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val
     50                  55                  60
```

```
Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn
 65                  70                  75                  80

Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala
                 85                  90                  95

Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His
            100                 105                 110

Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu
        115                 120                 125

Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser Ala Cys Gly Val Cys
    130                 135                 140

Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys Lys Gly Trp Pro Ile
145                 150                 155                 160

Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val Ser Leu Pro Asp Lys
                165                 170                 175

Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr Gly Gly Val His Ala
            180                 185                 190

Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu Ile Ile Arg Glu Asp
        195                 200                 205

Val Gly Arg His Asn Ala Ala Asp Lys Val Ile Gly Asn Met Leu Met
    210                 215                 220

Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu Val Met Ser Ser Arg
225                 230                 235                 240

Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met Ala Gly Ile Ser Gly
                245                 250                 255

Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln
            260                 265                 270

Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg Gly Asn Lys Phe Asn
        275                 280                 285

His Tyr Ala Gly Glu Leu Gly
    290                 295
```

<210> 727
<211> 1134
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1111)
<223> RXN00388

<400> 727
gaagagtact tcgaccacga cgactaacac cgcaatttaa aggcttttca agcctgcccc 60

acatcgaagc agttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac 115

```
                                                    Met Leu Pro Val Asn
                                                      1               5

caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc   163
Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile
                 10                  15                  20

atc tac gtt ctg gca ctc atc ctc tcc ctc gtc tac tac gta aaa caa   211
Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln
             25                  30                  35

caa ggc att atc gac gcc cgc cgc gag caa acc cgc gtc agc gaa ctc   259
Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu
         40                  45                  50

gtt ggt gca ggc ggc agc gct gat gtt gat act gac ctg cct gat gac   307
Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp
     55                  60                  65

atc gcc gac ggt gtc ctc gcc gac gaa gac ctt gca aaa cgc gaa gaa   355
Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu
 70                  75                  80                  85

acc gca cgc aaa cta gcc aac atg acc caa tct ctc atg tgg ctc ggc   403
Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly
                 90                  95                 100

gtc atg gtg cac ctc gta tcc gtc gtg atg cgc gcg ctg tct gcc agc   451
Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser
            105                 110                 115

cga ttc ccc ttc ggc aac ctg tat gaa tac atc ctc atg gtc acc ctc   499
Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile Leu Met Val Thr Leu
        120                 125                 130

ttc gcc atg atc gga gcc gta ctc atc ctg cag cgc cca caa ttc cgc   547
Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln Arg Pro Gln Phe Arg
    135                 140                 145

gtg gta tgg cca tgg atc ctc acc cca atg ctg gca ctg ctc ttc tac   595
Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu Ala Leu Leu Phe Tyr
150                 155                 160                 165

ggt ggc acc cag ctg tac tcc gac gca gca cca gtc gtt cca gca ctg   643
Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro Val Val Pro Ala Leu
                170                 175                 180

cag tcc ttc tgg ttc ccg atc cac gtt tcc tcc gtc tcc atc ggc gca   691
Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser Val Ser Ile Gly Ala
            185                 190                 195

tcc atc ggt atc gtc tcc ggt att gca tcc ctg ctg tac ata ctg cgc   739
Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu Leu Tyr Ile Leu Arg
        200                 205                 210

atg tgg caa cca aag ggt aaa gaa aag ggc ttc ttc ggc gca gta gca   787
Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe Phe Gly Ala Val Ala
    215                 220                 225

aaa cca ctc cca tcc gga aaa acc ctg gat aac ctg gca tac aag acc   835
Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn Leu Ala Tyr Lys Thr
```

```
230                 235                 240                 245

gcg atc tgg act gtc cca atc ttc ggc ctg ggc atc atc ttg ggt gcc   883
Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly Ile Ile Leu Gly Ala
                250                 255                 260

atc tgg gca gaa gca gcc tgg ggt cgt ttc tgg gga tgg gat cct aag   931
Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp Gly Trp Asp Pro Lys
            265                 270                 275

gaa aca gtc tcc ttc atc acc tgg gtt ctc tac gct ggt tac ctc cac   979
Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr Ala Gly Tyr Leu His
        280                 285                 290

gca cgt gca act gct ggt tgg cgc aac acc aac gct gca tgg atc aac   1027
Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn Ala Ala Trp Ile Asn
    295                 300                 305

atc ctg gcg ctg gtc acg atg att ttt aat ctg ttc ttc atc aac atg   1075
Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu Phe Phe Ile Asn Met
310                 315                 320                 325

gtc gta tct ggt ctg cac tct tac gcc gga ctg aac taagcacttt        1121
Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu Asn
                330                 335

tggttggcgg ggt                                                   1134


<210> 728
<211> 337
<212> PRT
<213> Corynebacterium glutamicum

<400> 728
Met Leu Pro Val Asn Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe
  1               5                  10                  15

Val Ser Ala Tyr Ile Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val
            20                  25                  30

Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr
        35                  40                  45

Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr
    50                  55                  60

Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu
65                  70                  75                  80

Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser
                85                  90                  95

Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg
            100                 105                 110

Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile
        115                 120                 125

Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln
    130                 135                 140
```

```
Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu
145                 150                 155                 160

Ala Leu Leu Phe Tyr Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro
                165                 170                 175

Val Val Pro Ala Leu Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser
            180                 185                 190

Val Ser Ile Gly Ala Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu
        195                 200                 205

Leu Tyr Ile Leu Arg Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe
    210                 215                 220

Phe Gly Ala Val Ala Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn
225                 230                 235                 240

Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly
                245                 250                 255

Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp
            260                 265                 270

Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr
        275                 280                 285

Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn
    290                 295                 300

Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu
305                 310                 315                 320

Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu
                325                 330                 335

Asn
```

EP 2 050 764 A1

<210> 729
<211> 326
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(303)
<223> FRXA00388

<400> 729

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acc ctg gat aac ctg gca tac aag acc gcg atc tgg act gtc cca atc   48
Thr Leu Asp Asn Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile
  1               5                  10                  15

ttc ggc ctg ggc atc atc ttg ggt gcc atc tgg gca gaa gca gcc tgg   96
Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp
             20                  25                  30

ggt cgt ttc tgg gga tgg gat cct aag gaa aca gtc tcc ttc atc acc   144
```

```
Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr
         35                  40                  45

tgg gtt ctc tac gct ggt tac ctc cac gca cgt gca act gct ggt tgg   192
Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp
     50                  55                  60

cgc aac acc aac gct gca tgg atc aac atc ctg gcg ctg gtc acg atg   240
Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met
 65                  70                  75                  80

att ttt aat ctg ttc ttc atc aac atg gtc gta tct ggt ctg cac tct   288
Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser
                 85                  90                  95

tac gcc gga ctg aac taagcacttt tggttggcgg ggt                    326
Tyr Ala Gly Leu Asn
            100
```

<210> 730
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 730
Thr Leu Asp Asn Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile
  1   5   10   15

Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp
            20   25   30

Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr
         35   40   45

Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp
     50   55   60

Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met
 65   70   75   80

Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser
                 85   90   95

Tyr Ala Gly Leu Asn
            100

<210> 731
<211> 610
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(610)
<223> FRXA00386

<400> 731
gaagagtact tcgaccacga cgactaacac cgcaatttaa aggcttttca agcctgcccc 60

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acatcgaagc agttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac   115
                                            Met Leu Pro Val Asn
                                              1               5

caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc   163
Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile
                 10                  15                  20

atc tac gtt ctg gca ctc atc ctc tcc ctc gtc tac tac gta aaa caa   211
Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln
             25                  30                  35

caa ggc att atc gac gcc cgc cgc gag caa acc cgc gtc agc gaa ctc   259
Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu
         40                  45                  50

gtt ggt gca ggc ggc agc gct gat gtt gat act gac ctg cct gat gac   307
Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp
     55                  60                  65

atc gcc gac ggt gtc ctc gcc gac gaa gac ctt gca aaa cgc gaa gaa   355
Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu
 70                  75                  80                  85

acc gca cgc aaa cta gcc aac atg acc caa tct ctc atg tgg ctc ggc   403
Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly
                 90                  95                 100

gtc atg gtg cac ctc gta tcc gtc gtg atg cgc gcg ctg tct gcc agc   451
Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser
             105                 110                 115

cga ttc ccc ttc ggc aac ctg tat gaa tac atc ctc atg gtc acc ctc   499
Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile Leu Met Val Thr Leu
         120                 125                 130

ttc gcc atg atc gga gcc gta ctc atc ctg cag cgc cca caa ttc cgc   547
Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln Arg Pro Gln Phe Arg
     135                 140                 145

gtg gta tgg cca tgg atc ctc acc cca atg gct ggc act tgg ttt tct   595
Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala Gly Thr Trp Phe Ser
150                 155                 160                 165

acg gtg gca ccc agc                                              610
Thr Val Ala Pro Ser
                170
```

<210> 732
<211> 170
<212> PRT
<213> Corynebacterium glutamicum

<400> 732

```
Met Leu Pro Val Asn Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe
  1               5                  10                  15

Val Ser Ala Tyr Ile Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val
             20                  25                  30
```

```
Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr
         35                  40                  45

Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr
     50                  55                  60

Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu
 65                  70                  75                  80

Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser
                 85                  90                  95

Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg
            100                 105                 110

Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile
        115                 120                 125

Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln
    130                 135                 140

Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala
145                 150                 155                 160

Gly Thr Trp Phe Ser Thr Val Ala Pro Ser
                165                 170
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<210> 733
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXA00945

<400> 733

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tcacagtacc acccacaagc cacaaggagg gtatggaggt gggcgtctaa agccaaattt 60

ttcccggtgt ttgaggcgat tgcaccgtac actaatgtgc atg ctt gaa cgc ctc   115
                                            Met Leu Glu Arg Leu
                                              1               5

aaa cgc cta gat ccg ctc att gtc ctc att gtg ctg gct gtc att gtg   163
Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val Leu Ala Val Ile Val
                 10                  15                  20

gcg atc atc att cca gtt cgc ggg gtt gct gcg gat tgg ttt gat gtc   211
Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala Asp Trp Phe Asp Val
            25                  30                  35

gcc gtc aag att gcc att gcg ctg ctg ttt ttt ctt tat ggt gcc cgc   259
Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe Leu Tyr Gly Ala Arg
        40                  45                  50

cta tcc acc caa gag gcg ctg aat ggt ctg aag cac tgg agg ctt cac   307
Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys His Trp Arg Leu His
    55                  60                  65
```

```
ctg act att ttg gcg atc act ttc gga ata ttc cca ctt atc ggc att   355
Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe Pro Leu Ile Gly Ile
 70                  75                  80                  85

ggg ctc gag ccg atg act gca ttt gtg tcg gaa gat att tat cgg gga   403
Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu Asp Ile Tyr Arg Gly
                90                  95                 100

att ttg ttc ctc acg ctc gtt ccg tcc acc gtg cag tca tcg gtg gcg   451
Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val Gln Ser Ser Val Ala
            105                 110                 115

ttt acc tcg atc gct aaa ggc aac gta gct ggt gcg att gtg tcg gca   499
Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly Ala Ile Val Ser Ala
        120                 125                 130

tcg ctc tcc aac ctt gcg ggt gtt ttc ctc act ccg ctg ctg gtc atg   547
Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr Pro Leu Leu Val Met
    135                 140                 145

ctc atc atg tct gcg ggc ggg gga gtt cac gtg gat tcc cag gtc ttc   595
Leu Ile Met Ser Ala Gly Gly Gly Val His Val Asp Ser Gln Val Phe
150                 155                 160                 165

ctc gac att gcg att cag ctt ctg ctg ccg ttc atc ctc ggc cag gta   643
Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe Ile Leu Gly Gln Val
                170                 175                 180

tgt agg cgt tgg gtg aag aat ttt gcg gcc aac aaa gca aca aaa atc   691
Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn Lys Ala Thr Lys Ile
            185                 190                 195

gtg gac cgc ggc tcg atc gcg atg gtc gtg tac tcc gcg ttt tct gcc   739
Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr Ser Ala Phe Ser Ala
        200                 205                 210

ggc atg gtg gct ggc att tgg tcc act gtg agc gtt cta gag att atc   787
Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser Val Leu Glu Ile Ile
    215                 220                 225

tac ctc att gtt ttc gct att ctg ctg gtg atg gcc atg ctg tgg ttc   835
Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met Ala Met Leu Trp Phe
230                 235                 240                 245

acg ctg ttc atg gct aca cgc ctt gga ttt aac cgg gca gat tcc atc   883
Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn Arg Ala Asp Ser Ile
                250                 255                 260

gct att cag ttc tgc gga acc aag aaa tcc ctg gcc aca ggc ctc cca   931
Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu Ala Thr Gly Leu Pro
            265                 270                 275

atg gcg gca gtc atc ttc ggt ggc gcc aat atc ggc ctg ctc atc ttg   979
Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile Gly Leu Leu Ile Leu
        280                 285                 290

ccg ttg atg atc ttc cac caa gtc cag ctg atg att tgt gca tgg ctt   1027
Pro Leu Met Ile Phe His Gln Val Gln Leu Met Ile Cys Ala Trp Leu
    295                 300                 305

gca gct cgt tat ggt cgt gat gcg cag gaa cag aaa gcc aac gcc       1072
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DEMANDE - DEMAND

Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln Lys Ala Asn Ala
310 315 320

taaaagtcct cagtagctag cca 1095

<210> 734
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 734
Met Leu Glu Arg Leu Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val
1 5 10 15

Leu Ala Val Ile Val Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala
20 25 30

Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe
35 40 45

Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys
50 55 60

His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe
65 70 75 80

Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu
85 90 95

Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val
100 105 110

Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly
115 120 125

Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr
130 135 140

Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Gly Val His Val
145 150 155 160

Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe
165 170 175

Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn
180 185 190

Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr
195 200 205

Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser
210 215 220

Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met
225 230 235 240

Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn
245 250 255

Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu

```
            260                 265                 270

Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile
        275                 280                 285

Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met
    290                 295                 300

Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln
305                 310                 315                 320

Lys Ala Asn Ala
```

<210> 735
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> RXN02556

<400> 735

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tgccatcata ttaaggccaa attgcttgga tcctgggatt tatttaatta gattaaatcc 60

gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc   115
                                           Leu Ile Val Ser Thr
                                             1               5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg   163
Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
                10                  15                  20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg   211
Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
            25                  30                  35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct   259
Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
        40                  45                  50

aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg   307
Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
    55                  60                  65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat   355
Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp
70                  75                  80                  85

gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg   403
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val
                90                  95                  100

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg   451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu
            105                 110                 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct   499
```

```
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro
        120                 125                 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg   547
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu
    135                 140                 145

atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc   595
Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly
150                 155                 160                 165

gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca   643
Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala
                170                 175                 180

acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca   691
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro
            185                 190                 195

ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag   739
Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln
        200                 205                 210

ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att   787
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile
    215                 220                 225

gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta   835
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val
230                 235                 240                 245

tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt   883
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val
                250                 255                 260

ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc   931
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly
            265                 270                 275

tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac   979
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp
        280                 285                 290

gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg   1027
Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val
    295                 300                 305

gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa   1075
Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu
310                 315                 320                 325

atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att   1123
Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile
                330                 335                 340

cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag   1171
Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys
            345                 350                 355

aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta   1219
Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val
```

```
        360                 365                 370

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca    1268
Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser
    375                 380                 385

ccccagaact tcc                                                  1281


<210> 736
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 736
Leu Ile Val Ser Thr Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala
  1               5                  10                  15

Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys
             20                  25                  30

Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
         35                  40                  45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly
     50                  55                  60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65                  70                  75                  80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
                 85                  90                  95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
            100                 105                 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
        115                 120                 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
    130                 135                 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
145                 150                 155                 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
                165                 170                 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
            180                 185                 190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
        195                 200                 205

Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
    210                 215                 220

Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
225                 230                 235                 240

Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
```

09529-0050

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                245                 250                 255

Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
            260                 265                 270

Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
        275                 280                 285

Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
    290                 295                 300

Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
305                 310                 315                 320

Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
                325                 330                 335

Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
            340                 345                 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
        355                 360                 365

Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
    370                 375                 380

Ile Ser
385


<210> 737
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> FRXA02556

<400> 737
tgccatcata ttaaggccaa attgcttgga tcctgggatt tatttaatta gattaaatcc 60

gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc   115
                                            Leu Ile Val Ser Thr
                                              1               5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg   163
Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
                10                  15                  20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg   211
Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
            25                  30                  35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct   259
Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
        40                  45                  50

aac acc ttc aac ggt ggc aat cag aag caa ggc gat cag cag aag gcg   307
Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
```

```
     55                  60                  65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat   355
Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp
 70                  75                  80                  85

gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg   403
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val
                90                  95                 100

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg   451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu
            105                 110                 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct   499
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro
        120                 125                 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg   547
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu
    135                 140                 145

atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc   595
Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly
150                 155                 160                 165

gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca   643
Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala
                170                 175                 180

acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca   691
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro
            185                 190                 195

ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag   739
Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln
        200                 205                 210

ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att   787
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile
    215                 220                 225

gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta   835
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val
230                 235                 240                 245

tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt   883
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val
                250                 255                 260

ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc   931
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly
            265                 270                 275

tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac   979
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp
        280                 285                 290

gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg  1027
Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val
    295                 300                 305
```

```
gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa   1075
Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu
310                 315                 320                 325

atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att   1123
Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile
                330                 335                 340

cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag   1171
Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys
            345                 350                 355

aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta   1219
Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val
        360                 365                 370

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca    1268
Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser
    375                 380                 385

ccccagaact tcc                                                   1281
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US 2005/0196848 A1

<210> 738
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 738

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Leu Ile Val Ser Thr Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala
  1               5                  10                  15

Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys
             20                  25                  30

Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
         35                  40                  45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly
     50                  55                  60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65                  70                  75                  80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
                 85                  90                  95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
            100                 105                 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
        115                 120                 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
    130                 135                 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
145                 150                 155                 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
```

```
                165                 170                 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
            180                 185                 190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
        195                 200                 205

Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
    210                 215                 220

Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
225                 230                 235                 240

Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
                245                 250                 255

Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
            260                 265                 270

Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
        275                 280                 285

Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
    290                 295                 300

Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
305                 310                 315                 320

Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
                325                 330                 335

Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
            340                 345                 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
        355                 360                 365

Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
    370                 375                 380

Ile Ser
385
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US09/509,260

<210> 739
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1177)
<223> RXA01392

<400> 739
gtctgcaatc accccgaaca tttgttcaat cgttgatttt cattccactt cgtaatattg 60

ttgacatatc atctaaattt ccaagagagg acaccacaca gtg gct aac acg tca 115
                                              Val Ala Asn Thr Ser
                                                1   5

```
tcc gat tgg gca ggc gcc cca caa aat gca tca gca gac ggc gag ttc   163
Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser Ala Asp Gly Glu Phe
                 10                  15                  20

gtt cgc gat acc aac tac atc gat gac cgc atc gtc gca gac gtt cca   211
Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile Val Ala Asp Val Pro
            25                  30                  35

gcg gga tcc gaa cca att gct cag gaa gat ggc act ttc cat tgg cct   259
Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly Thr Phe His Trp Pro
        40                  45                  50

gtc gag gct ggt cgc tac cgt tta gtc gct gcc cgc gca tgt cca tgg   307
Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala Arg Ala Cys Pro Trp
    55                  60                  65

gca cac cgc act gtt atc acc cgt cgt ctt ctc ggc ctg gag aac gtg   355
Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu Gly Leu Glu Asn Val
70                  75                  80                  85

atc tcg ctt ggt ctg acc ggc ccg act cac gac gtt cgt tcc tgg act   403
Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp Val Arg Ser Trp Thr
                90                  95                 100

ttc gat tta gat cca aac cat ctt gat ccc gtg ctg cag att cct cgt   451
Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val Leu Gln Ile Pro Arg
            105                 110                 115

cta cag gac gcg tat ttc aac cgc ttc ccc gat tac ccg cgc ggc att   499
Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp Tyr Pro Arg Gly Ile
        120                 125                 130

act gtc cca gcg ctc gtg gag gaa tcg tct aag aag gtc gtc acc aac   547
Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys Lys Val Val Thr Asn
    135                 140                 145

gat tac cct tcc atc acc atc gat ttc aat ctt gag tgg aag cag ttc   595
Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu Glu Trp Lys Gln Phe
150                 155                 160                 165

cac cgt gag ggt gcg cct aac ctc tac ccc gcg gag ctg cgc gag gag   643
His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala Glu Leu Arg Glu Glu
                170                 175                 180

atg gcg ccg gtg atg aag cgc atc ttc act gag gtc aac aac ggc gta   691
Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu Val Asn Asn Gly Val
            185                 190                 195

tac agg acc ggc ttt gcc ggt agc cag gaa gcg cac aac gag gcg tac   739
Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala His Asn Glu Ala Tyr
        200                 205                 210

aag cgg ctt tgg gtt gcg ttg gac tgg cta gaa gat cgc tta tcg acg   787
Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu Asp Arg Leu Ser Thr
    215                 220                 225

cga cgt tac ctc atg ggg gat cac atc acc gag gcg gat atc cgc ctc   835
Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu Ala Asp Ile Arg Leu
230                 235                 240                 245
```

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tac cca acc ctc gtg cgt ttc gat gcc gtc tac cac gga cac ttc aag   883
Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr His Gly His Phe Lys
                250                 255                 260

tgt ggc cgc aac aag atc acc gaa atg ccg aat cta tgg ggc tac ctg   931
Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn Leu Trp Gly Tyr Leu
            265                 270                 275

cgg gat ctt ttc cag acc cca ggc ttt ggc gac acc acc gat ttc acc   979
Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp Thr Thr Asp Phe Thr
        280                 285                 290

gaa atc aag cag cac tac tac atc acc cac gcg gag att aac ccc acc   1027
Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala Glu Ile Asn Pro Thr
    295                 300                 305

cgg atc gtt cca gtc gga cca gat ctg tct ggt ttc gcg aca cca cac   1075
Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly Phe Ala Thr Pro His
310                 315                 320                 325

ggc cgt gaa aag ctc ggc gga tcc cca ttt gct gaa ggt gtt act ctg   1123
Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala Glu Gly Val Thr Leu
                330                 335                 340

cct ggc cca att cct gcg ggc gaa gaa gtg aaa aac cct gaa cct ttt   1171
Pro Gly Pro Ile Pro Ala Gly Glu Glu Val Lys Asn Pro Glu Pro Phe
            345                 350                 355

cag aag taactaaggc cgcaatccct cga                                 1200
Gln Lys
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US09/893,209

<210> 740
<211> 359
<212> PRT
<213> Corynebacterium glutamicum

<400> 740

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Val Ala Asn Thr Ser Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser
  1               5                  10                  15

Ala Asp Gly Glu Phe Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile
             20                  25                  30

Val Ala Asp Val Pro Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly
         35                  40                  45

Thr Phe His Trp Pro Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala
     50                  55                  60

Arg Ala Cys Pro Trp Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu
 65                  70                  75                  80

Gly Leu Glu Asn Val Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp
                 85                  90                  95

Val Arg Ser Trp Thr Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val
            100                 105                 110

Leu Gln Ile Pro Arg Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp
```

```
        115                 120                 125

Tyr Pro Arg Gly Ile Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys
    130                 135                 140

Lys Val Val Thr Asn Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu
145                 150                 155                 160

Glu Trp Lys Gln Phe His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala
                165                 170                 175

Glu Leu Arg Glu Glu Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu
            180                 185                 190

Val Asn Asn Gly Val Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala
        195                 200                 205

His Asn Glu Ala Tyr Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu
    210                 215                 220

Asp Arg Leu Ser Thr Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu
225                 230                 235                 240

Ala Asp Ile Arg Leu Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr
                245                 250                 255

His Gly His Phe Lys Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn
            260                 265                 270

Leu Trp Gly Tyr Leu Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp
        275                 280                 285

Thr Thr Asp Phe Thr Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala
    290                 295                 300

Glu Ile Asn Pro Thr Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly
305                 310                 315                 320

Phe Ala Thr Pro His Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala
                325                 330                 335

Glu Gly Val Thr Leu Pro Gly Pro Ile Pro Ala Gly Glu Glu Val Lys
            340                 345                 350

Asn Pro Glu Pro Phe Gln Lys
        355
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<210> 741
<211> 1227
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1204)
<223> RXA00800

<400> 741
gactccgcag ggatggccta caagtacggt cacggactta atttctagat tgtaggtagt 60

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ctcgtgggca caactgaaat cttattgaaa aggagtgtcc atg agc act gta gtg   115
                                           Met Ser Thr Val Val
                                             1               5

cct gga att gtc gca ctg tcc aag ggt gca ccg gta gaa aaa gta aac   163
Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro Val Glu Lys Val Asn
                 10                  15                  20

gtt gtt gtc cct gat cca ggt gct aac gat gtc atc gtc aag att cag   211
Val Val Val Pro Asp Pro Gly Ala Asn Asp Val Ile Val Lys Ile Gln
             25                  30                  35

gcc tgc ggt gtg tgc cac acc gac ttg gcc tac cgc gat ggc gat att   259
Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr Arg Asp Gly Asp Ile
         40                  45                  50

tca gat gag ttc cct tac ctc ctc ggc cac gag gca gca ggc att gtt   307
Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu Ala Ala Gly Ile Val
     55                  60                  65

gag gag gta ggc gag tcc gtc acc cac gtt gag gtc ggc gat ttc gtc   355
Glu Glu Val Gly Glu Ser Val Thr His Val Glu Val Gly Asp Phe Val
 70                  75                  80                  85

atc ttg aac tgg cgt gca gtg tgc ggc gag tgc cgt gca tgt aag aag   403
Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys Arg Ala Cys Lys Lys
                 90                  95                 100

ggc gag cca aag tac tgc ttt aac acc cac aac gcc tct aag aag atg   451
Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn Ala Ser Lys Lys Met
             105                 110                 115

acc ctg gaa gac ggc acc gag ctg tcc cca gca ctg ggt att ggc gcg   499
Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala Leu Gly Ile Gly Ala
         120                 125                 130

ttc ttg gaa aag acc ctg gtc cac gaa ggc cag tgc acc aag gtt aac   547
Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln Cys Thr Lys Val Asn
     135                 140                 145

cct gag gaa gat cca gca gca gct ggc ctt ctg ggt tgt ggc atc atg   595
Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu Gly Cys Gly Ile Met
150                 155                 160                 165

gca ggc ctt ggc gct gcg gtg aac acc ggt gat att aag cgt ggc gag   643
Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp Ile Lys Arg Gly Glu
                 170                 175                 180

tcc gta gca gtc ttc ggc ctt ggt ggc gtg ggc atg gca gct att gct   691
Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly Met Ala Ala Ile Ala
             185                 190                 195

ggc gcc aag att gct ggc gct tcc aag atc att gct gtt gat atc gat   739
Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile Ala Val Asp Ile Asp
         200                 205                 210

gag aag aag ctg gag tgg gcg aag gaa ttc ggc gca acc cac acc att   787
Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly Ala Thr His Thr Ile
     215                 220                 225

aat tcc tct ggt ctt ggt ggc gaa ggt gat gcc tct gag gtc gtg gca   835
```

```
Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala Ser Glu Val Val Ala
230                 235                 240                 245

aag gtt cgt gag ctc acc gat ggt ttc ggc acc gat gtc tcc atc gat   883
Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr Asp Val Ser Ile Asp
                250                 255                 260

gcg gta ggc atc atg ccg acc tgg cag cag gcg ttt tac tcc cgt gac   931
Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala Phe Tyr Ser Arg Asp
            265                 270                 275

cat gca ggc cgc atg gtg atg gtg ggc gtt cca aac ctg acg tct cgc   979
His Ala Gly Arg Met Val Met Val Gly Val Pro Asn Leu Thr Ser Arg
        280                 285                 290

gta gat gtt cct gcg att gat ttt tac ggt cgc ggt gga tcc gtg cgc   1027
Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg Gly Gly Ser Val Arg
    295                 300                 305

cct gca tgg tac ggc gac tgc ctg cct gag cgt gat ttc cca act tat   1075
Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg Asp Phe Pro Thr Tyr
310                 315                 320                 325

gtg gat ctg cac ctg cag ggt cgt ttc cca ctg gat aag ttt gtt tct   1123
Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu Asp Lys Phe Val Ser
                330                 335                 340

gag cgt att ggt ctt gat gat gtt gaa gag gct ttc aac acc atg aag   1171
Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala Phe Asn Thr Met Lys
            345                 350                 355

gct ggc gac gtg ctg cgt tct gtg gtg gag atc taaatggctc acgacggatt 1224
Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile
        360                 365

gcg                                                               1227
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<210> 742
<211> 368
<212> PRT
<213> Corynebacterium glutamicum

<400> 742

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Met Ser Thr Val Val Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro
  1               5                  10                  15

Val Glu Lys Val Asn Val Val Val Pro Asp Pro Gly Ala Asn Asp Val
             20                  25                  30

Ile Val Lys Ile Gln Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr
         35                  40                  45

Arg Asp Gly Asp Ile Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu
     50                  55                  60

Ala Ala Gly Ile Val Glu Glu Val Gly Glu Ser Val Thr His Val Glu
 65                  70                  75                  80

Val Gly Asp Phe Val Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys
                 85                  90                  95
```

Arg Ala Cys Lys Lys Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn
100 105 110

Ala Ser Lys Lys Met Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala
115 120 125

Leu Gly Ile Gly Ala Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln
130 135 140

Cys Thr Lys Val Asn Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu
145 150 155 160

Gly Cys Gly Ile Met Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp
165 170 175

Ile Lys Arg Gly Glu Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly
180 185 190

Met Ala Ala Ile Ala Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile
195 200 205

Ala Val Asp Ile Asp Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly
210 215 220

Ala Thr His Thr Ile Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala
225 230 235 240

Ser Glu Val Val Ala Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr
245 250 255

Asp Val Ser Ile Asp Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala
260 265 270

Phe Tyr Ser Arg Asp His Ala Gly Arg Met Val Met Val Gly Val Pro
275 280 285

Asn Leu Thr Ser Arg Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg
290 295 300

Gly Gly Ser Val Arg Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg
305 310 315 320

Asp Phe Pro Thr Tyr Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu
325 330 335

Asp Lys Phe Val Ser Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala
340 345 350

Phe Asn Thr Met Lys Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile
355 360 365

<210> 743
<211> 1011
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(988)
<223> RXA02143

<400> 743
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ccctatgccc ttcacttcca cagtcgagat tcaaagggaa atg atg gaa acc aac 115
Met Met Glu Thr Asn
1 5

ccg cag acc cca gag gga aat agc atg gct aaa ccc tct gct aag aag 163
Pro Gln Thr Pro Glu Gly Asn Ser Met Ala Lys Pro Ser Ala Lys Lys
10 15 20

gtc aag aat cgc cgc aag gtc cgg cgc acc gtc gca ggt gca ttg gct 211
Val Lys Asn Arg Arg Lys Val Arg Arg Thr Val Ala Gly Ala Leu Ala
25 30 35

ctg acc att gga ctg agc gga gca gga atc ctc gca acc gcg atc act 259
Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu Ala Thr Ala Ile Thr
40 45 50

cca gat gct caa gtt gct acc gct cag cgt gac gat cag gca ctt atc 307
Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp Asp Gln Ala Leu Ile
55 60 65

tcc gag ggt aaa gac ctc tac gat gtc gcc tgc atc acc tgc cac ggc 355
Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys Ile Thr Cys His Gly
70 75 80 85

gta aac ctc caa ggt gtt gag gac cgc ggt cct tcc ctc gta ggt gtt 403
Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro Ser Leu Val Gly Val
90 95 100

ggc gaa ggc gca gtg tac ttc caa gtt cac tcc ggc cgt atg cca ata 451
Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser Gly Arg Met Pro Ile
105 110 115

ctg cgt aac gag gct cag gct gag cgc aag gct cct cgt tac acc gag 499
Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala Pro Arg Tyr Thr Glu
120 125 130

gca cag acc ctt gcg atc gct gca tat gtt gca gct aat ggc ggt ggc 547
Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala Ala Asn Gly Gly Gly
135 140 145

cca gga ctc gtt tac aac gag gac ggc acc ctc gcc atg gag gag ctc 595
Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu Ala Met Glu Glu Leu
150 155 160 165

cgt ggc gaa aac tac gac gga cag att acc tcc gcc gac gtc gct cgc 643
Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser Ala Asp Val Ala Arg
170 175 180

ggc gga gat ctg ttc cgc ctg aac tgt gca tcc tgc cac aac ttc act 691
Gly Gly Asp Leu Phe Arg Leu Asn Cys Ala Ser Cys His Asn Phe Thr
185 190 195

ggt cgt ggt ggc gca ctg tcc tct ggt aag tac gca cca aac ctg gat 739

```
Gly Arg Gly Gly Ala Leu Ser Ser Gly Lys Tyr Ala Pro Asn Leu Asp
        200                 205                 210

gct gca aac gag cag gaa atc tac cag gct atg ctt acc ggt cct cag   787
Ala Ala Asn Glu Gln Glu Ile Tyr Gln Ala Met Leu Thr Gly Pro Gln
    215                 220                 225

aac atg cct aag ttc tcc gat cgt cag ctc tcc gca gat gag aag aag   835
Asn Met Pro Lys Phe Ser Asp Arg Gln Leu Ser Ala Asp Glu Lys Lys
230                 235                 240                 245

gac atc atc gcc ttc atc aag tcc acc aag gag act cca tca cct ggt   883
Asp Ile Ile Ala Phe Ile Lys Ser Thr Lys Glu Thr Pro Ser Pro Gly
                250                 255                 260

ggt tac tca ctc ggt agc ttg ggc cca gtg gct gag ggt ctg ttc atg   931
Gly Tyr Ser Leu Gly Ser Leu Gly Pro Val Ala Glu Gly Leu Phe Met
            265                 270                 275

tgg gta ttc ggc atc ttg gtc ctc gtg gcc gcc gct atg tgg att gga   979
Trp Val Phe Gly Ile Leu Val Leu Val Ala Ala Ala Met Trp Ile Gly
        280                 285                 290

tca cgt tca tgagtaacaa caacgacaaa cag                            1011
Ser Arg Ser
    295
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09522400.seq

<210> 744
<211> 296
<212> PRT
<213> Corynebacterium glutamicum

<400> 744

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Met Met Glu Thr Asn Pro Gln Thr Pro Glu Gly Asn Ser Met Ala Lys
  1               5                  10                  15

Pro Ser Ala Lys Lys Val Lys Asn Arg Arg Lys Val Arg Arg Thr Val
             20                  25                  30

Ala Gly Ala Leu Ala Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu
         35                  40                  45

Ala Thr Ala Ile Thr Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp
     50                  55                  60

Asp Gln Ala Leu Ile Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys
 65                  70                  75                  80

Ile Thr Cys His Gly Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro
                 85                  90                  95

Ser Leu Val Gly Val Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser
            100                 105                 110

Gly Arg Met Pro Ile Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala
        115                 120                 125

Pro Arg Tyr Thr Glu Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala
    130                 135                 140
```

```
Ala Asn Gly Gly Gly Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu
145                 150                 155                 160

Ala Met Glu Glu Leu Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser
                165                 170                 175

Ala Asp Val Ala Arg Gly Gly Asp Leu Phe Arg Leu Asn Cys Ala Ser
            180                 185                 190

Cys His Asn Phe Thr Gly Arg Gly Gly Ala Leu Ser Ser Gly Lys Tyr
        195                 200                 205

Ala Pro Asn Leu Asp Ala Ala Asn Glu Gln Glu Ile Tyr Gln Ala Met
    210                 215                 220

Leu Thr Gly Pro Gln Asn Met Pro Lys Phe Ser Asp Arg Gln Leu Ser
225                 230                 235                 240

Ala Asp Glu Lys Lys Asp Ile Ile Ala Phe Ile Lys Ser Thr Lys Glu
                245                 250                 255

Thr Pro Ser Pro Gly Gly Tyr Ser Leu Gly Ser Leu Gly Pro Val Ala
            260                 265                 270

Glu Gly Leu Phe Met Trp Val Phe Gly Ile Leu Val Leu Val Ala Ala
        275                 280                 285

Ala Met Trp Ile Gly Ser Arg Ser
    290                 295
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<210> 745
<211> 502
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> RXN03096

<400> 745
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cgcaggcgcc gttgtcacct cactgctcac cttgtacacc atg gtt ctg gtc tgg 115
                                            Met Val Leu Val Trp
                                              1   5

tcc aag gcc ttc tgg cgc gac cgt aaa gac gcc ccc gat gga gca acc 163
Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala Pro Asp Gly Ala Thr
                 10   15   20

gca cta gca aga ccc gca cct ttg gta gat atc caa gac gaa gtc gcc 211
Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile Gln Asp Glu Val Ala
             25   30   35

gtt aaa gac cgc aac gat gtc gga cgg atg cct tgg ggc atg gtc ttc 259
Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro Trp Gly Met Val Phe
         40   45   50

tcc act gcc ctg ttg gtt tcc gca tcc ctt gct gta tcc gtg ctc gca 307
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```
Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala Val Ser Val Leu Ala
     55                  60                  65

gga cca ctg tca tct att act gga cgc gcc gcc gaa tcc gca caa gat   355
Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala Glu Ser Ala Gln Asp
 70                  75                  80                  85

gtc aac atc tac cgc gcc gca gta ctc ggc cca act acc tcg acc cat   403
Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro Thr Thr Ser Thr His
                 90                  95                 100

cac gca cac tcg aga tgg agc gtt acg acg cca acc gcg atg aca tca   451
His Ala His Ser Arg Trp Ser Val Thr Thr Pro Thr Ala Met Thr Ser
            105                 110                 115

acc acc gcg tcg aca cca atg gaa cgg agg acc aac cat gat cag tgg   499
Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr Asn His Asp Gln Trp
        120                 125                 130

att                                                               502
Ile
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SEQUENCE LISTING

<210> 746
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 746

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Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala
  1               5                  10                  15

Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile
             20                  25                  30

Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro
         35                  40                  45

Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala
     50                  55                  60

Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala
 65                  70                  75                  80

Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro
                 85                  90                  95

Thr Thr Ser Thr His His Ala His Ser Arg Trp Ser Val Thr Thr Pro
            100                 105                 110

Thr Ala Met Thr Ser Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr
        115                 120                 125

Asn His Asp Gln Trp Ile
    130
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<210> 747
<211> 504
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(481)
<223> RXN02036

<400> 747
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gccctcatct ctgctgcagt ggcggctctc ggagggtggt gtg cat att cct ttt 115
Val His Ile Pro Phe
1 5

ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc 163
Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys
10 15 20

gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211
Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser
25 30 35

acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259
Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala
40 45 50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg 307
Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val
55 60 65

cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc 355
Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe
70 75 80 85

gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403
Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe
90 95 100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag 451
Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys
105 110 115

gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg 501
Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
120 125

ttt 504

<210> 748
<211> 127
<212> PRT
<213> Corynebacterium glutamicum

<400> 748
Val His Ile Pro Phe Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys
1 5 10 15

Gly Gly Gly Ser Cys Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro
20 25 30

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Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala
         35                  40                  45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala
     50                  55                  60

Phe Arg Ser Gly Val Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala
 65                  70                  75                  80

Thr Ser Val Gly Phe Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile
                 85                  90                  95

Ala Gly Leu Cys Phe Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg
            100                 105                 110

Gln Val Ala Arg Lys Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
        115                 120                 125
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<210> 749
<211> 882
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(859)
<223> RXN02765

<400> 749

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tctgaacttt tccgcatcga cccagatgag gtttaccccg acgacgacgc cacctgcgaa 60

ttcaacccat ggccgtatcc tcgcggattt taggagataa atg tct aat caa tta   115
                                            Met Ser Asn Gln Leu
                                              1               5

ccc gat cac gtc cgc gac gcc ttc caa gta ggt gcg gga cct gcc gaa   163
Pro Asp His Val Arg Asp Ala Phe Gln Val Gly Ala Gly Pro Ala Glu
                 10                  15                  20

caa ctc ggt caa gct tgg gac ttc gga ttc cgc gtc ggc aac act gtg   211
Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg Val Gly Asn Thr Val
             25                  30                  35

ttc gcc aaa gtg acg gcg ccg gaa gtg tcg ggc tgg tcg tcg aaa acc   259
Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly Trp Ser Ser Lys Thr
         40                  45                  50

cgc gaa acc ctg aaa cca gaa ggc gtg cgc gtc gta cga ccg atc cgc   307
Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val Val Arg Pro Ile Arg
     55                  60                  65

tcc acc gac ggc cga ttt gtg gtt gcg ggg tgg cgc gca tcg gtg ttc   355
Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp Arg Ala Ser Val Phe
 70                  75                  80                  85

tct acg gga acg atc agc aag cga gtc gat gag acg gtc gtt gcg ggt   403
Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu Thr Val Val Ala Gly
                 90                  95                 100

ctt cgt ttg gca gat gca tta gtg gat acg cat gca ccg gaa cct gtg   451
```

```
Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His Ala Pro Glu Pro Val
            105                 110                 115

gac aat gtg ttt aac cgt gct gat gtg cag gcc tgg gaa gag cag ccc   499
Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala Trp Glu Glu Gln Pro
        120                 125                 130

ggt cga atc ggt gaa ttg ttg gag ccg att aat cgc gtg aac cag gtt   547
Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn Arg Val Asn Gln Val
    135                 140                 145

ggt cat gcg gat atg ttg gcg aca acg ctg tat gcg gga act cag cca   595
Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr Ala Gly Thr Gln Pro
150                 155                 160                 165

cct gca gtg acg gat ttg gtg cca gtg ctg cgt ccg cat ggt ttc act   643
Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg Pro His Gly Phe Thr
                170                 175                 180

gcg gca ttg gtg atc gtt gat ggg ttg ctg ctg ggt gcg gtt gat gag   691
Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu Gly Ala Val Asp Glu
            185                 190                 195

gga att ctg cgg agg ttt tcg cat ttg ccg gaa att gag cag ctg gtt   739
Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val
        200                 205                 210

ttg agg gca ttt ttg ttc cgt cga aac ttg cag gag ttc tct gag aac   787
Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln Glu Phe Ser Glu Asn
    215                 220                 225

aac gat ccg aat gtt att tcg aac cta aac agg gtg gaa tcg aca ctc   835
Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg Val Glu Ser Thr Leu
230                 235                 240                 245

gtg tcg tat gtt tct gac aag att tgaggtatgt cggaatacaa acc         882
Val Ser Tyr Val Ser Asp Lys Ile
                250
```

<210> 750
<211> 253
<212> PRT
<213> Corynebacterium glutamicum

<400> 750

```
Met Ser Asn Gln Leu Pro Asp His Val Arg Asp Ala Phe Gln Val Gly
  1               5                  10                  15

Ala Gly Pro Ala Glu Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg
             20                  25                  30

Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly
         35                  40                  45

Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val
     50                  55                  60

Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp
 65                  70                  75                  80
```

```
Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu
                 85                  90                  95

Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His
            100                 105                 110

Ala Pro Glu Pro Val Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala
        115                 120                 125

Trp Glu Glu Gln Pro Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn
    130                 135                 140

Arg Val Asn Gln Val Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr
145                 150                 155                 160

Ala Gly Thr Gln Pro Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg
                165                 170                 175

Pro His Gly Phe Thr Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu
            180                 185                 190

Gly Ala Val Asp Glu Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu
        195                 200                 205

Ile Glu Gln Leu Val Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln
    210                 215                 220

Glu Phe Ser Glu Asn Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg
225                 230                 235                 240

Val Glu Ser Thr Leu Val Ser Tyr Val Ser Asp Lys Ile
                245                 250
```

US 2003/0175945 A1

<210> 751
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXN02206

<400> 751

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ggcaggatct gctgctgcgg ctaggagggt tatctcttca ttcacccgat ctaccgtact 60

accttatgac ctcagtagtg tggtgggcgt gaaacagcga atg gtc ggt tca agt   115
                                            Met Val Gly Ser Ser
                                              1               5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg   163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
                 10                  15                  20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat   211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
             25                  30                  35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc   259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
```

```
         40                  45                  50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg   307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
     55                  60                  65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc   355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
 70                  75                  80                  85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat   403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
                 90                  95                 100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg   451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
            105                 110                 115

ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg   499
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
        120                 125                 130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga   547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly
    135                 140                 145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca   595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala
150                 155                 160                 165

gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg   643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu
                170                 175                 180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta   691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu
            185                 190                 195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act   739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr
        200                 205                 210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca   787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr
    215                 220                 225

gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc   835
Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile
230                 235                 240                 245

att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc   883
Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro
                250                 255                 260

gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct   931
Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala
            265                 270                 275

gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag   979
Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys
        280                 285                 290
```

US 9,932,567 B2

```
gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat   1027
Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp
    295                 300                 305

gtc tcc ctg tgacttggtc caattacatt cac                            1059
Val Ser Leu
310
```

<210> 752
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 752

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Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr
  1               5                  10                  15

Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe
            20                  25                  30

Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn
        35                  40                  45

Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala
    50                  55                  60

Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn
65                  70                  75                  80

Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
                85                  90                  95

Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
            100                 105                 110

Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu
        115                 120                 125

Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
    130                 135                 140

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
145                 150                 155                 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
                165                 170                 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
            180                 185                 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
        195                 200                 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
    210                 215                 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
225                 230                 235                 240
```

09892136.030208

```
Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
                245                 250                 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
            260                 265                 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
        275                 280                 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
    290                 295                 300

Gln Ala Leu Asp Asp Val Ser Leu
305                 310


<210> 753
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXN02554

<400> 753
gcttttgaag tgtgtcgcgt gtgcggactg aaatagtttc cgcttcaact tggttgctaa 60

ggataggctc cataaaaata accaaaggcg gaaaatttca atg tca cac act aag   115
                                            Met Ser His Thr Lys
                                              1               5

cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc   163
Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala
                10                  15                  20

agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt   211
Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly
            25                  30                  35

gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg   259
Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala
        40                  45                  50

gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc   307
Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
    55                  60                  65

ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta   355
Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
70                  75                  80                  85

gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat   403
Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
                90                  95                  100

ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att   451
Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
            105                 110                 115
```

```
att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac   499
Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
        120                 125                 130

att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att   547
Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
    135                 140                 145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta   595
Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
150                 155                 160                 165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac   643
Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
                170                 175                 180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat   691
Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
            185                 190                 195

aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
        200                 205

aac                                                               747
```

<210> 754
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 754

```
Met Ser His Thr Lys Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val
  1               5                  10                  15

Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys
             20                  25                  30

Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
         35                  40                  45

Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
     50                  55                  60

Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
 65                  70                  75                  80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
                 85                  90                  95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
            100                 105                 110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
        115                 120                 125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
    130                 135                 140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
```

```
145                 150                 155                 160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
                165                 170                 175

Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe
            180                 185                 190

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
        195                 200                 205
```

<210> 755
<211> 933
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> RXN01204

<400> 755

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ttacagcgag tttttcagac gtccatcgca ccgtgcacaa caacatttca ggtgcacggc 60

ccgaacacgg gagagaacgc tgagcgttac aacactgtcc atg aag ggc gaa ttc   115
                                          Met Lys Gly Glu Phe
                                            1               5

cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat   163
His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp
                10                  15                  20

agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg   211
Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp
            25                  30                  35

ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc   259
Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu Leu Met Thr Ala Val
        40                  45                  50

gtt gtg gtc ttc ttc ctt tgg gct atg cgc aag cca aag ctt gtt ccg   307
Val Val Val Phe Phe Leu Trp Ala Met Arg Lys Pro Lys Leu Val Pro
    55                  60                  65

cat ggc gtc cag aat ttt gca gag tac gca ctc gat ttc gtt ggt att   355
His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu Asp Phe Val Gly Ile
70                  75                  80                  85

cac atc gct gaa gac atc ctc gga aag aag aaa ggt cgt cgg ttc ctg   403
His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys Gly Arg Arg Phe Leu
                90                  95                  100

ccg atc ctg gcc acc atc ttc ttc gcg gct ctg ttg atg aac ctt gca   451
Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu Leu Met Asn Leu Ala
            105                 110                 115

acg atc atc ccg gga cta aac atc tcc tcc aac tca cgt att gca ttc   499
```

```
Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn Ser Arg Ile Ala Phe
        120                 125                 130

cca atc gtg atg gcg gta gct ggt tac atc gcg ttt atc tac gca ggc   547
Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala Phe Ile Tyr Ala Gly
    135                 140                 145

tct aag cgt tac gga ttc ttc aaa tat gtg aag tct tct gtt gtg att   595
Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys Ser Ser Val Val Ile
150                 155                 160                 165

ccg aac att cca cca gca ctt cac gtc ttg gtg gtt cca att gag ttc   643
Pro Asn Ile Pro Pro Ala Leu His Val Leu Val Val Pro Ile Glu Phe
                170                 175                 180

ttc tct aca ttc atc ttg agg cca gtc acc ctg gca ctg cgt ttg atg   691
Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu Ala Leu Arg Leu Met
            185                 190                 195

gcc aac ttc ctt gct ggc cac atc atc ctg gtt ctg ctt ttc tcc gca   739
Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val Leu Leu Phe Ser Ala
        200                 205                 210

acg aac ttc ttc ttc ttc cag ttc aac gga tgg aca gca atg tcc ggc   787
Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp Thr Ala Met Ser Gly
    215                 220                 225

gta acc atc ttg atg gca gta ctc ttc acg gtt tac gag atc att gtt   835
Val Thr Ile Leu Met Ala Val Leu Phe Thr Val Tyr Glu Ile Ile Val
230                 235                 240                 245

atc ttc ctg cag gca tac atc ttc gct ctg ctg gtc gct gta tac att   883
Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu Val Ala Val Tyr Ile
                250                 255                 260

gag ctt tca ctt cac gcg gat tct cac tagatgaaaa aggtcgctat         930
Glu Leu Ser Leu His Ala Asp Ser His
            265                 270

taa                                                              933


<210> 756
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 756
Met Lys Gly Glu Phe His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro
  1               5                  10                  15

Gly His Val Thr Asp Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp
             20                  25                  30

Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu
         35                  40                  45

Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
     50                  55                  60

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
```

```
65                  70                  75                  80

Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
                85                  90                  95

Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
            100                 105                 110

Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
        115                 120                 125

Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
    130                 135                 140

Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
145                 150                 155                 160

Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
                165                 170                 175

Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
            180                 185                 190

Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
        195                 200                 205

Leu Leu Phe Ser Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
    210                 215                 220

Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
225                 230                 235                 240

Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu
                245                 250                 255

Val Ala Val Tyr Ile Glu Leu Ser Leu His Ala Asp Ser His
            260                 265                 270
```

<210> 757
<211> 862
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(862)
<223> FRXA01204

<400> 757
ttacagcgag tttttcagac gtccatcgca ccgtgcacaa caacatttca ggtgcacggc 60

ccgaacacgg gagagaacgc tgagcgttac aacactgtcc atg aag ggc gaa ttc 115
Met Lys Gly Glu Phe
1 5

cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163
His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp
10 15 20

agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211

```
Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp
            25                  30                  35

ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc   259
Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu Leu Met Thr Ala Val
        40                  45                  50

gtt gtg gtc ttc ttc ctt tgg gct atg cgc aag cca aag ctt gtt ccg   307
Val Val Val Phe Phe Leu Trp Ala Met Arg Lys Pro Lys Leu Val Pro
    55                  60                  65

cat ggc gtc cag aat ttt gca gag tac gca ctc gat ttc gtt ggt att   355
His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu Asp Phe Val Gly Ile
70                  75                  80                  85

cac atc gct gaa gac atc ctc gga aag aag aaa ggt cgt cgg ttc ctg   403
His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys Gly Arg Arg Phe Leu
                90                  95                  100

ccg atc ctg gcc acc atc ttc ttc gcg gct ctg ttg atg aac ctt gca   451
Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu Leu Met Asn Leu Ala
            105                 110                 115

acg atc atc ccg gga cta aac atc tcc tcc aac tca cgt att gca ttc   499
Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn Ser Arg Ile Ala Phe
        120                 125                 130

cca atc gtg atg gcg gta gct ggt tac atc gcg ttt atc tac gca ggc   547
Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala Phe Ile Tyr Ala Gly
    135                 140                 145

tct aag cgt tac gga ttc ttc aaa tat gtg aag tct tct gtt gtg att   595
Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys Ser Ser Val Val Ile
150                 155                 160                 165

ccg aac att cca cca gca ctt cac gtc ttg gtg gtt cca att gag ttc   643
Pro Asn Ile Pro Pro Ala Leu His Val Leu Val Val Pro Ile Glu Phe
                170                 175                 180

ttc tct aca ttc atc ttg agg cca gtc acc ctg gca ctg cgt ttg atg   691
Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu Ala Leu Arg Leu Met
            185                 190                 195

gcc aac ttc ctt gct ggc cac atc atc ctg gtt ctg ctt ttc ttc gca   739
Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val Leu Leu Phe Phe Ala
        200                 205                 210

acg aac ttc ttc ttc ttc cag ttc aac gga tgg aca gca atg tcc ggc   787
Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp Thr Ala Met Ser Gly
    215                 220                 225

gta acc atc ttg atg gca gta ctc ttc acg gtt tac gag atc att gtt   835
Val Thr Ile Leu Met Ala Val Leu Phe Thr Val Tyr Glu Ile Ile Val
230                 235                 240                 245

atc ttc ctg cag gca tac atc ttc gct                              862
Ile Phe Leu Gln Ala Tyr Ile Phe Ala
                250
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<210> 758

<211> 254
<212> PRT
<213> Corynebacterium glutamicum

<400> 758

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Met Lys Gly Glu Phe His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro
  1               5                  10                  15

Gly His Val Thr Asp Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp
             20                  25                  30

Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu
         35                  40                  45

Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
     50                  55                  60

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
 65                  70                  75                  80

Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
                 85                  90                  95

Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
            100                 105                 110

Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
        115                 120                 125

Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
    130                 135                 140

Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
145                 150                 155                 160

Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
                165                 170                 175

Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
            180                 185                 190

Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
        195                 200                 205

Leu Leu Phe Phe Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
    210                 215                 220

Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
225                 230                 235                 240

Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala
                245                 250
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<210> 759
<211> 1764
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1741)
<223> RXA01201

<400> 759
tcgggcaaac tcgagcgtct gcgggcaagc ttcgcataaa gacacgacga attagacaac 60

attagtaatg ctggaagaaa caaccgagag caggaagaac atg gcg gag ctg acg 115
Met Ala Glu Leu Thr
1 5

atc tcc tcc gat gag atc cgt agc gcg att gcg aac tac acc tcg agc 163
Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala Asn Tyr Thr Ser Ser
10 15 20

tac tcc gcg gag gcc tcc cgt gag gag gtc ggc gtg gtt att tcg gcc 211
Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly Val Val Ile Ser Ala
25 30 35

gct gac ggt atc gcc cag gtt tcg ggc ctc ccg tca gta atg gcg aat 259
Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro Ser Val Met Ala Asn
40 45 50

gag ctc ctc gaa ttc ccg ggc ggc gtc atc ggc gtc gca cag aac ctt 307
Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly Val Ala Gln Asn Leu
55 60 65

gaa gct gac cga gtc ggc gtc gtg gtc ctg ggt aac tac gag cta ctt 355
Glu Ala Asp Arg Val Gly Val Val Val Leu Gly Asn Tyr Glu Leu Leu
70 75 80 85

aaa gaa ggc gac caa gtt cgt cgt act gga gac gtt ctg tct atc cca 403
Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp Val Leu Ser Ile Pro
90 95 100

gtc ggc gag gca ttc ctt ggc cgc gtt atc aac ccc ctt ggc cag cca 451
Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn Pro Leu Gly Gln Pro
105 110 115

att gac ggc ctg ggc gaa att gca tcc gaa gag gac cgc gtc ctc gag 499
Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu Asp Arg Val Leu Glu
120 125 130

ctt cag gca cca acc gtg ctt gag cgc cag cct gtc gag gag cct ttg 547
Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro Val Glu Glu Pro Leu
135 140 145

gca acc ggc atc aag gct atc gat gca atg acc cca atc ggc cgc ggt 595
Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr Pro Ile Gly Arg Gly
150 155 160 165

cag cgt cag ctg atc att ggt gac cgt aag act ggc aag acc gca gtc 643
Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr Gly Lys Thr Ala Val
170 175 180

tgt gtc gat acc atc ctt aac cag aag gcc aac tgg gag acc ggc gac 691
Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn Trp Glu Thr Gly Asp
185 190 195

aag acc aag cag gtt cgc tgc atc tac gtc gca atc ggt cag aag ggc 739
Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala Ile Gly Gln Lys Gly
200 205 210

09025480.0025480

```
tcc acc att gca gcc ctg cgt aag acc ctc gag gag cag ggc gct ctc   787
Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu Glu Gln Gly Ala Leu
    215                 220                 225

gag tac acc acc atc gtg gct gca ccc gct tcc gat gct gca ggc ttc   835
Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser Asp Ala Ala Gly Phe
230                 235                 240                 245

aag tgg ctt gca cca ttc gct ggc gct gct ctc gcc cag cac tgg atg   883
Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu Ala Gln His Trp Met
                250                 255                 260

tac cag ggc aac cac gtc ctg gtc atc tac gat gat ctg acc aag cag   931
Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp Asp Leu Thr Lys Gln
            265                 270                 275

gct gag gca tac cgt gct atc tcc ctg ctg ctg cgt cgc cca ccg ggc   979
Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly
        280                 285                 290

cgc gaa gca tac cca ggt gac gtc ttc tac ctg cac tcc cgt ctg ctg   1027
Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu
    295                 300                 305

gag cgc gct gcg aag ctg tcc gat gaa cta ggc gca ggt tct att aca   1075
Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly Ala Gly Ser Ile Thr
310                 315                 320                 325

gca ctg cca atc att gag acc aag gct aat gac gtt tcc gcc ttc att   1123
Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp Val Ser Ala Phe Ile
                330                 335                 340

cct acc aac gtg att tcc atc acc gac ggt cag gta ttc ctt gag tcc   1171
Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln Val Phe Leu Glu Ser
            345                 350                 355

gac ctg ttc aac cgt ggc gtt cgc ccg gcg atc aac gtc ggt gta tcc   1219
Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile Asn Val Gly Val Ser
        360                 365                 370

gtc tcc cgt gtc ggt ggc gca gct cag acc aag ggt atg aag aag gtt   1267
Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys Gly Met Lys Lys Val
    375                 380                 385

gcc ggt tct ctc cgt ctg gat ctg gct gca ttc cgc gac ctg gaa gca   1315
Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe Arg Asp Leu Glu Ala
390                 395                 400                 405

ttc gct acc ttc gca tct gac ttg gat gct gca tcc aag tct cag ctt   1363
Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala Ser Lys Ser Gln Leu
                410                 415                 420

gag cgt ggc cag cgc ctc gtt cag ctg ttg att cag tct gag aac gca   1411
Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile Gln Ser Glu Asn Ala
            425                 430                 435

cct cag gct gtt gag tac cag atc att tct ctc tgg ctt gca ggc gaa   1459
Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu Trp Leu Ala Gly Glu
        440                 445                 450
```

```
ggc gca ttc gac aac gtt cct gtt gaa gat gtt cgt cgc ttc gag tcc   1507
Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val Arg Arg Phe Glu Ser
    455                 460                 465

gaa ctg cac gag tac tta ggc tcc aac gct gca cag gtc tac gag cag   1555
Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala Gln Val Tyr Glu Gln
470                 475                 480                 485

atc gct ggt gga gct cag ctt tcc gac gag tcc aag gaa acc ttg ctc   1603
Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser Lys Glu Thr Leu Leu
                490                 495                 500

aag gca acc gaa gat ttc aag agc gct ttc cag acc acc gat ggc acc   1651
Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln Thr Thr Asp Gly Thr
            505                 510                 515

cct gtc atc aac gag cct gag gtt gaa gca ctc gat gca ggc cag gtc   1699
Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu Asp Ala Gly Gln Val
        520                 525                 530

aag aaa gac cag ctc acc gtt tcc cgc aag gtc agc aag aag           1741
Lys Lys Asp Gln Leu Thr Val Ser Arg Lys Val Ser Lys Lys
    535                 540                 545

taaggcagcg agcctacact aaa                                        1764
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<210> 760
<211> 547
<212> PRT
<213> Corynebacterium glutamicum

<400> 760

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Met Ala Glu Leu Thr Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala
  1               5                  10                  15

Asn Tyr Thr Ser Ser Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly
             20                  25                  30

Val Val Ile Ser Ala Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro
         35                  40                  45

Ser Val Met Ala Asn Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly
     50                  55                  60

Val Ala Gln Asn Leu Glu Ala Asp Arg Val Gly Val Val Val Leu Gly
 65                  70                  75                  80

Asn Tyr Glu Leu Leu Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp
                 85                  90                  95

Val Leu Ser Ile Pro Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn
            100                 105                 110

Pro Leu Gly Gln Pro Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu
        115                 120                 125

Asp Arg Val Leu Glu Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro
    130                 135                 140

Val Glu Glu Pro Leu Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
```

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```
145                 150                 155                 160

Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
                165                 170                 175

Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn
            180                 185                 190

Trp Glu Thr Gly Asp Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala
        195                 200                 205

Ile Gly Gln Lys Gly Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu
    210                 215                 220

Glu Gln Gly Ala Leu Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser
225                 230                 235                 240

Asp Ala Ala Gly Phe Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu
                245                 250                 255

Ala Gln His Trp Met Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp
            260                 265                 270

Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu
        275                 280                 285

Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu
    290                 295                 300

His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly
305                 310                 315                 320

Ala Gly Ser Ile Thr Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp
                325                 330                 335

Val Ser Ala Phe Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
            340                 345                 350

Val Phe Leu Glu Ser Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile
        355                 360                 365

Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys
    370                 375                 380

Gly Met Lys Lys Val Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe
385                 390                 395                 400

Arg Asp Leu Glu Ala Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala
                405                 410                 415

Ser Lys Ser Gln Leu Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile
            420                 425                 430

Gln Ser Glu Asn Ala Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu
        435                 440                 445

Trp Leu Ala Gly Glu Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val
    450                 455                 460

Arg Arg Phe Glu Ser Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala
465                 470                 475                 480
```

Doc. No. 1000-0000

```
Gln Val Tyr Glu Gln Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser
                485                 490                 495

Lys Glu Thr Leu Leu Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln
            500                 505                 510

Thr Thr Asp Gly Thr Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu
        515                 520                 525

Asp Ala Gly Gln Val Lys Lys Asp Gln Leu Thr Val Ser Arg Lys Val
    530                 535                 540

Ser Lys Lys
545
```

<210> 761
<211> 1572
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1549)
<223> RXN01193

<400> 761

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gtgtggccaa ccaggcacgt caggcacaga tcacccagga aatcacagag attgttggtg 60

gcgcaggcgc gctcgccgac agcggagaaa gtgactaatt atg act aca gct ctt   115
                                        Met Thr Thr Ala Leu
                                          1               5

gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt   163
Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg
                  10                  15                  20

gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca   211
Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro
              25                  30                  35

gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag   259
Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys
          40                  45                  50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc   307
Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile
      55                  60                  65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct   355
Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala
  70                  75                  80                  85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt   403
Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val
                  90                  95                 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc   451
Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser
              105                 110                 115
```

```
ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca   499
Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro
        120                 125                 130

cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc   547
Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly
    135                 140                 145

atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc   595
Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
150                 155                 160                 165

ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa   643
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu
                170                 175                 180

atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca   691
Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala
            185                 190                 195

ggt gtt ggt gag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg   739
Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met
        200                 205                 210

gaa gaa atg ggc gtt ctc cag gac acc gcc ctg gtg ttc ggt cag atg   787
Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu Val Phe Gly Gln Met
    215                 220                 225

gat gag cca cca gga gtc ggt atg cgc gtg gct ctg tcc ggc ctg acc   835
Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala Leu Ser Gly Leu Thr
230                 235                 240                 245

atg gcg gag tac ttc cgc gat gtt cag aac cag gac gtg ctg ctg ttc   883
Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe
                250                 255                 260

atc gac aac atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc   931
Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr
            265                 270                 275

ctt ctg ggt cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct   979
Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala
        280                 285                 290

gac gag atg ggt gtt ctc cag gag cgc att acc tcc acc aag ggc cgt   1027
Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg
    295                 300                 305

tcg att acc tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc   1075
Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr
310                 315                 320                 325

gac ccg gct cca gcg acc acc ttc gct cac ttg gat gca acc acc gag   1123
Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu
                330                 335                 340

ctt gac cgc tcc att gct tcc aag ggt att tac cca gca gtg aac cca   1171
Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro
            345                 350                 355
```

Doc No. 1000

```
ctg acc tcc acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt   1219
Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg
        360                 365                 370

cac tac gag gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag   1267
His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys
    375                 380                 385

gaa ctt cag gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa   1315
Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu
390                 395                 400                 405

gag gac aag atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg   1363
Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu
                410                 415                 420

ggt cag aac ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc   1411
Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser
            425                 430                 435

tac gtg cca ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac   1459
Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn
        440                 445                 450

ggc gac ttc gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt   1507
Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly
    455                 460                 465

ttg gac gat gtc gaa gct gca tac aag aag ctg acc gga aag           1549
Leu Asp Asp Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys
470                 475                 480

taaggtagag acacatggct gaa                                        1572
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<210> 762
<211> 483
<212> PRT
<213> Corynebacterium glutamicum

<400> 762

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Met Thr Thr Ala Leu Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala
  1               5                  10                  15

Gly Arg Val Val Arg Val Ile Gly Ala Val Val Asp Val Glu Phe Pro
            20                  25                  30

Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr
        35                  40                  45

Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu
    50                  55                  60

Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu
65                  70                  75                  80

Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro
                85                  90                  95

Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
            100                 105                 110
```

Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly
115 120 125

Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu
130 135 140

Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val
145 150 155 160

Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
165 170 175

Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly
180 185 190

Thr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp
195 200 205

Leu Phe Leu Glu Met Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu
210 215 220

Val Phe Gly Gln Met Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala
225 230 235 240

Leu Ser Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln
245 250 255

Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly
260 265 270

Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr
275 280 285

Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr
290 295 300

Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro
305 310 315 320

Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu
325 330 335

Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr
340 345 350

Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala
355 360 365

Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile
370 375 380

Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met
385 390 395 400

Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg
405 410 415

Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr
420 425 430

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```
Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe
        435                 440                 445

Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe
    450                 455                 460

Asn Gly Leu Gly Gly Leu Asp Asp Val Glu Ala Ala Tyr Lys Lys Leu
465                 470                 475                 480

Thr Gly Lys
```

<210> 763
<211> 778
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (15)..(755)
<223> FRXA01193

<400> 763

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caccaggagt cggtatg cgc gtg gct ctg tcc ggc ctg acc atg gcg gag    50
               Met Arg Val Ala Leu Ser Gly Leu Thr Met Ala Glu
                 1               5                  10

tac ttc cgc gat gtt cag aac cag gac gtg ctg ctg ttc atc gac aac    98
Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn
         15                  20                  25

atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc ctt ctg ggt   146
Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly
     30                  35                  40

cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct gac gag atg   194
Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met
 45                  50                  55                  60

ggt gtt ctc cag gag cgc att acc tcc acc aag ggc cgt tcg att acc   242
Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr
                 65                  70                  75

tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc gac ccg gct   290
Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala
             80                  85                  90

cca gcg acc acc ttc gct cac ttg gat gca acc acc gag ctt gac cgc   338
Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg
         95                  100                 105

tcc att gct tcc aag ggt att tac cca gca gtg aac cca ctg acc tcc   386
Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser
    110                 115                 120

acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt cac tac gag   434
Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu
125                 130                 135                 140

gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag gaa ctt cag   482
```

```
Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln
                145                 150                 155

gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa gag gac aag   530
Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys
            160                 165                 170

atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg ggt cag aac   578
Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn
        175                 180                 185

ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc tac gtg cca   626
Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro
    190                 195                 200

ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac ggc gac ttc   674
Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe
205                 210                 215                 220

gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt ttg gac gat   722
Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp
                225                 230                 235

gtc gaa gct gca tac aag aag ctg acc gga aag taaggtagag acacatggct 775
Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys
            240                 245

gaa                                                               778
```

<210> 764
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 764

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Met Arg Val Ala Leu Ser Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp
  1               5                  10                  15

Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg Phe
             20                  25                  30

Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser
         35                  40                  45

Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln
     50                  55                  60

Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala
 65                  70                  75                  80

Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr
                 85                  90                  95

Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser
            100                 105                 110

Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile
        115                 120                 125

Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg
```

```
    130                 135                 140

Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala
145                 150                 155                 160

Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala
                165                 170                 175

Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala
            180                 185                 190

Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr
        195                 200                 205

Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro
    210                 215                 220

Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp Val Glu Ala Ala
225                 230                 235                 240

Tyr Lys Lys Leu Thr Gly Lys
                245
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09605-0020US1

<210> 765
<211> 739
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(739)
<223> FRXA01203

<400> 765

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gtgtggccaa ccaggcacgt caggcacaga tcacccagga aatcacagag attgttggtg 60

gcgcaggcgc gctcgccgac agcggagaaa gtgactaatt atg act aca gct ctt   115
                                          Met Thr Thr Ala Leu
                                            1               5

gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt   163
Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg
                  10                  15                  20

gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca   211
Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro
              25                  30                  35

gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag   259
Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys
          40                  45                  50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc   307
Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile
      55                  60                  65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct   355
Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala
  70                  75                  80                  85
```

```
gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt   403
Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val
                 90                  95                 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc   451
Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser
            105                 110                 115

ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca   499
Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro
        120                 125                 130

cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc   547
Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly
    135                 140                 145

atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc   595
Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
150                 155                 160                 165

ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa   643
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu
                170                 175                 180

atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca   691
Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala
            185                 190                 195

ggt gtt ggt aag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg   739
Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met
        200                 205                 210
```

<210> 766
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 766

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Met Thr Thr Ala Leu Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala
  1               5                  10                  15

Gly Arg Val Val Arg Val Ile Gly Ala Val Val Asp Val Glu Phe Pro
             20                  25                  30

Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr
         35                  40                  45

Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu
     50                  55                  60

Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu
 65                  70                  75                  80

Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro
                 85                  90                  95

Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
            100                 105                 110

Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly
```

```
        115                 120                 125

Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu
    130                 135                 140

Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val
145                 150                 155                 160

Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
                165                 170                 175

Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly
            180                 185                 190

Thr Ser Val Phe Ala Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp
        195                 200                 205

Leu Phe Leu Glu Met
    210
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US20090305363A1

<210> 767
<211> 363
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(340)
<223> RXN02821

<400> 767

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aagtcgccca gatagcgagc ggaccactcg gtcaactgaa taaccccact aaacacttca 60

cagcccgaac acacgggcac cagaaaggga acgacacctc atg aac gag atc atc   115
                                            Met Asn Glu Ile Ile
                                              1               5

ctg gca cag gac gca acc gag tcc acc atc acc gga ctt ggc gct gtc   163
Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr Gly Leu Gly Ala Val
                10                  15                  20

ggc tac ggc atc gca acc atc gga cct ggc ctc ggc atc ggc atc ctg   211
Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu
            25                  30                  35

gtt ggt aag gct ctc gag ggt atg gca cgt cag cct gag atg gct gga   259
Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly
        40                  45                  50

cag ctc cgt acc acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg   307
Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu
    55                  60                  65

gca ctg atc ggc ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga 360
Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
70                  75                  80

aag                                                               363
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<210> 768
<211> 80
<212> PRT
<213> Corynebacterium glutamicum

<400> 768
Met Asn Glu Ile Ile Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr
1 5 10 15

Gly Leu Gly Ala Val Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu
20 25 30

Gly Ile Gly Ile Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln
35 40 45

Pro Glu Met Ala Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala
50 55 60

Phe Val Glu Ala Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
65 70 75 80

<210> 769
<211> 303
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(280)
<223> FRXA02821

<400> 769
agcccgaaca cacgggcacc agaaagggaa cgacacctca tgaacgagat catcttggca 60

caggacgcaa ccgagtccac catcaccgga ccttggcgct gtg ggc tac ggc atc 115
Val Gly Tyr Gly Ile
1 5

gca acc atc gga cct ggc ctc ggc atc ggc atc ttg gtt ggt aag gct 163
Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu Val Gly Lys Ala
10 15 20

ctc gag ggt atg gca cgt cag cct gag atg gct gga cag ctc cgt acc 211
Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly Gln Leu Arg Thr
25 30 35

acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg gca ctg atc ggc 259
Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu Ala Leu Ile Gly
40 45 50

ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga aag 303
Leu Val Ala Gly Phe Leu Phe
55 60

<210> 770
<211> 60

<212> PRT
<213> Corynebacterium glutamicum

<400> 770
Val Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile
1 5 10 15

Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala
20 25 30

Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala
35 40 45

Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
50 55 60

<210> 771
<211> 632
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(609)
<223> RXA01200

<400> 771
ggc tgt ctt cgg tgg aaa agt gag cca tct gtt ctc gaa gtc ctc aag 48
Gly Cys Leu Arg Trp Lys Ser Glu Pro Ser Val Leu Glu Val Leu Lys
1 5 10 15

gac gcc gca gag cag acc tgg tcc act cca cgc gag ttc cgc gct gga 96
Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly
20 25 30

cta gtc caa ctt ggc cgt cgc gcc ctt ctt cgc tct gcg gag aaa cag 144
Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln
35 40 45

ggt cag ctt ggt cag gtg gaa gat gaa ctg ttc cga ctc agc cga atc 192
Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
50 55 60

ctg gat cgc gaa agc aag ctg act cag ctt ctt tca gat cgc act cag 240
Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
65 70 75 80

gaa att ggc ggt cga cgt gac ctc ctg gct aag gtg ctc tac ggc aag 288
Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
85 90 95

gta act gct gtt acc gaa gcc ctc gca ctg cag gct att ggt cgc cct 336
Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
100 105 110

gag cac aac cca att gac gat atc gca gct ttg gct ggc gct gta gca 384
Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
115 120 125

gag cta cag ggt cgt tcc gtt gca cat gtc gtt acc gca gtt gaa ctc 432

```
Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
    130                 135                 140

aac gag gga cag caa caa gcg cta gct gaa aag ctg gga cgt att tat   480
Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
145                 150                 155                 160

ggt cgt gcg atg agc atc cac tcc gag gtt gat acc agc ctc ctc ggt   528
Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
                165                 170                 175

gga atg atc atc cgc gtc gga gac gaa gta att gac ggc agc acc tcg   576
Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser
            180                 185                 190

ggc aaa ctc gag cgt ctg cgg gca agc ttc gca taaagacacg acgaattaga 629
Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala
        195                 200

caa                                                               632
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<210> 772
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 772

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Gly Cys Leu Arg Trp Lys Ser Glu Pro Ser Val Leu Glu Val Leu Lys
  1               5                  10                  15

Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly
             20                  25                  30

Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln
         35                  40                  45

Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
     50                  55                  60

Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65                  70                  75                  80

Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
                 85                  90                  95

Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
            100                 105                 110

Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
        115                 120                 125

Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
    130                 135                 140

Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
145                 150                 155                 160

Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
                165                 170                 175
```

Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser
180 185 190

Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala
195 200

<210> 773
<211> 495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)
<223> RXA01194

<400> 773
acttcgacca ctacccagag caggctttca acggcctcgg tggtttggac gatgtcgaag 60

ctgcatacaa gaagctgacc ggaaagtaag gtagagacac atg gct gaa atc acc 115
Met Ala Glu Ile Thr
1 5

gtt gaa ctg gtg tct gta gag cgc atg ctg tgg gcc ggc cag gcc tcc 163
Val Glu Leu Val Ser Val Glu Arg Met Leu Trp Ala Gly Gln Ala Ser
10 15 20

atc gtg act gca cag acc acc gag ggt gag atc ggc gtg ctg ccc gat 211
Ile Val Thr Ala Gln Thr Thr Glu Gly Glu Ile Gly Val Leu Pro Asp
25 30 35

cac gag cct ctt ctc ggc caa ttg gtt gag aac ggt gtc gtg acc atc 259
His Glu Pro Leu Leu Gly Gln Leu Val Glu Asn Gly Val Val Thr Ile
40 45 50

cag ccg atc gac ggc gaa aag ctt atc gcc ggc gtt tcg gat gga ttc 307
Gln Pro Ile Asp Gly Glu Lys Leu Ile Ala Gly Val Ser Asp Gly Phe
55 60 65

ctc tcc gta tct aag gaa aag gtg acg atc ctc gcg gac ttc gcc gtc 355
Leu Ser Val Ser Lys Glu Lys Val Thr Ile Leu Ala Asp Phe Ala Val
70 75 80 85

tgg gcg aat gag gtt gat acc gca tcc gcc gag gct gac ctt aat tcg 403
Trp Ala Asn Glu Val Asp Thr Ala Ser Ala Glu Ala Asp Leu Asn Ser
90 95 100

gac gac gag ctg gcc aag gca cac gcc gag gct ggg ctg cgc gcg gtc 451
Asp Asp Glu Leu Ala Lys Ala His Ala Glu Ala Gly Leu Arg Ala Val
105 110 115

cgc cgc agc agc gaa ggt ctc taaacctccg tttagctgaa gta 495
Arg Arg Ser Ser Glu Gly Leu
120

<210> 774
<211> 124
<212> PRT
<213> Corynebacterium glutamicum

<400> 774
Met Ala Glu Ile Thr Val Glu Leu Val Ser Val Glu Arg Met Leu Trp
1 5 10 15

Ala Gly Gln Ala Ser Ile Val Thr Ala Gln Thr Thr Glu Gly Glu Ile
20 25 30

Gly Val Leu Pro Asp His Glu Pro Leu Leu Gly Gln Leu Val Glu Asn
35 40 45

Gly Val Val Thr Ile Gln Pro Ile Asp Gly Glu Lys Leu Ile Ala Gly
50 55 60

Val Ser Asp Gly Phe Leu Ser Val Ser Lys Glu Lys Val Thr Ile Leu
65 70 75 80

Ala Asp Phe Ala Val Trp Ala Asn Glu Val Asp Thr Ala Ser Ala Glu
85 90 95

Ala Asp Leu Asn Ser Asp Asp Glu Leu Ala Lys Ala His Ala Glu Ala
100 105 110

Gly Leu Arg Ala Val Arg Arg Ser Ser Glu Gly Leu
115 120

<210> 775
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1075)
<223> RXA01202

<400> 775
agaaagacca gctcaccgtt tcccgcaagg tcagcaagaa gtaaggcagc gagcctacac 60

taaatgactg tccaagcaac tgaagggagg cgtgtgaacc atg gca aca att cgt 115
Met Ala Thr Ile Arg
1 5

gaa ttg cgt gac cga att cgt tcg gtt aac tca acc aag aag atc acc 163
Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser Thr Lys Lys Ile Thr
10 15 20

aag gct caa gag ctc atc gcc acc tct cgc atc acc aag gca cag ggt 211
Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile Thr Lys Ala Gln Gly
25 30 35

cgc gtc gcg gca gct gcg ccg tac gcc gag gaa atc cag cgc gtg ctg 259
Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu Ile Gln Arg Val Leu
40 45 50

gag cgc ctc gcg tcg gca agc tcc cta gac cac cca atg ctg cgt gag 307
Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His Pro Met Leu Arg Glu
55 60 65

cgt gaa ggc ggc aag cga gcc gcc gtg ctc gtg gtt act tct gac cgc 355

```
Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val Val Thr Ser Asp Arg
 70                  75                  80                  85

ggc atg gct ggt ggc tac aac cac aac gtt ctg aaa aag gca gcg gag   403
Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu Lys Lys Ala Ala Glu
                 90                  95                 100

ctg gaa aag ctt ctt gct gaa agt gga tac gaa gtg gtt cgt tat gtc   451
Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu Val Val Arg Tyr Val
            105                 110                 115

acc ggc aaa aag ggc gtc gac tac tac aag ttc cgc gct gaa gat gtg   499
Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe Arg Ala Glu Asp Val
        120                 125                 130

gct ggc acc tgg act gga ttc tca cag gat cca gac tgg gca gct acc   547
Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro Asp Trp Ala Ala Thr
    135                 140                 145

cac aac gtg cgc cgt cac ctc att gat ggt ttc acc gcc agc tct gaa   595
His Asn Val Arg Arg His Leu Ile Asp Gly Phe Thr Ala Ser Ser Glu
150                 155                 160                 165

ggt gaa gct gca tgg cgc gag gga ctg aac cta cca gaa ggc cag gat   643
Gly Glu Ala Ala Trp Arg Glu Gly Leu Asn Leu Pro Glu Gly Gln Asp
                170                 175                 180

atc cag ggc ttc gac cag gtt cac gtg gtc tac acc gag ttc atc tcc   691
Ile Gln Gly Phe Asp Gln Val His Val Val Tyr Thr Glu Phe Ile Ser
            185                 190                 195

atg ctg act caa aac cca gta gtg cac caa ctg ctg cct gtt gag cca   739
Met Leu Thr Gln Asn Pro Val Val His Gln Leu Leu Pro Val Glu Pro
        200                 205                 210

gtc atc gaa gat gaa att ttc gaa aaa ggc gag gat ctg ctg tcc tct   787
Val Ile Glu Asp Glu Ile Phe Glu Lys Gly Glu Asp Leu Leu Ser Ser
    215                 220                 225

tcc ggc gaa gtc gaa ccc gac tac gag ttc gag ccg gat gca gac act   835
Ser Gly Glu Val Glu Pro Asp Tyr Glu Phe Glu Pro Asp Ala Asp Thr
230                 235                 240                 245

ctg ctt gag gca ctg ctt ccg cag tac gtc tct cgt agg ctg ttc tcc   883
Leu Leu Glu Ala Leu Leu Pro Gln Tyr Val Ser Arg Arg Leu Phe Ser
                250                 255                 260

atc ttc ttg gag gct gca gct gca gag tcc gct tca cgt cga aac gcg   931
Ile Phe Leu Glu Ala Ala Ala Ala Glu Ser Ala Ser Arg Arg Asn Ala
            265                 270                 275

atg aag tct gcg act gac aac gct acg gaa ctg gtc aag gac ctg tcc   979
Met Lys Ser Ala Thr Asp Asn Ala Thr Glu Leu Val Lys Asp Leu Ser
        280                 285                 290

cgt gtg gcc aac cag gca cgt cag gca cag atc acc cag gaa atc aca   1027
Arg Val Ala Asn Gln Ala Arg Gln Ala Gln Ile Thr Gln Glu Ile Thr
    295                 300                 305

gag att gtt ggt ggc gca ggc gcg ctc gcc gac agc gga gaa agt gac   1075
Glu Ile Val Gly Gly Ala Gly Ala Leu Ala Asp Ser Gly Glu Ser Asp
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310 315 320 325

taattatgac tacagctctt gaa 1098

<210> 776
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 776

Met Ala Thr Ile Arg Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser
1 5 10 15

Thr Lys Lys Ile Thr Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile
20 25 30

Thr Lys Ala Gln Gly Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu
35 40 45

Ile Gln Arg Val Leu Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His
50 55 60

Pro Met Leu Arg Glu Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val
65 70 75 80

Val Thr Ser Asp Arg Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu
85 90 95

Lys Lys Ala Ala Glu Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu
100 105 110

Val Val Arg Tyr Val Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe
115 120 125

Arg Ala Glu Asp Val Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro
130 135 140

Asp Trp Ala Ala Thr His Asn Val Arg Arg His Leu Ile Asp Gly Phe
145 150 155 160

Thr Ala Ser Ser Glu Gly Glu Ala Ala Trp Arg Glu Gly Leu Asn Leu
165 170 175

Pro Glu Gly Gln Asp Ile Gln Gly Phe Asp Gln Val His Val Val Tyr
180 185 190

Thr Glu Phe Ile Ser Met Leu Thr Gln Asn Pro Val Val His Gln Leu
195 200 205

Leu Pro Val Glu Pro Val Ile Glu Asp Glu Ile Phe Glu Lys Gly Glu
210 215 220

Asp Leu Leu Ser Ser Ser Gly Glu Val Glu Pro Asp Tyr Glu Phe Glu
225 230 235 240

Pro Asp Ala Asp Thr Leu Leu Glu Ala Leu Leu Pro Gln Tyr Val Ser
245 250 255

Arg Arg Leu Phe Ser Ile Phe Leu Glu Ala Ala Ala Ala Glu Ser Ala
260 265 270

```
Ser Arg Arg Asn Ala Met Lys Ser Ala Thr Asp Asn Ala Thr Glu Leu
        275                 280                 285

Val Lys Asp Leu Ser Arg Val Ala Asn Gln Ala Arg Gln Ala Gln Ile
    290                 295                 300

Thr Gln Glu Ile Thr Glu Ile Val Gly Gly Ala Gly Ala Leu Ala Asp
305                 310                 315                 320

Ser Gly Glu Ser Asp
                325
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<210> 777
<211> 1773
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1750)
<223> RXN02434

<400> 777

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cttcaatagt caaaaccagc aaactaattt tttaagtttt acgtaactgg ccccaccgct 60

tgtggcaggc cttgcgtttt gacattgaag gacccttttt atg cgc act ttt gcc   115
                                              Met Arg Thr Phe Ala
                                                1               5

gct tat att gcc att gat ggc ctc agc ttt tcc tac ccc aac acc cac   163
Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser Tyr Pro Asn Thr His
                10                  15                  20

gtt tta agc gat att tcg ctc acc gtt gcc aat ggc gat atc gcc gga   211
Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn Gly Asp Ile Ala Gly
            25                  30                  35

ctg att ggt gaa aac ggc gca gga aaa tcc acc ctg ctc agc ctc atc   259
Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Leu Ile
        40                  45                  50

gct ggc gtc atg gaa ccc gac cag ggc agg att tac ctc ccc gaa cgc   307
Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile Tyr Leu Pro Glu Arg
    55                  60                  65

acc gga ttc atc gcc caa gaa aca gac tta ccg ttt gaa caa ccc gtg   355
Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro Phe Glu Gln Pro Val
70                  75                  80                  85

cag tcg ctt atc gac gcc gcc gtc gcc cca gtg cgc gcg gtc gat gcc   403
Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val Arg Ala Val Asp Ala
                90                  95                  100

gcg att aca gat ttg tcc acc aag ctt ggc gac gcc tcc ctc agc gcc   451
Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp Ala Ser Leu Ser Ala
            105                 110                 115

gaa gag cag gcg caa gtc gcc aca gat ttc gat gca gcg cta ggc gct   499
Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp Ala Ala Leu Gly Ala
```

```
        120                 125                 130

gca gaa gaa ctc gga ctg tgg gaa tta gat gca cgt att gaa acc atc   547
Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala Arg Ile Glu Thr Ile
    135                 140                 145

gtc gcg ggt ctc ggc ctt gcc gag gtg gat cgc agc act ccc att ggt   595
Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg Ser Thr Pro Ile Gly
150                 155                 160                 165

gag ctt tcc ggc ggt cag cgc cgc aga ttc gca ttg gca gcg ctg ctg   643
Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala Leu Ala Ala Leu Leu
                170                 175                 180

ttg gaa cca cac gat gct ctg att ttc gat gag ccc acc aac cac ctc   691
Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu Pro Thr Asn His Leu
            185                 190                 195

gac gac aca gcc gta gat ttc ctc atc tcg gag att tcc cgt ttc aaa   739
Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu Ile Ser Arg Phe Lys
        200                 205                 210

ggt cca gtg ctg atc gcc agc cac gat cgc ttc ttc ctc gac tcc gtc   787
Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe Phe Leu Asp Ser Val
    215                 220                 225

tgt acc gag tta atc gac ctc gat cct gca ctt gga cct gag ggc gga   835
Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu Gly Pro Glu Gly Gly
230                 235                 240                 245

tcc ggc gaa gaa gta aaa caa gcc gtg tct ttt ggt ggt gga ttt tct   883
Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe Gly Gly Gly Phe Ser
                250                 255                 260

gaa tac atc aaa gaa cgc gag acc cgc cgc acc cgc tgg gct cag ttg   931
Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr Arg Trp Ala Gln Leu
            265                 270                 275

tac acc gca caa gaa acc gag cgg gaa aaa ctc gaa gaa acc acc ggc   979
Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu Glu Glu Thr Thr Gly
        280                 285                 290

acc acc gaa tcg gat att ttc cac agc tcg gtt tcc aaa tcg gaa gct  1027
Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val Ser Lys Ser Glu Ala
    295                 300                 305

aaa atc acc gcg aaa ttt tac gca gac cgg gca gct aaa act caa ggc  1075
Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala Ala Lys Thr Gln Gly
310                 315                 320                 325

aac cgc gtc cgc tcc gcc aaa aac cgc ctg aag gaa ttg gaa cgc tat  1123
Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys Glu Leu Glu Arg Tyr
                330                 335                 340

gaa atc cca gca cct cca aag cca ctg gaa ttc caa ggc atc cca gaa  1171
Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe Gln Gly Ile Pro Glu
            345                 350                 355

gcc tcc gga aac ggt cac ggt gaa aca cta gaa gtg cgg gct att gct  1219
Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu Val Arg Ala Ile Ala
        360                 365                 370
```

US 09/419,346

```
gtg gaa aac agg ctt caa ccc ttg act ttc cac atc gat ccc ggc gac   1267
Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His Ile Asp Pro Gly Asp
    375                 380                 385

cac atc ctg gtc gaa ggc ccc aac ggt gtc ggt aaa tcc acc ctg ctg   1315
His Ile Leu Val Glu Gly Pro Asn Gly Val Gly Lys Ser Thr Leu Leu
390                 395                 400                 405

agc gtt ctg gaa ggc gtg ctt gaa cca acc gaa ggt gaa ttg atc gtc   1363
Ser Val Leu Glu Gly Val Leu Glu Pro Thr Glu Gly Glu Leu Ile Val
                410                 415                 420

ccc gaa ggg ctg aaa gtt gcg cgc ctg aaa cag gac gat cag tgg acg   1411
Pro Glu Gly Leu Lys Val Ala Arg Leu Lys Gln Asp Asp Gln Trp Thr
            425                 430                 435

gaa aag cag ttg aac acc ccc gtc gac gaa ctg ttc gcc gcc cta tcg   1459
Glu Lys Gln Leu Asn Thr Pro Val Asp Glu Leu Phe Ala Ala Leu Ser
        440                 445                 450

aaa ggt ccg gtc gga ctc aac ctc gtg gag atg ggg ctg ttg agg gag   1507
Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met Gly Leu Leu Arg Glu
    455                 460                 465

acg tcg caa agc agc ccg cta cgg gcc cta tcg ctc ggc caa cgc cgg   1555
Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser Leu Gly Gln Arg Arg
470                 475                 480                 485

cgc gtc tcg ctc ggg ctc atc ctg gcg agc cca cca gat ctt ttg ctt   1603
Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro Pro Asp Leu Leu Leu
                490                 495                 500

ctt gac gag ccc acc aac cac ctc tcc ctc gcg ctg agc gaa gaa ctc   1651
Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala Leu Ser Glu Glu Leu
            505                 510                 515

gag tcg gcg ata gaa aaa ttc ccc ggt cgc gtt att ctg gcc agc cac   1699
Glu Ser Ala Ile Glu Lys Phe Pro Gly Arg Val Ile Leu Ala Ser His
        520                 525                 530

gat agg tgg atc aga aaa cgt tgg acg ggg aag aaa atc agc ctg agc   1747
Asp Arg Trp Ile Arg Lys Arg Trp Thr Gly Lys Lys Ile Ser Leu Ser
    535                 540                 545

cgt taaaccctac tgaacaggaa cct                                    1773
Arg
550
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09525160.1 - 09525160

[redacted]

<210> 778
<211> 550
<212> PRT
<213> Corynebacterium glutamicum

<400> 778

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Met Arg Thr Phe Ala Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser
  1               5                  10                  15

Tyr Pro Asn Thr His Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn
             20                  25                  30
```

```
Gly Asp Ile Ala Gly Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr
         35                  40                  45

Leu Leu Ser Leu Ile Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile
     50                  55                  60

Tyr Leu Pro Glu Arg Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro
 65                  70                  75                  80

Phe Glu Gln Pro Val Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val
                 85                  90                  95

Arg Ala Val Asp Ala Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp
            100                 105                 110

Ala Ser Leu Ser Ala Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp
        115                 120                 125

Ala Ala Leu Gly Ala Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala
    130                 135                 140

Arg Ile Glu Thr Ile Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg
145                 150                 155                 160

Ser Thr Pro Ile Gly Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala
                165                 170                 175

Leu Ala Ala Leu Leu Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu
            180                 185                 190

Pro Thr Asn His Leu Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu
        195                 200                 205

Ile Ser Arg Phe Lys Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe
    210                 215                 220

Phe Leu Asp Ser Val Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu
225                 230                 235                 240

Gly Pro Glu Gly Gly Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe
                245                 250                 255

Gly Gly Gly Phe Ser Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr
            260                 265                 270

Arg Trp Ala Gln Leu Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu
        275                 280                 285

Glu Glu Thr Thr Gly Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val
    290                 295                 300

Ser Lys Ser Glu Ala Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala
305                 310                 315                 320

Ala Lys Thr Gln Gly Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys
                325                 330                 335

Glu Leu Glu Arg Tyr Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe
            340                 345                 350
```

Sequence Listing

```
Gln Gly Ile Pro Glu Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu
        355                 360                 365

Val Arg Ala Ile Ala Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His
    370                 375                 380

Ile Asp Pro Gly Asp His Ile Leu Val Glu Gly Pro Asn Gly Val Gly
385                 390                 395                 400

Lys Ser Thr Leu Leu Ser Val Leu Glu Gly Val Leu Glu Pro Thr Glu
                405                 410                 415

Gly Glu Leu Ile Val Pro Glu Gly Leu Lys Val Ala Arg Leu Lys Gln
            420                 425                 430

Asp Asp Gln Trp Thr Glu Lys Gln Leu Asn Thr Pro Val Asp Glu Leu
        435                 440                 445

Phe Ala Ala Leu Ser Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met
    450                 455                 460

Gly Leu Leu Arg Glu Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser
465                 470                 475                 480

Leu Gly Gln Arg Arg Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro
                485                 490                 495

Pro Asp Leu Leu Leu Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala
            500                 505                 510

Leu Ser Glu Glu Leu Glu Ser Ala Ile Glu Lys Phe Pro Gly Arg Val
        515                 520                 525

Ile Leu Ala Ser His Asp Arg Trp Ile Arg Lys Arg Trp Thr Gly Lys
    530                 535                 540

Lys Ile Ser Leu Ser Arg
545                 550
```

<210> 779
<211> 1407
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1384)
<223> RXN00684

<400> 779
agtcacacct aaaagtgata gccatcacga atctttagga aaagtgattc aaacttcact 60

gtgatcggct tcggccacac acaagtgtca ggagatgaca atg act tcc cag act 115
Met Thr Ser Gln Thr
1 5

tcc caa caa tcc acc tca acc ggt gga tgc cca ttc ggg cac aca tca 163
Ser Gln Gln Ser Thr Ser Thr Gly Gly Cys Pro Phe Gly His Thr Ser
10 15 20

```
gag tcc acc agc cat cac ggc tac cag cct ttc gat atg cac aac ccg   211
Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe Asp Met His Asn Pro
            25                  30                  35

ttt cct gca tat aaa gaa ctc cgt cag gaa gag cca gtg atg ttc gat   259
Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu Pro Val Met Phe Asp
        40                  45                  50

gag cgc atc ggc tac tgg gtg gta acc aaa tat gac gac atc aaa acc   307
Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr Asp Asp Ile Lys Thr
    55                  60                  65

acc ttt gat gac tgg gaa aca ttc tcc tct gaa aat gca caa gcc cca   355
Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu Asn Ala Gln Ala Pro
70                  75                  80                  85

gtc cgc aag cgt gga cct cag gca acc caa atc atg acc gat ggc ggc   403
Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile Met Thr Asp Gly Gly
                90                  95                  100

ttc act gca tac tcc gga tta tca gct cgt att cca cca gag cac acc   451
Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile Pro Pro Glu His Thr
            105                 110                 115

cgc atc cgc gca atc gca caa aag gcc ttc acg cca cgc cgc tat aaa   499
Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr Pro Arg Arg Tyr Lys
        120                 125                 130

gca ctc gaa cca gat atc cga gca atg gtg att gat cgt gtg gag aaa   547
Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile Asp Arg Val Glu Lys
    135                 140                 145

atg ttg gcg aat gat caa cac gtc ggc gat atg gtg tca gat ctt gcc   595
Met Leu Ala Asn Asp Gln His Val Gly Asp Met Val Ser Asp Leu Ala
150                 155                 160                 165

tac gac att cca acc atc acg atc ctg acg ctg atc ggt gca gat att   643
Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu Ile Gly Ala Asp Ile
                170                 175                 180

ttc atg gtg gtc acc tac aag cgg tgg tca gat tcc cgt gcg gcc atg   691
Phe Met Val Val Thr Tyr Lys Arg Trp Ser Asp Ser Arg Ala Ala Met
            185                 190                 195

acc tgg ggc gat ctt agt gat gaa gag cag atc cca cac gca cac aat   739
Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile Pro His Ala His Asn
        200                 205                 210

ttg gtt gag tac tgg cag gaa tgc caa cgc atg gta gct gat gca cat   787
Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met Val Ala Asp Ala His
    215                 220                 225

gca cac ggt ggc gac aac ctc acc gct gat cta gtg cga gca cag caa   835
Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu Val Arg Ala Gln Gln
230                 235                 240                 245

gag ggt caa gaa atc acc gat cat gag att gct tct ttg ctg tac tcc   883
Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala Ser Leu Leu Tyr Ser
                250                 255                 260

ctg ctt ttt gcg ggg cac gaa aca acc acc acg ttg atc tcc aat tgt   931
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9950450.1

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Leu Leu Phe Ala Gly His Glu Thr Thr Thr Thr Leu Ile Ser Asn Cys
            265                 270                 275

ttc cga gtt ctc ctc gat cat cca gag cag tgg caa gcc att cta gag   979
Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp Gln Ala Ile Leu Glu
        280                 285                 290

aat cca aaa ctg att cct gcg gca gtg gat gag gtc ttg cgg tac tcc   1027
Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu Val Leu Arg Tyr Ser
    295                 300                 305

ggc tcg atc gtg ggg tgg cgt cga aaa gca tta aaa gac acc gag atc   1075
Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu Lys Asp Thr Glu Ile
310                 315                 320                 325

ggc ggc gtt gcc att aag gaa ggc gat ggt gtt ctg ctg ctc atg ggt   1123
Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val Leu Leu Leu Met Gly
                330                 335                 340

tcc gcg aac cgc gat gaa gct cgc ttt gaa aat ggc gag gaa ttc gat   1171
Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn Gly Glu Glu Phe Asp
            345                 350                 355

atc agc cgc gct aat gcg cgc gag cac ctg tct ttt ggt ttc ggc atc   1219
Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser Phe Gly Phe Gly Ile
        360                 365                 370

cac tat tgc cta gga aac atg ctg gcc aaa ctt caa gcc aag atc tgt   1267
His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu Gln Ala Lys Ile Cys
    375                 380                 385

ctc gag gaa gtc acc agg ctt gtt cct tcc ctg cac ttg gtt gcg gac   1315
Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu His Leu Val Ala Asp
390                 395                 400                 405

aaa gct atc ggg ttc cgg gag aac ctc tcc ttc cgc gtc ccc act tct   1363
Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe Arg Val Pro Thr Ser
                410                 415                 420

gtt ccc gtg act tgg aac gct taacgcttta ttaaataagg aga             1407
Val Pro Val Thr Trp Asn Ala
            425
```

<210> 780
<211> 428
<212> PRT
<213> Corynebacterium glutamicum

<400> 780

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Met Thr Ser Gln Thr Ser Gln Gln Ser Thr Ser Thr Gly Gly Cys Pro
  1               5                  10                  15

Phe Gly His Thr Ser Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe
             20                  25                  30

Asp Met His Asn Pro Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu
         35                  40                  45

Pro Val Met Phe Asp Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr
     50                  55                  60
```

```
Asp Asp Ile Lys Thr Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu
 65                  70                  75                  80

Asn Ala Gln Ala Pro Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile
                 85                  90                  95

Met Thr Asp Gly Gly Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile
            100                 105                 110

Pro Pro Glu His Thr Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr
        115                 120                 125

Pro Arg Arg Tyr Lys Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile
    130                 135                 140

Asp Arg Val Glu Lys Met Leu Ala Asn Asp Gln His Val Gly Asp Met
145                 150                 155                 160

Val Ser Asp Leu Ala Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu
                165                 170                 175

Ile Gly Ala Asp Ile Phe Met Val Val Thr Tyr Lys Arg Trp Ser Asp
            180                 185                 190

Ser Arg Ala Ala Met Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile
        195                 200                 205

Pro His Ala His Asn Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met
    210                 215                 220

Val Ala Asp Ala His Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu
225                 230                 235                 240

Val Arg Ala Gln Gln Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala
                245                 250                 255

Ser Leu Leu Tyr Ser Leu Leu Phe Ala Gly His Glu Thr Thr Thr Thr
            260                 265                 270

Leu Ile Ser Asn Cys Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp
        275                 280                 285

Gln Ala Ile Leu Glu Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu
    290                 295                 300

Val Leu Arg Tyr Ser Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu
305                 310                 315                 320

Lys Asp Thr Glu Ile Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val
                325                 330                 335

Leu Leu Leu Met Gly Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn
            340                 345                 350

Gly Glu Glu Phe Asp Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser
        355                 360                 365

Phe Gly Phe Gly Ile His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu
    370                 375                 380
```

09252160 - 050505

```
Gln Ala Lys Ile Cys Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu
385                 390                 395                 400

His Leu Val Ala Asp Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe
                405                 410                 415

Arg Val Pro Thr Ser Val Pro Val Thr Trp Asn Ala
            420                 425
```

<210> 781
<211> 978
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(955)
<223> RXN00387

<400> 781

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gatttctccg ccgactacct cgccaacggg ccaggccgag atg ttc cgc tcg aat   115
                                              Met Phe Arg Ser Asn
                                                1               5

att tcc tac gca gtc ggc gac gac atc caa aac gac cca gaa acc tgg   163
Ile Ser Tyr Ala Val Gly Asp Asp Ile Gln Asn Asp Pro Glu Thr Trp
                10                  15                  20

gaa gac tac gaa ctt cgc gtc aac cac cca ctg cgc atc gaa ggc gac   211
Glu Asp Tyr Glu Leu Arg Val Asn His Pro Leu Arg Ile Glu Gly Asp
            25                  30                  35

cgc gtc tac ctt cag ggc cac ggc ttc gcc cca aca ttc acc gtg acc   259
Arg Val Tyr Leu Gln Gly His Gly Phe Ala Pro Thr Phe Thr Val Thr
        40                  45                  50

tgg cca aat ggc gag acc cgc acc cag acc gtg cag tgg cgc cca gac   307
Trp Pro Asn Gly Glu Thr Arg Thr Gln Thr Val Gln Trp Arg Pro Asp
    55                  60                  65

gac ccg acc ttc ttc ctg tcc tca ggc gtg gtc cgt ttc gat cca ccc   355
Asp Pro Thr Phe Phe Leu Ser Ser Gly Val Val Arg Phe Asp Pro Pro
70                  75                  80                  85

gcc ggc atg tac cca gac ctt tac gag cgc cgc caa aac cag ttg gcc   403
Ala Gly Met Tyr Pro Asp Leu Tyr Glu Arg Arg Gln Asn Gln Leu Ala
                90                  95                  100

atc cag gga ctt ttc gca ccg acc gcg gaa tgg gaa ggc gac aac aac   451
Ile Gln Gly Leu Phe Ala Pro Thr Ala Glu Trp Glu Gly Asp Asn Asn
            105                 110                 115

gaa ctg ctg acc tcc tcc tac ccg gcg atg cgt gac cca gcc gtg gcg   499
Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg Asp Pro Ala Val Ala
        120                 125                 130

atc gat att tac cgc ggc gac aat ggc ctc gat acc ggc atc gga cag   547
Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp Thr Gly Ile Gly Gln
```

```
    135                 140                 145

tca ttg ttc agc ctg gac tct agt ctc atg cac agc ggc gtg ctg caa   595
Ser Leu Phe Ser Leu Asp Ser Ser Leu Met His Ser Gly Val Leu Gln
150                 155                 160                 165

aaa att gag cgc gtc aac ctc caa atc ggc gac acc gtc acc ctg gat   643
Lys Ile Glu Arg Val Asn Leu Gln Ile Gly Asp Thr Val Thr Leu Asp
                170                 175                 180

gat ggc acc acc gtc tcc ttc gac ggc gcg tca gaa ttt gcc aac tac   691
Asp Gly Thr Thr Val Ser Phe Asp Gly Ala Ser Glu Phe Ala Asn Tyr
            185                 190                 195

cag atc agc cgc gac ccc aca caa aac tgg gtg ctg gtc acc acc gtg   739
Gln Ile Ser Arg Asp Pro Thr Gln Asn Trp Val Leu Val Thr Thr Val
        200                 205                 210

att tcg ctg gtc tcc ctg gtt gga tcc ctg atg atc cga cgc cgc cgc   787
Ile Ser Leu Val Ser Leu Val Gly Ser Leu Met Ile Arg Arg Arg Arg
    215                 220                 225

att tgg gtg cgt ttc tat cca caa gaa aac gga acc acc cgc gtg gaa   835
Ile Trp Val Arg Phe Tyr Pro Gln Glu Asn Gly Thr Thr Arg Val Glu
230                 235                 240                 245

acc ggc gga ctt gcc cgc acc gac cgc gca ggc tgg ggt ggc gaa tac   883
Thr Gly Gly Leu Ala Arg Thr Asp Arg Ala Gly Trp Gly Gly Glu Tyr
                250                 255                 260

gag aaa ttc cac cgc gaa ctg ctg ggt ctg aag gag gaa gat gaa gac   931
Glu Lys Phe His Arg Glu Leu Leu Gly Leu Lys Glu Glu Asp Glu Asp
            265                 270                 275

gaa gag tac ttc gac cac gac gac taacaccgca atttaaaggc ttt         978
Glu Glu Tyr Phe Asp His Asp Asp
        280                 285
```

09252009

<210> 782
<211> 285
<212> PRT
<213> Corynebacterium glutamicum

<400> 782

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Met Phe Arg Ser Asn Ile Ser Tyr Ala Val Gly Asp Asp Ile Gln Asn
  1               5                  10                  15

Asp Pro Glu Thr Trp Glu Asp Tyr Glu Leu Arg Val Asn His Pro Leu
            20                  25                  30

Arg Ile Glu Gly Asp Arg Val Tyr Leu Gln Gly His Gly Phe Ala Pro
        35                  40                  45

Thr Phe Thr Val Thr Trp Pro Asn Gly Glu Thr Arg Thr Gln Thr Val
    50                  55                  60

Gln Trp Arg Pro Asp Asp Pro Thr Phe Phe Leu Ser Ser Gly Val Val
65                  70                  75                  80

Arg Phe Asp Pro Pro Ala Gly Met Tyr Pro Asp Leu Tyr Glu Arg Arg
```



```
                85                  90                  95

Gln Asn Gln Leu Ala Ile Gln Gly Leu Phe Ala Pro Thr Ala Glu Trp
            100                 105                 110

Glu Gly Asp Asn Asn Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg
        115                 120                 125

Asp Pro Ala Val Ala Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp
    130                 135                 140

Thr Gly Ile Gly Gln Ser Leu Phe Ser Leu Asp Ser Ser Leu Met His
```

APPENDIX A: DNA SEQUENCES

>RXA00013-upstream
CTGCAGAAAATTCGGGACGCATGATTGCACATATTACCCGCACCGATTGTGATTCTTAGA
ACGCCACCTTATTCAGCACACTTGGCCGACGGCATGCACA

>RXA00013
ATGGAAGGCATGACTAATCCAGAGCAGACACATCCCGCTGCAAGCCTCGAAGACATGATC
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CAGGCACTGGTGTACAACGCTGGACGTTTGGCATGGCGCATGCGCGAAAACGGTGTGGAT
ACGGATTACAAGACTTCTGTGTCTGATGTGGTCACGGATGCCGATCGTGCGGCCGAGGCC
TTCGTCGCAGGCGTTCTTGAAGCGTTGCGGCCTGAGGACGGCGTGCTTGGCGAGGAAGGC
GCGGACCGGGCGTCGAAAAGCGGAAAAACCTGGGTCATCGACCCGGTTGATGGCACCTAC
AACTTCACCCAGGGCTCAGATTATTGGTGCTCGGCGCTCGCGCTGGTCGAGGGCGATCCA
TCCGCGCCATCGCGCGTGCTTTTCGGCGCCGTACACCGCCCAGCCATGGGTTATACGTGG
TTCGGTGGCCCGGGAATCCGCACCACGCTCGACGGCAAGGAGCTAGATTTGCTTGTCGAC
GCCCCCCTCAATCAAATCTCCCTGGCCACCTACATCCACCCGTCACGCATCGCGGAACCT
GATATTCAAAAGGCGTGGATGAGCGTTGCCACCCACCCTGCAACGCTGCGCATGTTCGGC
GCCGGCTCCATCGATTTGGCCAACATCGCCGACGGCAGCATGGGCGCATGGGTGCAGCAC
AGCGTCGCAGATTGGGACTGGCTACCCGGCCGCGCACTCATCGAAGGCGTCGGCGGAGCG
TGCATCAAAGTGACCGCCGGCGGCGTCGAATGGTCCGTTGCAGGAAACGCGGAAGCAGTT
AGTGAGATCTCCGAAACTTTAAGCGCACTAGAC

>RXA00013-downstream
TAGCAACACATGAGCAAATATGC

>RXA00014-upstream
CATCAAAGTGACCGCCGGCGGCGTCGAATGGTCCGTTGCAGGAAACGCGGAAGCAGTTAG
TGAGATCTCCGAAACTTTAAGCGCACTAGACTAGCAACAC

>RXA00014
ATGAGCAAATATGCAGACGATTTAGCCTTAGCCCTCGAACTCGCCGAACTTGCCGATTCC
ATCACCCTCGACCGCTTCGAAGCCTCTGACCTGGAAGTATCCTCCAAGCCAGACATGACT
CCCGTCAGCGATGCCGACCTGGCGACCGAAGAAGCACTCCGCGAGAAAATCGCCACCGCC
CGCCCCGCCGACTCCATCCTCGGTGAAGAATTCGGTGGCGACGTAGAATTCAGCGGCCGC
CAGTGGATCATCGACCCCATCGACGGCACCAAAAACTACGTCCGCGGCGTCCCCGTATGG
GCAACCCTGATCGCGCTGCTCGACAACGGCAAACCCGTCGCAGGTGTCATCTCCGCACCC
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09609509 - 090704

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>RXA00206-upstream
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>RXA00206
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>RXA00224-upstream
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>RXA00224
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>RXA00225-upstream
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>RXA00225
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>RXA00235-upstream
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>RXA00235
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>RXA00246-upstream
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>RXA00246
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>RXA00246-downstream
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>RXA00251-upstream
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>RXA00251
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>RXA00268-upstream
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>RXA00268
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>RXA00288-upstream
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>RXA00288
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>RXA00290
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>RXA00293
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>RXA00296
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>RXA00309
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>RXA00310
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>RXA00317-upstream
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>RXA00317
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>RXA00328-upstream
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>RXA00328
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>RXA01193
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>RXA01201
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>RXA01225
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>RXA02404
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>RXA02414
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Docket No.: BGI-126CP

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09/29/2006 09:09:09

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>RXN03083
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>RXN03117
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>RXN03144
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>RXN03179
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>RXN03186
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>RXS00584 - 5'-Region
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>RXS00584 - coding Region
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>RXS00584 - 3'-Region
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>RXS01260 - 5'-Region
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>RXS01260 - coding Region
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>RXS01261 - 5'-Region
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>RXS01261 - coding Region
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>RXS01261 - 3'-Region
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>RXS01758 - 5'-Region
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>RXS01758 - coding Region
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>RXS02574 - 5'-Region
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>RXS02574 - coding Region
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>RXS02574 - 3'-Region
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>RXS02735 - 5'-Region
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>RXS02735 - coding Region
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>RXS02735 - 3'-Region
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>RXS03215 - coding Region
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ATCGGTGGCGGAACCGCAACCCTCCAGGTCAGCCGCATTTCCCAGGGACACCCAAACACCCTAGGTTTT
GAAGTGTTCTGTGAAAAGGGCTCCGTGCTCTTTGATTTCCGCAACTCAGGCGAATTCAAAATCTTCACC
CCAGCAACCTCCGGTGACATCAGCCAAGAAGCCGGCTACCGCACCATCACCATCGGACCAAAGCACCCA
TACTGGCGCGGCGGCCTTGCAATGGATGCACCAGGCGTGGGAATTGGCCAAAACGAAGGCTTCGTTTTC
CAGGCGCGCGCATTCCTCGAAGAAATCGCAGGAATCTCCGAAGCTGAAAGCCTGCCACGCTGCGCAACT
TTGGAAGAAGGGCTACACAATATGCAGCTCATTGATGCTGTATCACAGTCAGCTGCAGCAGGTGGCGAA
ACCGTTGCGGTCCCAGCGGCTGCTCTGATCCCTGCAAACAAC
RXS03215 - 3'-Region
TAGAAACTATTCAGAAAGCATCACCATGAA

>RXS03224 - 5'-Region
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TTGAACGCCGCGCCCGGCTAAGGTGGGAGGC

>RXS03224 - coding Region
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CTAGGCTGCAACGCCCTCATGCTGGGACCGGTATTCGAGTCCGTCAGCCACGGCTACGACACCCTCGAT
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CGGGGCATTGGAGTGCTTTTCGACGGCGTCTTCAATCATGTTTCCAGTTCCTCTAAATATCTCGACCTG
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GCTCTGATCGCGCTGCGCAGGCAACACCCGTGGTTGTATCAGGCGCACACCGAAGTCCTTGAGATTGCT
AATGAAGCGATGACCTATAAGTCCGTCGGTCTTGGAGGTGAAGAGCTGACAGTGCATCTTGATTTGGAA
GAGGTGTCTGTTCGGATCCTTGATGGCGAGAAGGTGCTGTTTCAGTACAGCGCT

>RXS03224 - 3'-Region
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>RXC00233 - 5'-Region

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TTAGACACAGACTCATGACAGAATAGAAGAC

>RXC00233 - coding Region
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GATATTTCTTACCGCAGCCCTGATGGAGTACCCGGTGTGGTGATGACCGCACCAAAACTGGATGACGGA
ACCCCATTCCCAACCCTGTACTACTTGACAGATCCACGCCTGACCACCGAGGCATCCCGCCTCGAGGTC
GCATTGGTAATGAAGTGGATGACTGATCGCCTTTCCACCGACGAAGAGCTTCGTGCCGACTACCAGCGC
GCCCACGAGCACTTCCTGGCAAAGCGCAACGCAATTGAAGATCTCGGCACGGATTTTTCCGGCGGTGGC
ATGCCTGACCGAGTGAAGTGCCTTCACGTCCTCATTGACTATGCACTGGCAGAAGGCCCACACCATTTC
CTT

>RXC00236 - 5'-Region
AATGCGAGAGTTCTAAAACGAGCCGGTAACATCGACCCCCATGAGTTCAGGGGTTAGAAAAGCAATGGG
ATTTGGATGCGGTTCGGTTTTGGCCGTCATC

>RXC00236 - coding Region
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TCCCTGGATGAAAATGGAGTTGCAACCCCTCCAATCATCGGCGTTCCACTTGATGGTTCACCGGGGTTT
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AACCAAATTGATGACGCAGCATTGAGTGCCGCAAACCTGTTGTGTTCCAACGATCGTGACTTGTCCACT
CCTGAAGGATGGACCGCAGCTGTTCATTCTTACAACATGTCTAATCAGTATTTGATGGACGTTCGAGAT
GCTGCCGCGTCCTACGCTTTACGACAGCCGGCGATC

>RXC00236 - 3'-Region
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>RXC00271 - 5'-Region
TAGTTTAAATCATGAGACATTTCACATATGGTTCTTTATCCGAGACATGTGTTGACGCTGTCTGCCCCT
TTTTGAAAATAACACTTTAAGGAGATGTGCC

>RXC00271 - coding Region
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TCAAGCGATTCCAGTGACAGCTCCACCTCCACTGATGCTGCAGGTGGCGACTCTTACCGAGTTGGCATC
AACCAGCTTGTTCAGCACCCTGCACTTGATGCAGCGACCACTGGTTTCAAGGAAGCTTTTGAAGAGGCA
GGCGTTGACGTCACCTTTGATGAGCAAAACGCTAACGGCGAGCAGGGCACTGCACTGACTATTTCTCAG
CAGTTCGCTTCTGACAATTTGGATCTCGTGTTGGCTGTTGCAACTCCAGCAGCACAGGCAACTGCGCAG
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GTGCAGGTCGATGAGGTCACCAAGGCTGCTGAGCCACTGGGGCTGTCCGTTAATACTCAGACTGTCACT
ACCGTGAACGAGATTCAGCAGGCTGTTGAAGCTCTCGGCGATGTTGATGTCATCTACGTTCCAACTGAC
AACATGGTTGTTTCCGGTATTTCTTCTCTGGTTCAGGTTGCTGAGCAGAAGCAGATCCCTGTGATCGGC
GCTGAGTCCGGCACTGTTGAGGGTGGCGCACTGGCAACCCTGGGTATCGATTACACCGAGCTTGGCCGC
CAGACTGGTGAGATGGCTCTGCGTATTCTGCAGGACGGCGAAGACCCAGCAACCATGCCTGTGGAGACT
GCAACTGAGTTCACCTACGTGATCAACGAAGATGCAGCAGAGCGCCAGGGCGTGGAGATCCCTCAAGAG
ATTTTGGATAAGGCCGAACGCGTA

>RXC00271 - 3'-Region
TGATCGGCGCTTTTGAGTTCGGA

>RXC00338 - 5'-Region
TCTTAGAAGGCGTAGTCACACCATTAACCTTGCCAGAATTTTTCAAGGCTTGGCTAGACTTGGGAAACG
AACATGCGGTACCAACCAGGGGAGTTAATGC

>RXC00338 - coding Region

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GATTGCACCCAGGCAGTGGCCGACAAGGCTGTGGACATGGGTTTGGACATGCTGATCATTCACCACCCA
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CTCGCCGAGCTCGTCGGCATCACGGCCGGGCGACCCATCGCGACACGGCTTTTAGGCGGCATGGACAAA
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GCGAATCCGGCAGAGGGGGACGTCGATAAGCTTTTTAAATCCCTTGAGCTGCGCATCGAGTTTGTTGCA
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TTCTTAAACGATGTGATTAAGCTCGGAGTGGACGTTTATGTCACTTCTGATCTGCGCCACCATCCAGTT
GATGAATATCTCCGAGAAGGTGGCCCTGCAGTAATCGATACTGCACACTGGGCCAGCGAATTTCCATGG
ACTTCCCAAGCCCAAGAAATTTTGCAGGACAAAGCCCCACAGGTTGAAGTTGATGTGATTTCGATCCGC
ACAGACCCCTGGACCATGTCTGCGCGAGCAGTGAAC

>RXC00338 - 3'-Region
TAAATTCTTGAGAACTAAAAAAG

>RXC00362 - 5'-Region
CACTTTTTGGGTGAAAATTCCACGAAGTTAATGCCGCTTTAAGTCAATTCAATCACATGTAACATGCTA
CGGTTTTTTCGGTCACTTAAAGGAGGCGCTT

>RXC00362 - coding Region
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ATTTCAGAAGCATTGCTAGTTGGATTAGTAGGAACTGCGCTTGTCGGCGGTGTAAATGCACCGACATTA
CTGATTGATGCTGTAGTGGATGCTGCTCAGTCGGAAGTTACTTTCGCAGGTATGGCCTTTGTTTTCATG
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CTTCGAGGTGGCGCAGGTTATGTTTCCACTCTTGGATCTGCGCTCATTGGACTCATCGCTGGATCAACG
GCTGGAAACTCCGCGACGGTTGGCTCAGTGACGATCCCTTGGATGAAAAAGACGGGATGGACTGCTGAA
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TGCATCATGTGCATTGTGGTGGCAACGCCACTGTCGTCAACAGCAACCGCGGCTGCGATTGGTGCTCCC
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CCAACGAAAATGTTCGTACCACTGATTACGTACTTTGTTGTCCCCATGATTCTGCTTGCTTGGCTAGTT
GGAATGGGATTCTTACCAGTGATTGTTCCTACGGGT

>RXC00362 - 3'-Region
TAAAGGGGTAAAAATGAACTCAA

>RXC00412 - 5'-Region
CTTTTGACGAACACCACGTCGCGTACGCTTCCTCGGGGCGTTAAACTATTTGTCTTCCAGCTTTTGTCC
CCCGACTTTTGTACGAATCGAGGACACCGTC

>RXC00412 - coding Region
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ACTCTTGTCCGCCTCATCAATGGCCTTGACTCCCCCACGAGCGGTTCGTTGCTGCTCAACGGCACCGAC
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CGCAAGGTAAACCGCGAACTGGGCATCACCATCGTTGTGATCACCCACGAAATGGAAGTTGTGCGTTCC
ATCGCAGACAAGGTTGCTGTGATGGAATCCGGCAAAGTTGTGGAATACGGCAGCGTCTACGAGGTGTTC
TCCAATCCACAAACACAGGTTGCTCAAAAGTTCGTGGCCACCGCGCTGCGTAACACCCCAGACCAAGTG
GAATCGGAAGATCTGCTTAGCCATGAGGGACGTCTGTTCACCATTGATCTGACTGAAACGTCCGGCTTC
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TTGCAACGCCAATCATTTGGCAAAATGACTGTTCGACTCACCGGCAACACCGCTGCGATTGAAGAGTTC
TATCAAACCTTGACCAAGACCACGACCATCAAGGAGATCACCCGA

>RXC00412 - 3'-Region
TGAACGAGATGATCCTCGCAGCT

>RXC00526 - 5'-Region
GGTGGAGCAGGCGGCGGCTCCTTTTAGTCCTGCGGCCCCTTTTGACCCTGCAGCCCCTGCCGTTTCTGC
CAAGCAAACCGTGGGCCAGGTGATTTAGCCT

>RXC00526 - coding Region
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AAATCAACGATGATGAACATCATTGGGTTGTTGGATAAGCCAACTGATGGCACGTACACCTTGGATGGC
GTGGATGTGTTGGATATCAGCGATGATGCTTTGGCGAGCCACCGCGCTAAATCGATTGGTTTTGTGTTT
CAGAACTTCAATCTGATTGGCCGGATCGATGCGTTGAAGAATGTGGAAATGCCCATGATGTATGCGGGC
ATTCCGGCTAAGCAGCGGAGAAGTCGTGCGGTTGAATTATTGGAAATGGTCGGGATGGGTGAGCGTCTC
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GATCCTGAGATCATTCTTGCTGATGAACCAACTGGTGCGTTGGATTCTGCAACGGGCCGGATGGTGATG
GATATTTTCCACCAGCTCAACAAGGAGCAGGGCAAAACCATCGTGTTTATTACTCACAACCCTGAGCTT
GCTGATGAATCTGATCGGGTGGTCACCATGGTTGACGGGCGCATCATTGGGTCTGAGGTGAAACACTCA

>RXC00526 - 3'-Region
TGAGCCTTGCAGAATCAATTCTT

>RXC01004 - 5'-Region
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TCACCCATGAAGAAGCAAAGGAGTACGAAAA

>RXC01004 - coding Region
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GAAAAGGTTCTCTACGCAACCGAGCACCTCTCCATCATGTTGGCGGGCGCTCAGTTCGGTATTACGGTC
TGTTCTCTGATTCTGGGTAAAGTCGCAGAACCTGCGATCGCCCACTTCATTGAGGTGCCTTTCACCTCC
TGGGGTGTTCCAAATGATTTGATCCACCCAATTTCCTTCGTCATCGCACTGGCGATCATCACCTGGTTG
CACATTCTCTTTGGTGAAATGGTGCCAAAGAACATCGCTATTGCTGGCCCTGAAACCTTAGGCATGTGG
CTTGCTCCAGTGCTCATTGCGTTTGTGAAGATTACCCGCCCGTTGATCGAGTTCATGAACTGGATCGCC
CGTCTGACCCTTCGCGCCTTTGGTGTGGAGCAAAAAAACGAGCTGGATTCCACCGTGGACCCAGAGCAG
CTGGCATCAATGATTTCCGAGTCCCGTTCCGAAGGCCTCCTTGATGCTGAAGAGCACGCCCGCCTGTCC
AAGGCGCTGCGCTCTGAGCAGCGTTCCATCAAGGAACTGGTGATTAAGGATGAGGACGTGCGCACGCTG
GCGTTCGGTAAATCTGGCCCGACCTTGCACCAGTTGGAGGAAGCAGTCCGCGAGACCGGTTTCTCCCGC
TTCCCTGTCACCGGCCGCGATGGATCCTACTTGGGTTATATCCACATCAAGGATATTTTGCCTCGTCTG
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GCCGACGGCCTCATGGATGACGTCTTGGATTTTATGCACTACCGCTCCGCGCACATGGCTCAGGTTCGC
CTCAAAGGTGAGCTTCTCGGCGTGATTACGCTGGAGGATCTCATCGAAGAATACGTGGGCACCGTCAAC
GATTGGACTCACGAAAGCTCCGACGAC

>RXC01004 - 3'-Region
TAGAAATAGTAACTGTGTTGGAC

>RXC01017 - 5'-Region
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TGCTAGAAAACTTTAAGAAAGAGGAAATAAT

>RXC01017 - coding Region
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AAGGAAGTCGAACAAGTCCGCGATATTGAAATCCAGTGGGTTCCAATGAGCCTCGCTGTCCTAAACGAA
GGCCGTGATCTCCCAGAGGATTACAAGGAGCGCATGAAGGCTGCATGGGGACCAGCACGCGTTTTCGCA
GCTGTCGCCACCGACCATGCTGACAAGCTCGGCGACCTGTACACCGCAATGGGTACCCGCATCCACAAC
GACGGTCGCGGACCAATCGAAGGTTCCTTCAATGATGTCATCGCAGAGGCACTTGAAGAGGTCGGCCTA
GACGCTGCACTTGGTGAAGTTGCAGACACCACCGAATGGGACGACGCACTTCGCGCATTCCACCAGACC
GCAATGGACGAGGTCGGCAACGATGTCGGAACCCCAGTGGTCAAGCTCGGCGACACCGCTTTCTTCGGC
CCAGTGCTCACCCGCATCCCACGCGGCGAGGAAGCAGGAGAGATCTTCGACGCTTCCTTCAAGCTCGCA
AGCTATCCCCACTTCTTTGAAATCAAGCGCAGCCGCACTGAGAACCCACAGTTCGAC

>RXC01017 - 3'-Region
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>RXC01021 - 5'-Region
CGAGAGGCTTTTTTGGCTCTAAGCCTTTTAGTCGTGCGAACGAAATCTTAAGCAGCCTCGGTGCCACCG
AGATCGATTGGTCGCTGTAAGGTATCTGATT

>RXC01021 - coding Region
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CTTGAGTGGGCCAGGACCGCTGTCGAGCAGCTTTCTGAACGTCGTGCAGAGATCAATGCACTGAATGTC
TTTCCTGTTCCAGATGCAGACACTGGATCAAACATGACCTACACCATGACAGCTGCGTTGGATGAAGCG
CTGAAACTGGGGGAGTTGGGTGATGTCGCAAGGATTACTGAGGCTTTGGCTGTTGGTTCTGTGCGTGGA
GCCCGAGGAAATTCTGGAGTAGTCCTTAGTCAGGTCCTTCGCGCTATTGCTCAGGCAGCTGCTGACGGG
GTTATTGATGGCCACACAATCCAAGAAGCGCTATCCATTGCTCGCTCCCTAGTTGATCGCGCAATTACA
GATCCTGTGGAGGGCACTGTTGTCACTGTGTTGCGTTCT

>RXC01212 - 5'-Region
TTTAGAAGCCACATGACATATGTCATGAAAATTATGTGCAAAGTGCAGTAATACTCCTGACATATGGCT
CTACCAGCGCCAATGCGAAGTAGGAAGAATT

>RXC01212 - coding Region
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AAAACCTCCACCTTGGAAGTCATCGAAGGACTTTCCGCACCCAGCTCCGGCACCGTGCGCATCTCCGGG
CTTGACCCCGTTGCCGACCGCGCGATCCTGCGCCCCGAGCTCGGCATCATGCTGCAATCAGGCGGCCTG
CCATCACAGCTCACCGTCGCCGAAACCATGGACATGTGGCACGGCACCTGCACGTATCCGCGCGCCATT
AAAGATGTGCTTGCCGACGTCGACCTCCTACACCGCGAAAACGTCAAGGTCGGCGCGCTTTCCGGAGGC
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CACGTCCGCATCGCCACCACCACCCTGCAGCAGCACACCTTAGAAATACTTACCTGGGCTGCAGAGACC
GGGATCGCGCTGGAAGGCTTCGCTGCAAAACCCGCCACCTTGGAATCCGTATTCATGGACATCGCCTCA
CTCGAGAACACCTCGCTGCAAACCGCC

>RXC01212 - 3'-Region
TAGAATCTTTAAGGAGACCACAA

>RXC01306 - 5'-Region
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TCACCCCGCTCCGAAGGAGAATCGCTAAGCC

>RXC01306 - coding Region
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ATTGAGTTCGCTTTGCTTGCAGCTAGGCGGAACCGGTTAGAGGAGACTGTGGAAACCTCGCGGTCTTCC
CGCGCTGCGTTGCGAAGCCTCAATGAACTTACTCTCATGCTCGCGGGCGCGCAGTTGGGAATCACCATG

GTGACTTTCGCGTTGGGTGCTATCACGAAGCCGTGGGTTCATTATGCTTTGATGCCGCTCTTCGAATGG
GCGCGTATACCGCTGGTTATGGCAGATGTCATTGCGTTTATTTTGTCGCTGTTTATCGTAACGTTTCTG
CACTTGGTCATCGGCGAAATGGCTCCGAAATCCTGGGCAATCGCGCATCCGGAGACGGCACTTCGAACT
ATCGCGATTCCCGCACGGGGCTTCATTAACCTGTTTCGTCCATTGCTGCAGTGGATCAACAAAATGGCG
AACGATTTGGTCCGCAAAGTTGGTGAAACTCCCGTTGATCGAGCTGCAGCTGGTGGCTATGACACCGAT
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AGCGGAATTATCAAGCTGGATAAAATCACGGTCGGTCAAACCCTGACCGCATCTCCATTTACGCACAGC
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GCCCCCTCCCACCTTTTCCCACACGTCATTCATGTGCGAGACACCCTTGGTGCCTCGCCAGACGAGAAG
GCTTCGAAGTGGTCTCGCCCAATCCTCACCGTTGCTGAGACCGACACGTTACACCAAGCGCTGGAATAC
ATGCGGGAGCATAACGAGCAGATCAGTGCGGTGCTTTCCGCTGATGGGAAAACGGTGCTTGGTGTAATA
ACTTGGGATCACATCTTGAAATACCTGTGGCCTGCATCGGTG
RXC01306 - 3′-Region
TAGCTAATTTGAGGTGCGCTGAA

>RXC01366 - 5′-Region
ATGCATGAAAACAAATTCTATGTGTGTTGAGCTGCCAAAAGGGGTTGGCGCGCCGATGATGACTGTCCA
AACCTAAACCAAAGGTCTAAACTTTGGCTTC

>RXC01366 - coding Region
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TATTCGGATTCCACTGCGGTGGTTGGTCCTTTGGCGCCTGCAGCAGAGCCCCATAGTTGGGATCTGTGT
GAGCATCATGCCGAGCGTATTACTGCGCCCCTTGGTTGGGAGATGCTGCGGGTGAACGACATCAAAGTC
GATGACGATGAGGATCTGACGGCTCTTGCTCAGGCTGTTCGTGAGGCTGGACGCACTGTGAGTGGTCTG
GTTCCTGAAGACGAAGTGGGCGGCAACCATCCGGTGAACCGGAGTGCGCGGATCGCGGAACAGAAGGTT
CACCGCAGGGGTCATCTCTATGTTGTGCCTGATCAGGACGAATCA

>RXC01366 - 3′-Region
TAAGGTTTGCTATTCGGATTGGA

>RXC01372 - coding Region
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ATAAGCACTCTTTTAGATCTTTTAGAAGCAGACCCCAGCATTATTTCCGACCGCTTGGAACACCTCGCC
GACTGCATTGATGAGGAAGTGGAATCGCTATCGCCGGAACGTGACGAACTAGTCAATCCCGGCCGAAAA
CTGCGCGCATACGTAGATCACGCACGGATCGTGCATACCGGCCGAACTGATGTGGGACTCGCGATTGCC
AACGTTATCGCCCCAATCTGGACCCGACGAGGCCTGGTATCAGCCGTGCTGGATTTTCCCGAGCTCATG
GAATCATTGCCGGAACTCCGCGGACCCGAGCCAATTACCGACGATATATTCCATGACCCATTCATAGAT
GACGAACCCGGGGGTGGTACCGTTTAGGGCTGTTGTCTGGGCCGAAGAGGAACCCGGAATCCCCGATGCC
ATGGCGCAAAGCTGCGACGGACCTAGCAAAGGGGCGCTGACACAAGCACTGCGTTTGCTGGTGCGCGGA
CAGTCAGCCACGACCTATTCCATTGAAGAAAAGGACTTG

>RXC01372 - 3′-Region
TAAATGGAGCTATTGGAAGGCTC

>RXC01659 - 5′-Region
TTGATGCGCGCCGCGGTGAGCAGCCTGCCGATCCAGAGCGTGAAGAATCTGATGATTTAGTCGAGATTG
ATACCGTCTCTGGATTCCGCCTGCTCAGTAC

>RXC01659 - coding Region
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GTGACTGCTGTGTGGATGGAATCTGATTGGGTGTTGGCGGAAACCATCAAGGGTTCCACGCCTTCCGAT
TGGGAAGAGATTTTGCGGCCGTTGGCGCTGCTCACGGACGCGTCTTTCACGTTGCCACCTCGTTCCACG
CGTGCGCAAACCTTGGATTTGAAGCATTTGGAACCAAGCCGTCTGAAGCCGGAGCAGCCAGAAAAGCCA
GCGTTTACTCCCAATGCTTCGGAAGAAGATTTGTCTCAGCCGTTGGTGATCCGCCCCGAGGAGCCGTTG
CAGATGCCGGTTCGCGGTGTGCAGGAAAGCCGCGGAGTGGTCGAGCCACGGTCATTGGGTGCGGATGAT
GTGGAGTCGATTGCGGAGGGCGATCCAGAGCGTCCGAGCGATCTTTATGGCACGCGTGTGCTGCGTGAT
CTCAATGGTCAGTCCAGTATTTTCCAAGATTCCACCGACGCGGATGAGCCACCAAAAAAGTGG

>RXC01659 - 3′-Region
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>RXC01663 - 5'-Region
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>RXC01663 - coding Region
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>RXC01663 - 3'-Region
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>RXC01693 - 5'-Region
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>RXC01693 - coding Region
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>RXC01693 - 3'-Region
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>RXC01703 - 5'-Region
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>RXC01703 - coding Region
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>RXC01703 - 3'-Region
TAGCCCCGATAGTGTATGTGCTG

>RXC02254 - coding Region
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RXC02254 - 3'-Region
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RXC02255 - 5'-Region
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RXC02255 - coding Region
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RXC02255 - 3'-Region
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RXC02435 - 5'-Region
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RXC02435 - coding Region
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RXC02435 - 3'-Region
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RXC03216 - 5'-Region
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RXC03216 - coding Region
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ATGCTGGTCAACATCGAACACGAGGATGTTTCACTCGGTCGCGAAGAAGGCGTCAACGAAGCCGCTAAG
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RXC03216 - 3'-Region
TAAAAAAACTACGCCTGCCCCGCAACGCTT

Docket No. BGI-126CP

APPENDIX B: AMINO ACID SEQUENCES

> RXA00013 (1-873, translated) 291 residues
MEGMTNPEQT HPAASLEDMI KTITKTFVIA HDQDSDEHLA QALVYNAGRL AWRMRENGVD
TDYKTSVSDV VTDADRAAEA FVAGVLEALR PEDGVLGEEG ADRASKSGKT WVIDPVDGTY
NFTQGSDYWC SALALVEGDP SAPSRVLFGA VHRPAMGYTW FGGPGIRTTL DGKELDLLVD
APLNQISLAT YIHPSRIAEP DIQKAWMSVA THPATLRMFG AGSIDLANIA DGSMGAWVQH
SVADWDWLPG RALIEGVGGA CIKVTAGGVE WSVAGNAEAV SEISETLSAL D

> RXA00014 (1-780, translated) 260 residues
MSKYADDLAL ALELAELADS ITLDRFEASD LEVSSKPDMT PVSDADLATE EALREKIATA
RPADSILGEE FGGDVEFSGR QWIIDPIDGT KNYVRGVPVW ATLIALLDNG KPVAGVISAP
ALARRWWASE GAGAWRTFNG SSPRKLSVSQ VSKLDDASLS FSSLSGWAER DLRDQFVSLT
DTTWRLRGYG DFFSYCLVAE GAVDIAAEPE VSLWDLAPLS ILVTEAGGKF TSLAGVDGPH
GGDAVATNGI LHDETLDRLK

> RXA00030 (1-390, translated) 130 residues
MRIEITSVFV DDQAKALDFY TTKLGFELKH DVTAGDYRWL TVVDPENPDG VQLLLEPNQH
PDAATYQAGI KRDGIPATQF YVDDVQEEYD SLKDKGVDFI MEPTDVGPSV IAILDDTVGN
LIQIVQLKQN

> RXA00032 (1-1509, translated) 503 residues
MNTPLQLNTE NLQEIASTSG VQIPAFNRAD VAPGIVHFGV GGFHRAHQAM YLNELMNEGK
ALDWGIIGMG VMPSDVRMRD ALASQDHLYT LTTKAPDGTL DQKIIGSIID YVFAPEDPAR
AVATLAQDSI RIVSLTVTEG GYNIDPATED FDHTNPRIVA DREALQAGDT STLQTFFGLI
TAALISRKES GSTPFTIMSC DNIQGNGDLA KRFFLAFAHS VSSELGEWVE NNVAFPNSMV
DRITPETTDG DRDDIKEIGY IDAWPVVSED FTQWVLEDAF TQGRPAYEEV GVQVVSDVEP
YELMKLRLLN ASHQGLCYFG HLAGHHMVHD VMADTRFQDF LLAYMEREAT PTLKELPGVD
LDAYRRQLIA RFGNAAVKDT VPRLCAESSD RIPKWLLPVV RENLAAGRDV TLSAAIVASW
ARYAEGTDEQ GNPIKIVDRL SERVQENASG NRTDILSFIR DRGIFGDLVD AEPFTKAYSE
TLSSLHDRGA EATIDALLTQ VTV

> RXA00038 (1-1158, translated) 386 residues
MSFAEHAIIW HVYPLGALGA PIRPEAPAPV THRLPNLIGW LDYVVELGCN ALMLGPVFES
VSHGYDTLDF YRIDPRLGTE EDMDALLEAA NQRGIGVLFD GVFNHVSSSS KYLDLTTGAS
FEGHDILAEL DHTNPAVVDL VVDVMNHWLD RGIAGWRLDA VYAIAPEFWE KVLPEVRRKH
PHAWIVGEMI HGDYSDYVKS SGIDSVTEYE LWKAIWSSIK ERNFFELEWT LSRHNEFLDT
FVPQTFIGNH DVTRIATRIG QSNAILAAAI LFTVGGTPSI YYGDEQGFTG LKEDNVFGDD
AIRPPLPAEF SPLGTWIENI YKALIALRRQ HPWLYQAHTE VLEIANEAMT YKSVGLGGEE
LTVHLDLEEV SVRILDGEKV LFQYSA

> RXA00041 (1-1242, translated) 414 residues
MHTELSSLRP AYHVTPPQGR LNDPNGMYVD GDTLHVYYQH DPGFPFAPKR TGWAHTTTPL
TGPQRLQWTH LPDALYPDAS YDLDGCYSGG AVFTDGTLKL FYTGNLKIDG KRRATQNLVE
VEDPTGLMGG IHRRSPKNPL IDGPASGFTP HYRDPMISPD GDGWKMVLGA QRENLTGAAV
LYRSTDLENW EFSGEITFDL SDAQPGSAPD LVPGGYMWEC PNLFTLRDEE TGEDLDVLIF
CPQGLDRIHD EVTHYASSDQ CGYVVGKLEG TTFRVLRGFS ELDFGHEFYA PQVAVNGSDA
WLVGWMGLPA QDDHPTVARE GWVHCLTVPR KLHLRNHAIY QELLLPEGES GVIRSVLGSE
PVRVDIRGNI SLEWDGVRLS VDRGGDRRVA EVKPGELVIA DDNTAIEITA GDGQ

> RXA00042 (1-759, translated) 253 residues
MDIIICKDEQ EVGKAAAALI APFATKGGTL GLATGSSPLS TYQELIRMYE AGEVSFKNCK
AFLLDEYVGL TRDDENSYFK TIRKEFTDHI DIVDEEVYSP DGANPDPYEA AAEYEAKIAA
ESVDVQILGI GGNGHIAFNE PSSSLSGLTK VQALHPKTVE DNARFFNTIE EVPTHALTQG
LGTLSRAQNI VLVATGEGKA DAIRGTVEGP LTAMCPGSIL QMHNNATIIV DEAAASKLEN
ADHYRLMEQL KLR

> RXA00043 (1-1164, translated) 388 residues

MAEVVHYQEN AGQAVKKIEG RIVTPHGVID GFLQLENGII TELSGEPAPK NAGFHPELPT
IVPSFIDLHN HGGNGGAFPT GTQDQARNAA QYHREHGTTV MLASMVSAPA DALAAQVENL
IPLCEEGLLC GIHLEGPFIN ACRCGAQNPD FIFPGNPTDL AQVIHAGKGW IKSITVAPET
DNLTELLDLC AAHHIIASFG HTDADFDTTT SAIALAKEKN VTVTATHLFN AMPPLHHRDP
GSVGALLAAA RAGDAYVELI ADGVHLADGT VDLARSNNAF FITDAMEAAG MPDGEYILGV
LNVTVTDGVA RLRDGGAIAG GTSTLASQFV HHVRRGMTLI DATLHTSTVA AKILGLSDHE
IVKSNPVNFV VFDSNGQLQQ VHLDHQVI

> RXA00055 (1-138, translated) 46 residues
VDVVDIARWQ FGITTVYHFI FVPLTIGLAP LVAIMQTFWQ VTGKEH

> RXA00098 (1-1620, translated) 540 residues
MADISTTQVW QDLTDHYSNF QATTLRELFK EENRAEKYTF SAAGLHVDLS KNLLDDATLT
KLLALTEESG LRERIDAMFA GEHLNNTEDR AVLHTALRLP AEADLSVDGQ DVAADVHEVL
GRMRDFATAL RSGNWLGHTG HTIKKIVNIG IGGSDLGPAM ATKALRAYAT AGISAEFVSN
VDPADLVSVL EDLDAESTLF VIASKTFTTQ ETLSNARAAR AWLVEKLGEE AVAKHFVAVS
TNAEKVAEFG IDTDNMFGFW DWVGGRYSVD SAVGLSLMAV IGPRDFMRFL GGFHAMDEHF
RTTKFEENVP ILMALLGVWY SDFYGAETHA VLPYSEDLSR FAAYLQQLTM ESNGKSVHRD
GSPVSTGTGE IYWGEPGTNG QHAFFQLIHQ GTRLVPADFI GFARPKQDLP AGERTMHDLL
MSNFFAQTKV LAFGKNAEEI AAEGVAPELV NHKVMPGNRP TTTILAEELT PSILGALIAL
YEHIVMVQGV IWDINSFDQW GVELGKQQAN DLAPAVSGEE DVDSGDSSTD SLIKWYRANR

> RXA00148 (1-1998, translated) 666 residues
MTSIPNFSDI PLTAETRASE SHNVDAGKVW NTPEGIDVKR VFTQADRDEA QAAGHPVDSL
PGQKPFMRGP YPTMYTNQPW TIRQYAGFST AAESNAFYRR NLAAGQKGLS VAFDLATHRG
YDSDNERVVG DVGMAGVAID SILDMRQLFD GIDLSSVSVS MTMNGAVLPI LAFYIVAAEE
QGVGPEQLAG TIQNDILKEF MVRNTYIYPP KPSMRIISNI FEYTSLKMPR FNSISISGYH
IQEAGATADL ELAYTLADGI EYIRAGKEVG LDVDKFAPRL SFFWGISMYT FMEIAKLRAG
RLLWSELVAK FDPKNAKSQS LRTHSQTSGW SLTAQDVYNN VARTAIEAMA ATQGHTQSLH
TNALDEALAL PTDFSARIAR NTQLLLQQES GTVRPVDPWA GSYYVEWLTN ELANRARKHI
DEVEEAGGMA QATAQGIPKL RIEESAARTQ ARIDSGRQAL IGVNRYVAEE DEEIEVLKVD
NTKVRAEQLA KLAQLKAERN DAEVKAALDA LTAAARNEHK EPGDLDQNLL KLAVDAARAK
ATIGEISDAL EVVFGRHEAE IRTLSGVYKD EVGKEGTVSN VERAIALADA FEAEEGRRPR
IFIAKMGQDG HDRGQKVVAS AYADLGMDVD VGPLFQTPAE AARAAVDADV HVVGMSSLAA
GHLTLL

RXA00149 (1-1848, translated) 616 residues
LTDLTKTAVP EELSENLETW YKAVAGVFAR TQKKDIGDIA VDVWKKLIVT TPDGVDINPL
YTRADESQRK FTEVPGEFPF TRGTTVDGER VGWGVTETFG HDSPKNINAA VLNALNSGTT
TLGFEFSEEF TAADLKVALE GVYLNMAPLL IHAGGSTSEV AAALYTLAEE AGTFFAALTL
GSRPLTAQVD GSHSDTIEEA VQLAVNASKR ANVRAILVDG SSFSNQGASD AQEIGLSIAA
GVDYVRRLVD AGLSTEAALK QVAFRFAVTD EQFAQISKLR VARRLWARVC EVLGFPELAV
APQHAVTARA MFSQRDPWVN MLRSTVAAFA AGVGGATDVE VRTFDDAIPD GVPGVSRNFA
HRIARNTNLL LLEESHLGHV VDPAGGSYFV ESFTDDLAEK AWAVFSGIEA EGGYSAACAS
GTVTAMLDQT WEQTRADVAS RKKKLTGINE FPNLAESPLP ADRRVEPAGV RRWAADFEAL
RNRSDAFLEK NGARPQITMI PLGPLSKHNI RTGFTSNLLA SGGIEAINPG QLVPGTDAFA
EAAQAAGIVV VCGTDQEYAE TGEGAVEKLR EAGVERILLA GAPKSFEGSA HAPDGYLNMT
IDAAATLADL LDALGA

> RXA00195 (1-561, translated) 187 residues
VTKKILILGS TGSIGTQALD VIADNSDKFE VVGIAAGGSQ PDLVISQAQQ LGLAADKVAV
ADAQAAAVIS KALGGEIISG TDAAKILVET TKADTVLNAL VGSLGLAATL ATLESGAHLA
LANKESLVAG GEFVTSKAKL GQIIPVDSEH SAMAQCLRSG TRDEVARIVL TASGGPFRAG
PGRRCGR

> RXA00196 (1-615, translated) 205 residues
MWEVTPEQAA AHPTWAMGQM NTLNSATLIN KGLELIEATL LFETDADLID VTVHPQSIIH
SMITFTDGAT IAQASPPSMK LPIALALDWP HRVPKAQPAL DFTAAHTWAF EPVDDAAFPA
VQLARHVAKQ KGTYPAVYNA ANEEAAEAFL RGRIKFPQIV DVVDEVLQGA SQFAGVASHV
DDILATESEA RARANALINR LATNL

> RXA00202 (1-942, translated) 314 residues
MYARKLIALS ASVVLAFSLS ACNRESSGTS ADGGSADGSI TLALSTQTNP FFVQLRDGAQ
EKADELGVTL NVQDASDDAA TQANQLNNAV TTGAGVVIVN PTDSDAVVPS VEALNQADIP
VVAVDRSSNG GEVASFVASD NVAGGAQAAA ALAEAIGGEG EILMLQGIAG SSASRDRGQG
FEEEIAKHEG ISIVAKQTAN FDRGEGLDVA TNLLQAHPNV KAIFAENDEM ALGAIEALGA
RAGEDVIVVG FDGTNDGLAA VEDGRMLATV AQQPEELGAK AVEEAAKLLR GEDAETEVPV
EVVTVKLDNV ADFK

> RXA00206 (1-1038, translated) 346 residues
MEDMRIATLT SGGDCPGLNA VIRGIVRTAS NEFGSTVVGY QDGWEGLLGD RRVQLYDDED
IDRILLRGGT ILGTGRLHPD KFKAGIDQIK ANLEDAGIDA LIPIGGEGTL KGAKWLSDNG
IPVVGVPKTI DNDVNGTDFT FGFDTAVAVA TDAVDRLHTT AESHNRVMIV EVMGRHVGWI
ALHAGMAGGA HYTVIPEVPF DIAEICKAME RRFQMGEKYG IIVVAEGALP REGTMELREG
HIDQFGHKTF TGIGQQIADE IHVRLGHDVR TTVLGHIQRG GTPTAFDRVL ATRYGVRAAR
ACHEGSFDKV VALKGESIEM ITFEEAVGTL KEVPFERWVT AQAMFG

> RXA00224 (1-951, translated) 317 residues
MSISYVLVEQ LDGRPEPVTL ELITAARALG DVVAVVVGEP GAGVNLAAEL GNWGAAQVVS
AEISGASNRL ILPAVDALHI LAANNPGPIV IAATASGNEI AGRLAARLAS GVLTDVVGIN
ADRTAQQSIF GDTIQVSAAV GGASPLYTLR PGALDGVAVP ATGELATIEI PGATAKDVTI
TSFTPSTQSD RPELPQAKVV IAGGRGVGSE ENFRSIVEPL ADALGGAVGA TRDAVDLGYY
PGEYQVGQTG VTVSPDLYIG LGISGAIQHT SGMQTAKKVI VINNDEDAPI FQIADLGVVG
DLFDIAPALI EEINKRK

> RXA00225 (1-786, translated) 262 residues
MSTIVVLVKN VPDTWSKRTL EADFTLDREG VDRVLDEINE FALEQALRLR ESNPDAGYRV
VALSAGPAGG EEALRKALSM GADEAIQLSD DALAGSDLLG TAWALNNAIN TIAGVALIVT
GSASSDGSMG ALPGVLAEYR QVPALTNLSA LKVEGASITA TRIDNHGTYE LQAALPAVVS
ISDKADKPRF PNFKGIMAAK KAEIKKLSLA EIGVAPEQVG LSHAATAVTA AADRPERSQG
DVIGASGAAE KIAEYLASEN LI

> RXA00235 (1-1275, translated) 425 residues
VAEIMHVFAR EILDSRGNPT VEAEVFLDDG SHGVAGVPSG ASTGVHEAHE LRDGGDRYLG
KGVLKAVENV NEEIGDELAG LEADDQRLID EAMIKLDGTA NKSRLGANAI LGVSMAVAKA
AADSAGLPLF RYIGGPNAHV LPVPMMNIIT GGAHADSGVD VQEFMIAPIG AETFSEALRN
GAEVYHALKS VIKEKGLSTG LGDEGGFAPS VGSTREALDL IVEAIEKAGF TPGKDIALAL
DVASSEFFKD GTYHFEGGQH SAAEMANVYA ELVDAYPIVS IEDPLQEDDW EGYTNLTATI
GDKVQIVGDD FFVTNPERLK EGIAKKAANS ILVKVNQIGT LTETFDAVDM AHRAGYTSMM
SHRSGETEDT TIADLAVALN CGQIKTGAPA RSDRVAKYNQ LLRIEQLLGD AGVYAGRSAF
PRFQG

> RXA00246 (1-1035, translated) 345 residues
MTTAAPQEFT AAVVEKFGHD VTVKDIDLPK PGPHQALVKV LTSGICHTDL HALEGDWPVK
PEPPFVPGHE GVGEVVELGP GEHDVKVGDI VGNAWLWSAC GTCEYCITGR ETQCNEAEYG
GYTQNGSFGQ YMLVDTRYAA RIPDGVDYLE AAPILCAGVT VYKALKVSET RPGQFMVISG
VGGLGHIAVQ YAAAMGMRVI AVDIADDKLE LARKHGAEFT VNARNEDSGE AVQKYTNGGA
HGVLVTAVHE AAFGQALDMA RRAGTIVFNG LPPGEFPASV FNIVFKGLTI RGSLVGTRQD
LAEALDFFAR GLIKPTVSEC SLDEVNGVLD RMRNGKIDGR VAIRF

> RXA00251 (1-708, translated) 236 residues
MKKKIAVVTG ATGGMGIEIV KDLSRDHIVY ALGRNPEHLA ALAEIEGVEP IESDIVKEVL
EEGGVDKLKN LDHVDTLVHA AAVARDTTIE AGSVAEWHAH LDLNVIVPAE LSRQLLPALR
AASGCVIYIN SGAGNGPHPG NTIYAASKHA LRGLADAFRK EEANNGIRVS TVSPGPTNTP
MLQGLMDSQG TNFRPEIYIE PKEIANAIRF VIDAGETTQI TNVDVRPRIE LADRKD

> RXA00268 (1-831, translated) 277 residues
MARGFFLGAT AGRTTLTGEG LQHMDGHSPV LASTNEGVET YDPSFAYEIA HLVHRGIDRM
YGPGKGEDVI YYITIYNEPT PQPAEPEGLD VEGLHKGIYL YSRGEGTGHE ANILASGVGM

QWALKAASIL EADYGVRANI YSATSWVNLA RDGAARNKAQ LRNPGADAGE AFVTTQLKQT
SGPYVAVSDF STDLPNQIRE WVPGDYTVLG ADGFGFSDTR PAARRFFNID AESIVVAVLN
SLAREGKIDV SVAAQAAEKF KLDDPTSVSV DPNAPEE

> RXA00288 (1-1011, translated) 337 residues
MSAQMDTPDP TMSAVAMLDS IPSDQPDFLI DVEVDRPTPG PHDLLVHIEA VSINPVDTKV
RMRAGKQKHP KILGFDAAGE VVAVGSQVTL FNVGDKVFYA GSNQRPGSNA EYQVVDERLV
GHAPQSLGAH DAAALPLVAL TAWESLFDRL GVTQSTTGTL LVLGGSGGVP SALIQLARAL
TGLKVVATAS RPESQEWVTK LGAHEVIDHS KDLSEQISDV DFVFSSWTTG REVELATLMK
PQSHLVLIDD PVDPNLGAFK QKAIALHWEF MFTRAMFNTP DMGEQGKILN KIADMVDRGQ
FESVTATVLD GLNAANIMEG HRLVEQGKTS GKIVVRV

> RXA00290 (1-963, translated) 321 residues
MTIDLQRSTQ NLTHEEIFEA HEGGKLSISS TRPLRDMRDL SLAYTPGVAQ VCEAIKEDPE
VARTHTGIGN TVAVISDGTA VLGLGDIGPQ ASLPVMEGKA QLFSSFAGLK AIPIVLDVHD
VDALVETIAA IAPSFGAINL EDISAPRCFE VERRLIERLD IPVMHDDQHG TAVVILAALR
NSLKLLDRKI EDLKIVISGA GAAGVAAVDM LTNAGATDIV VLDSRGIIHD SREDLSPVKA
ALAEKTNPRG ISGGINEAFT GADLFIGVSG GNIGEDALKL MAPEPILFTL ANPTPEIDPE
LSQKYGAIVA TGPVLTCLTR S

> RXA00293 (1-912, translated) 304 residues
MKIFVGFGDY PLTTKALKEA GAEIVDSLEK AEGFVFTQTP GTEFPLLPDG VRWVQFPNAG
LNAYFTAGQI DDKRRWSNAS GVYGQQVAEA AMALLLGLIH MHPTMVRADS WAPSTQIDQQ
TRWLDGATVA IVGAGGIGKH LAAMLKPFGA KSLAVSRTGT PTQDFDATEP ISNLHQVLAD
ADHVVLCVPL TADTYHLIGK AELKAMQSTA ILINVARGEV VDTEALVDAL DAQEISGAGL
DVTDPEPLPD DHPLWGRSNV IITPHVANTL TSMDRMLAPV VAENYRRFLA GEKMLTEVDI
HKGY

> RXA00296 (1-2835, translated) 945 residues
TIKFNRLDPE VFSQHSRAKL RTDMTTRAAY SSDAGIFRRV PAAVAEPENV EQIRDAIAVA
VARGWSVVGR GGGSSVAGNA IGEGLIIDTS RYFNRILDID PVAQTAVVEP GVVCDALRDA
AAEFGLTYGP DPSTHSRCTI GGMVANNACG SHSVAFGTAA ENLVDVTLML SDGREVTVTK
DGCDDAEINQ KLTDLASKNQ DLISKELGRF PRQVSGYGLH YLAHDMAKAM AGTEGTIGII
TRLTVKLVPT PKVKALAVLA FDTVFDAARA AAKLRLPGVA TIEGMGGDLL AALRSKQGQS
EAGQNLPGNR IGIEAGGWLY CETGSDTLQA AVQAAEEVAT AVDTIDYVVV SEPSEMRELW
RIRESSAGIV TRLADGGEAW PNWEDSAVPP ENLADYLRDL YALMDKFDYQ GIPFGHFGEG
CVHVRISFDF STKEGLKKFE AFMNEASTLV ASYGGSLSGE HGDGRARSSF LDRMYSAEMR
ALFEEFKLIF DPQRIFNPGV LVWADPVMQG LRMDPGQRAL DITPVHKFSK DKGSMINAVN
RCVGVSACRS ESDAMCPSFQ ITGDEVHSTR GRARLLSEMF RGESIADGYR SEEVNEALDL
CLSCKACASE CPVNVDMSTY KAEFLDKHYA GRLRPMAHYV MGWLPLLGHV AHKIPLLPTL
IDATMQSALT APVVRKVGGL ADRPLISFAH RSLRKYKPKK NSGETVVLWP DSFNTNLDTG
PAHAAIKTLE ALGYNVVIPD GFVCCGLTWH STGQLSMTKK VLEQTAKVMK PYLDQGLTVV
GLEPSCTVML QDEATELSDN PDLARLAALT KPFAEVIAPK ITELVESGSL QLTESTALTQ
VHCHERSLGD PQQSALVLEA LGVKDEQIAT GCCGLAGNWG FEKDHAEMSF ALGERELFPK
VRKAEGHVIA DGFSCRTQIE QGTGKQATHL AEVVLSILEQ NNMAQ

> RXA00309 (1-312, translated) 104 residues
MGQCTVALYR EHSYYTATPW RGTWAADGGG VLMTQAIHYI DLLYWLLGEP VEVFGYTNSF
KHGDNIEVED SAVATVRFES GALATISATT AAEPALGAQV QVMG

> RXA00310 (1-435, translated) 145 residues
MSDKIWKVGI IGCGAISRNH IEAVQAIPGA EVSAVCDVDG AKASETAAKY GISPSFTSVD
EILASGVDIV AVCTPHPTHE TVVLAAAAAG VHVLCEKPIA IELDSAQRMI DACESAGVQL
GVLFQRRFWP AAQKMKKEPS WANAR

> RXA00317 (1-339, translated) 113 residues
VTTPSKKTLL FDLDGTLVDS FPGIRTSFLH TLHEKNWEIP SEERISQVPG PPMEWTFQDL
GMTPEQAQDA LQTYLEHYGQ VGWDLSEAFP GMRDLLIPLI YEGFRLCTAT FQG

> RXA00327 (1-384, translated) 128 residues
MIQAALWIVL FLFADRLSNP LVFVSAIMFA ISFSSPVANF GFDTICEKLD RRVMVAGTGM
ANMSAYICAM LATQIIGFLL DWNADGHAYT WSNFQVAWLG LGAVWLAGMI GLAVCLLLQR
RKNIAFRR

> RXA00328 (1-492, translated) 164 residues
VGVERGKVSA KALVVWLTAM CVYIVAIAGR TSFGVAGVHA IDRFDIDASR LAVFTSVQVG
VYVLAQIPMG MLVDRFDARK LLLAGALILA AGQLILGFTD SYMIAIFARV LISVGDSSAF
LSVMRLLPNW FPMSWTPVLQ QLTGAFGFVG QFSPRCRFCT YSTP

> RXA00329 (1-1224, translated) 408 residues
MAAITSRTSF GVAGVEAIDR FQVDATRIAV FTSVQVGVYA FAQIPMGILI DKFGPRKLLA
IGALVMGIGQ LILGFTDSYS IAIIARVFIG AGDASIFLSV MRILPFWFPL KHTPIFTQLT
TCLGQLGQFF SAVPFMALLG AQGWPVAFVS LGSVVALIAI AALVAVRDTP DPQPKPVESA
QEADKPSLRA SLKLIVRNPI TWQGFFIHYV LMVWQTVFSM MWGVPLMTLG MGLSATTAGL
VLSINTLCMV VSAPIIGIIS ARLGYRRDVV AIALSFVQSA VWLVFLASDA PRGLMAIILV
NIVMGLTTAA SGYGFDTIRE RLDRKILAAG TGLANMGGFL SSMVAAQVMG FLLDHSAHGS
TYTWVDFRFG FLAILVTWAV GVTGFVVARL KGGPGRRLLA QIRSTKDF

> RXA00340 (1-1146, translated) 382 residues
VKLVIEADGG SRGNPGVAGS GTVVYSDNKA EVLKEIAYVV GTKATNNVAE YRGLLEGLKA
ARELGATSVD VYMDSKLVVE QMSGRWKIKH PDMKVLAIEA KEIASEIGSV SYTWIPREKN
KRADALSNVA MDAAAAGKPV GVVGDSASVS SASSVAGSEK EDLNCTETKP TNWNGATTDP
TRFLLLRHGQ TAMSVARLYS GRSNPELSEL GEKQAAAAAR RLAQTGGIDA IVSSPLTRTM
QTAEAAAAAL GMKVRVIDDL IETDFGLWDG KSFSEAHEQD PELHTKWLTD SSVAPPGGES
LQTVNRRVKK ARESLQREYG AANVLVVSHV TPIKAIMRQA LDAGPSFFQK AHLDLASLSI
AEFYEDGPTC VRLFNDTSHL EA

> RXA00379 (1-207, translated) 69 residues
MSEIVVAQSI GQQFADVAAS GPLFLGILAA ALAGLVSFAS PCVVPLVPGY ISYLAGVVGG
EVEYSAHAT

> RXA00381 (1-606, translated) 202 residues
MTQTIVHLVR HGEVHNPEKI LYGRMPGYRL SSRGRSQAAR TAASFEGHDV TYIAASPLQR
VQETSEPFIK VTGLELITDE DLLEAGNRFE GLRTKGWRSQ LWNPVRWPLM YNPTLPSWGE
HYTDILERMM AAVERARVAA EGHEAILVTH QLPIVCVQRH ARGQSLSHNP ATRQCDLASV
TSLVFQDDQI VGVHYNEPAQ EI

> RXA00385 (1-339, translated) 113 residues
LGGVFALGWT PCLGPTLAAI ISISAGTEGM TAARGVILIV GYCLGLGLPF LLIALGSSKA
LTGVEWLRKH SRTLQIIGGV FLILVGVALL SGSWAIFINW VRQWTVEYGA TLL

> RXA00386 (1-510, translated) 170 residues
MLPVNQTYAQ FSDTAFVSAY IIYVLALILS LVYYVKQQGI IDARREQTRV SELVGAGGSA
DVDTDLPDDI ADGVLADEDL AKREETARKL ANMTQSLMWL GVMVHLVSVV MRALSASRFP
FGNLYEYILM VTLFAMIGAV LILQRPQFRV VWPWILTPMA GTWFSTVAPS

> RXA00388 (1-303, translated) 101 residues
TLDNLAYKTA IWTVPIFGLG IILGAIWAEA AWGRFWGWDP KETVSFITWV LYAGYLHARA
TAGWRNTNAA WINILALVTM IFNLFFINMV VSGLHSYAGL N

> RXA00406 (1-975, translated) 325 residues
DPVEVAADTQ EMIITRIIDN ASVQAASVLR RPVSSARAMA QVRPVTDGRG ASVFGLPGRY
AAEWAALANG TAVRELDFHD TFLAAEYSHP GDNIPPILAA AQQAGKGGKD LIRGIATGYE
IQVNLVRGMC LHEHKIDHVA HLGPSAAAGI GTLLDLDVDT IYQAIGQALH TTTATRQSRK
GAISSWKAFA PAFAGKMSIE AVDRAMRGEG APSPIWEGED GVIAWLLSGL DHIYTIPLPA
EGEAKRAILD TYTKEHSAEY QSQAPIDLAR SMGEKLAAQG LDLRDVDSIV LHTSHHTHYV
IGTGSNDPQK FDPDASRETL DHSIM

> RXA00427 (1-432, translated) 144 residues

LLPGIASLFN GALISAYAME RIGVPDYRLF IRGDEVEYHR RLVRSGLPFG TCLTTAYLHP
DGSDEFKPIL GGRMHTQYPD NDFKRFFTYR NRGYLMSQPG MRKLLPQEYA RFAWFFLVQK
RDVKGFREWL RLHKLGRDEK FNRP

> RXA00483 (1-1464, translated) 488 residues
VLVTGATGYI GGRLITELLA AGFQVRATSR KKTSLQRFDW YEDVEAVEAD LTDATELDTL
FKDVDVVYYL VHSMGGKNVD FEEQEQRTAE NVIQAADQAG IKQIVYLSGL HPRNRKIEEL
SKHMRSREKV AQILLAGQTP ALILRAATII GSGSASFEII RHLTERLPRM IAPQWITNQI
EPLAIRDVLH YLISAADLKD PVNRSCDIGC GKSYEFADLL RIYADVRGLK RHVNSVPLNL
PMDKLSGLWI SLVTPVPFQL SFPLAQSMAE DAVTEEHSIK DIISDPPDGF IEYREAVELA
LAAEFDRGVP TSWDRSWTVQ QPWAGQPTDP EWAGKAVYED VRTEDTDLRA AQVWPIIEGL
GGVNGWYSAP LLWRLRGIAD RLIGGPGLGG RRDPRHLKLG DRIDWWRVTE IDPPHRLVLT
AEMKVDGGAW LILEVADKEN GGCTYTQRAI FEPKGLPGYL YWWVVSPFHA IIFPYMRSNI
LKAARKLT

> RXA00511 (1-513, translated) 171 residues
ELRKNTLVGT VMSNLGLKIA MDEAGITLRT TKVGDRYVLE DLNAGGFSLG GEQSGHIVLP
DHGTTGDGTL TGLSIMARMA ETGKSLGELA QAMTVLPQVL INVPVSDKST IVSHPSVVAA
IAEAEAELGA TGRVLLRASG TEELFRVMVE AGDKEQARRI AGRLAAVVAE V

> RXA00512 (1-618, translated) 206 residues
MSSATTTDVR KGLYGVIADY TAVSKVMPET NSLTYRGYAV EDLVENCSFE EVFYLLWHGE
LPTAQQLAEF NERGRSYRSL DAGLISLIHS LPKEAHPMDV MRTAVSYMGT KDSEYFTTDS
EHIRKVGHTL LAQLPMVLAM DIRRRKGLDI IAPDSSKSVA ENLLSMVFGT GPESPASNPA
DVRDFEKSLI LYAEHSFNAS TFTARV

> RXA00514 (1-408, translated) 136 residues
HERSYAPERA LRRETIELWN KISTVEDPEW TRRYHSVDPA EKAFGARAVI TFKDGTVVED
ELAVANAHPL GARPFAREQY IQKFRTLAEG VVSEKEQDRF LDAAQRTHEL EDLSELNIEL
DADILAKAPV IPEGLF

> RXA00517 (1-1041, translated) 347 residues
MPEVTVNAQQ LTVLCTDILT KTGVPAADAH LVGDSLVQAD LWGHPSHGVL RLPWYVRRLH
SGAMTTHAHV EVLNDLGAVL ALDGHNGIGQ VLADHARKEA VTRAMMFGIG AVSVRNSNHF
GTAMYYTRKA AAQGCVSILT TNASPAMAPW GGREKRIGTN PWSIAAPFGE TATVVDIANT
AVARGKIYHA RQTNMPIPET WAITSEGAPT TDPAEAINGV VLPMAGHKGY AISFMMDVLS
GVLTGSQHST KVHGPYDPTP PGGAGHLFIA LDVAAFRDPQ DFDDALSDLV GEVKSTPKAQ
NTEEIFYPGE SEDRAHRKNS AHGISLPEKT WMELQELAIE NHVVTHR

> RXA00518 (1-297, translated) 99 residues
VLPVLAARHD GEKWVAMYEN MRDAMDARTG IKPNLDFPAG PAYHLLGFPV DFFTPLFVIA
RVAGWTAHIV EQYENNSLIR PLSEYNGEEQ REVAPIEKR

> RXA00521 (1-1059, translated) 353 residues
LDAADEVQIK HIAADGTETI LKDSLKLLEG EVLDGTVLSA KALDAFLLEQ VARAKAEGIL
FSAHLKATMM KVSDPIIFGH VVRAYFADVF AQYGEQLLAA GLNGENGLAA ILSGLESLDN
GEEIKAAFEK GLEDGPDLAM VNSARGITNL HVPSDVIVDA SMPAMIRTSG HMWNKDDQEQ
DTLAIIPDSS YAGVYQTVIE DCRKNGAFDP TTMGTVPNVG LMAQKAEEYG SHDKTFRIEA
DGVVQVVSSN GDVLIEHDVE ANDIWRACQV KDAPIQDWVK LAVTRSRLSG MPAVFWLDPE
RAHDRNLASL VEKYLADHDT EGLDIQILYP VEATQLSIDR IRRGEDTISV TGN

> RXA00606 (1-1749, translated) 583 residues
MASVPPLLGF VSKEGMITAF MDAPIGNSYV VLLLVGAAIG AVLTFTYSAK LVLGAFVDGP
RDMSHVKEAP VSLWLPAALP GLMSLPLVLV LSLFDAPVSA AATSAAGEAA HMHLALWHGI
NTPLLISLGV LVAGILGVLF RKELWKIAET SPFPIATGND ILSMLVYRAN LLGKFFGRMA
DSMSPRRHLV SLIVLLWALA AFATIHPSVQ LAPKQPGIDR WIDLIPLAII ALSVFGLLTT
RNRLSAAVLV GTVGVGVSFQ MLLLGAPDVA LTQFLVEGLV VVIIMMVVRH QPANFKRIKP
SRRRSTVLVA VLAAFAAFMA VWGLLGRHER SELAMWYLNQ GPEITSGANV VNTILVEFRA
LDTLGELSVL GMAAVVIGAM VASMPRHPFA KGTHPRPFGQ SQLNSIPLRM LLKVLVPALC
FLSFMVFMRG HNDPGGGFIA ALIAGGALML LYLSKAKDGR IFRPNVPFIL TGAGILMAVF

SGVLGLTHGS FLYAIHFNFV GQHWTTSMIF DLGVYLAVLG MVSMAINGLG GYLRPGTDNA
DLDYARRSGP LPATPTVEPE PEGDEDWPEP INPAGDNKEE ANR

> RXA00608 (1-765, translated) 255 residues
MAMDVLLPIF VAVPLAASAI AVLLPWRLIR DILHIIVPFA GIFAGIWLFA HTAEHGPIAH
NVGLYVGGVA IPFAADTFSA IMLITTSIVA VAANWFATIV GETRARFYPA LTLMLITGVN
GALLTADLFN FFVFIEVMLL PSYGLIAMTG TWARLASGRI FVLVNLSAST LLVAGVGIVY
GVIGSVNIAA LQDVVEGNPL VASAMGIVVI AIAVKAGVFP VHTWLPRTYP GTSAAVMGLF
SGLHTKVAVY MLYRI

> RXA00635 (1-921, translated) 307 residues
GTDFPYSDFL PKDNVAQVDI NGAHIGRRTT VKYPVTGDVA ATIENILPHV KEKTDRSFLD
RMLKAHERKL SSVVETYTHN VEKHVPIHPE YVASILNELA DKDAVFTVDT GMCNVWHARY
IENPEGTRDF VGSFRHGTMA NALPHAIGAQ SVDRNRQVIA MCGDGGLGML LGELLTVKLH
QLPLKAVVFN NSSLGMVKLE MLVEGQPEFG TDHEEVNFAE IAAAAGIKSV RITDPKKVRE
QLAEALAYPG PVLIDIVTDP NALSIPPTIT WEQVMGFSKA ATRTVFGGGV GAMIDLARSN
IRNIPTP

> RXA00679 (1-1266, translated) 422 residues
MNTSAETGIL IIGANQSGVQ LAISLRATGF TESITLLGEE DHRPYQRPAL SKEFLQDKID
KERLIFRSNE YWEENNIRLV KGVRIERIEK NDDGSGVAYG AGQEFAFRRL ALAVGARPRH
LDLPGATLEG VTYLRNADDA LALKAMIGSV TDAVVVGGGF IGLEAACSLH DLGKNVTVLE
YGPRLIGRAV GEETAAFFLE QHRSRGVNIV LDARMKQFVG KDGKLSGIEL EDGTVIPAQL
VIVGIGVIPN TELAAVLGLD INNGIVVDKH AVASDGTTIA IGDVANIPNP IPGSPADERI
RLESVNNAIE HAKIAAYSLV GQPEAYAGIP WFWSNQGDLK LQIAGLTLGY DSTVIRQDPE
KKKFSVLYYR GDNIIAADCV NAPLDFMAVR SALSRNQNIP ADLAADISQP LKKLAVDLEV
TR

> RXA00680 (1-318, translated) 106 residues
MSTIHFIDHA GKTRTIEATV GDSVMETAVR NGVPGIVAEC GGSLSCATCH VFVDPAQYDA
LPPMEEMEDE MLWGAAVDRE DCSRLSCQIK VTEGMDLSLT TPETQV

> RXA00682 (1-1899, translated) 633 residues
MANKSFPKPS DLPVPKGAEG WEDLYPYYLV FQDKLMDQEN EKFWFCDSQH WPTVFKPFET
IGGEFAVKCL GQYNARHLMI PNANGIEFRV HLGYLYMSPI PVPEDQIAER VPMFQERITH
YFQNWEPMLA NWKERVLGTI NELESLEFKP LPDYVPIDDI VSGKAKDGTE VLMENFDRLI
QLAYQNWQYH FEFLNLGYIA YLDFFNFCKE VFPDIPDQSI SMMVQGVDME LFRPDDELKI
LAQLAVDLGL QTHFANPDDP QATLAAIAKA EGGATWIARW EEAQDPWFNF TVGNGFYGHD
KYWIEHLELP LGYIADYIRR LDEGQTISRP KDELIAEKER VVEEYRDLLD GEQLAQFDAK
CGLAATAYPY VENHNFYIEH WTMSVFWRKV RELSRTLQGY GFWENEDDML YLNRTEVRDV
LFDLATAWGV GAPGGPIGTI IWPEEIERRK AIVTALKTAR PAPALNTPPE SITEPFTRML
WGITTEQVQS WLGNDEDAEE GTLKGMAASP GVVEGYARVI LSADDLSEIQ QDEILVAPVT
APSWGPIFGK IKATVTDIGG MMSHAAIVCR EYGLPAVTGT GAASTTIKTG DYLKVDGTKG
KVVIVDPDAP RIEGPGAHSH AHSVAAHGVD THA

> RXA00683 (1-1092, translated) 364 residues
MTNSLNIPFV QRFDEGLDPV LEVLGGKGAS LVTMTDAGMP VPPGFVVTTA SFDEFIREAG
VAEHIDKFLN DLDAEDVKEV DRVSAIIRDE LCSLDVPENA RFAVHQAYRD LMERCGGDVP
VAVRSSATAE DLPDASFAGQ QDTYLWQVGL SAVTEHIRKC WASLFTSRAI IYRLKNNIPN
EGLSMAVVVQ KMVNSRVAGV AITMNPSNGD RSKITIDSSW GVGEMVVSGE VTPDNILLDK
ITLQVVSEHI GSKHAELIPD ATSGSLVEKP VDEERANRRS LTDEEMLAVA QMAKRAEKHY
KCPQDIEWAL DADLPDGENL LLLQSRPETI HSNGVKKETP TPQAAKTIGT FDFSSITVAM
TGTK

> RXA00686 (1-804, translated) 268 residues
MAGGNREPGR TVTSKVIAVL GAFEHTMRPL GVTEIAELAD LPPSTTHRLV SELTEGGLLS
KKSDGRYQLG LRIWELAQNT GRQLRDTARP FIQELYSLTS ETAQLVVRDK DEALLIDRAY
GTKKIPRSAR VGGRLPLNST AVGKILLAFD EPWVKQSYLK LPLNASTPKT IVNPDVLAAQ
LKQIHSQGFA ITHDEQRIGG ASIAVPVWHT GKLGAALGLV VPTAQAANLE RYLPILQATS
QRITKATALI PLDTLLASHK NAERKGDT

> RXA00700 (1-804, translated) 268 residues
MINAITLKPK TFLTLSFLAV LSIVIFFWPL IVNPESFLSD KAQAPLYIAI VIPLVLAAVI
AEISENGFDV KAVAMLGVLT AMVAVVRPFG AGAAGFEAVF FVLILGGRAF GPGFGFILGN
TGLFASALLT AGIGPWLPYQ MLAAAWVSFG AGLLPQVRGK KEMLIIVLYA IVSSLGYGTM
MNMSFWPYAI GVTSGLSFTP GAPVLENLHT FMLFCLTTSM GWDLGRAFFT SVLLLLTAKP
VLGALRRASR RAAFGVERDF GEAGVPRV

> RXA00703 (1-2286, translated) 762 residues
MTTPPTEISN VNPTANEFDD PDVGRRITSA AGVPGVLHAL QHAVPNRALL PLLTMNKPGG
IDCPGCAWPE PSTANLGVVE FCENGAKAVA EETTPDRAGK EFWAEHSIYD LREKTDHWLG
KRGRITEPMF YDRSSGDDHY RPISWDRAFA IIASKLREIE PDEAVFYTSG RAPNEPAYML
QLLARRLGTN NLPDCGNMCH ESTGTALGET LGLGKGSVVM EDFYNTDLLI SVGQNPGTNH
PRALTAFKEL KENGGKILAL NPMPETGLMK FREPQSVKGA LSISDKLADE YLQIRLDGDR
AFFQALNKEL IRRDALDHAF LDKFCSGVDE TIEHLKSLDD EVLLKGCGLT AAEINKAADM
VEKSDTVVVS WTLGVTQHKN AVYTIREMVN FLLLTGNIGK PGAGTAPLRG HSNVQGDRTM
GIWEKMPEAF LAALENEFGF DVPRKHGFDT VNSLRAMREG KTKFFLSLGG NLVRVSSDTS
VVEKGMESNE LTVHLSTKPN GSQAWPGEQS LILPVIARTD KDVQKSGVQR VTVEDSAGAV
HASTGKRTAN KDLNLKSECD IIGTIGKQTF GDAFWQPMID NYDVVRDHIE ATIPGFHDFN
RRIDNPGGFL LPNGPRERIF NTSNGKAQLT VNETNVIELP KDYLLMNTVR SHDQYNSTIY
GLDDRYRGVR NGRRVVFVNP QDCKQRGLKD GDIVDIVSVF DDGERRAPNF RVVEYDTARD
CVTTYFPEAN VLVPLDSVAE KSNTPVSKSV VVRLEATGRT AS

> RXA00705 (1-885, translated) 295 residues
PRVVSTDEQV FVNTRPDTVA VEEPLEIRVN GTALTTTMRT PGHDIELVHG LLLSEGLITD
ASEVFTARYC AGAVGPDNQN TYNVLELDVI PKDNPARDPV QNPSHNPEGS QHEALHIPTF
QPVRELNLVA AQRNVLTTSA CGVCGTTSIE QLMNKKGWPI TPITPDPRMI VSLPDKLKSK
QKIFDKTGGV HAAGLATLDG EMLIIREDVG RHNAADKVIG NMLMAGKLPL ENTILVMSSR
ASFELVQKAA MAGISGVIAV GAATSLAIEA AQDSGIFLAG FVRGNKFNHY AGELG

> RXA00782 (1-882, translated) 294 residues
MSIFLNSDSR IIIQGITGSE GSEHARRILA SGAKLVGGTN PRKAGQTILI NDTELPVFGT
VKEAMEETGA DVTVIFVPPA FAKAAIIEAI DAHIPLCVII TEGIPVRDAS EAWAYAKKVG
HTRIIGPNCP GIITPGESLA GITPANIAGS GPIGLISKSG TLTYQMMYEL SDIGISTAIG
IGGDPIIGTT HIDALEAFEA DPETKAIVMI GEIGGDAEER AADFISKHVT KPVVGYVAGF
TAPEGKTMGH AGAIVTGSEG TARAKKHALE AVGVRVGTTP SETAKLMREV VAAL

> RXA00783 (1-1272, translated) 424 residues
LKHLLLREDF VKDAEGSKHG PEMELAVDLF EYQARDLFET HGVPVLKGIV ASTPEAARKA
AEEIGGLTVV KAQVKVGGRG KAGGVRVAPT SAQAFDAADA ILGMDIKGHT VNQVMVAQGA
DIAEEYYFSI LLDRANRSYL AMCSVEGGME IEILAKEKPE ALAKVEVDPL TGIDEDKARE
IVTAAGFETE VAEKVIPVLI KIWQVYYEEE ATLVEVNPLV LTDDGDVIAL DGKITLDDNA
DFRHDNRGAL AESAGGLDIL ELKAKKNDLN YVKLDGSVGI IGNGAGLVMS TLDIVAAAGE
RHGGQRPANF LDIGGGASAE SMAAGLDVIL GDSQVRSVFV NVFGGITACD VVAKGIVGAL
DVLGDQATKP LVVRLDGNNV VEGRRILAEY NHPLVTVVEG MDAAADHAAH LANLAQHGQF
ATAN

> RXA00794 (1-1005, translated) 335 residues
MNLKNPETPD RNLAMELVRV TEAAALASGR WVGRGMKNEG DGAAVDAMRQ LINSVTMKGV
VVIGEGEKDE APMLYNGEEV GTGFGPEVDI AVDPVDGTTL MAEGRPNAIS ILAAAERGTM
YDPSSVFYMK KIAVGPEAAG KIDIEAPVAH NINAVAKSKG INPSDVTVVV LDRPRHIELI
ADIRRAGAKV RLISDGDVAG AVAAAQDSNS VDIMMGTGGT PEGIITACAM KCMGGEIQGI
LAPMNDFERQ KAHDAGLVLD QVLHTNDLVS SDNCYFVATG VTNGDMLRGV SYRANGATTR
SLVMRAKSGT IRHIESVHQL SKLQEYSVVD YTTAT

> RXA00799 (1-1584, translated) 528 residues
LQFRDLDGDG VLAPYEDWRL TPAERAADLV KRMNVEEKAG LMIIGSHYPG YSPLAPESEG
KDAEKCEPLL NPVDMWREDN PITGVPFTEP VLATSSTENA INLRNQRYLI VRDNLPARGL
ATWTNAVQEV AERSRLGIPV AFASNPRNHV ALVAQFGVNE SAGVFSEWPG ELGLAALRDA
ELMETFGTEA AKEWRAGGVH KLYGYMADLA SEPRWSRFNG TFGEDPELIS DYIAAVVRGL

QGPELSKNSV STTIKHFPGG GVRLDGHDPH FHWGQTNEYP TEDALGKYHL PPFQAAIDAG
CASIMPYYAR PMNNSANQLD QQLWQNPTTQ FEEVAFAYNR TFIQDLLRDA MGHRGYVNSD
SGVIDAMMWG VEELSEPERF AAAVRAGTDI FSDMANPRRL LEAVAEGHLD ESELNQPVQR
LLEEIFQLGL FENPYVSEDE AEKIIGAPEV SALGNKAQLD SVTLLRNNPI RAATGSCSKP
EDLPIGYWPY QDRRGSTTAG SSHSRRTPRG NLGVFRVRSR SCNRVGSP

> RXA00800 (1-1104, translated) 368 residues
MSTVVPGIVA LSKGAPVEKV NVVVPDPGAN DVIVKIQACG VCHTDLAYRD GDISDEFPYL
LGHEAAGIVE EVGESVTHVE VGDFVILNWR AVCGECRACK KGEPKYCFNT HNASKKMTLE
DGTELSPALG IGAFLEKTLV HEGQCTKVNP EEDPAAAGLL GCGIMAGLGA AVNTGDIKRG
ESVAVFGLGG VGMAAIAGAK IAGASKIIAV DIDEKKLEWA KEFGATHTIN SSGLGGEGDA
SEVVAKVREL TDGFGTDVSI DAVGIMPTWQ QAFYSRDHAG RMVMVGVPNL TSRVDVPAID
FYGRGGSVRP AWYGDCLPER DFPTYVDLHL QGRFPLDKFV SERIGLDDVE EAFNTMKAGD
VLRSVVEI

> RXA00825 (1-933, translated) 311 residues
MRTVVTGGAG FIGSHLVDLL IKEGHEVVVI DNLSRGRLEN LSDAEATGKL TFVEADLLDV
DFNEFLGTHK PEVIFHLAAQ IDVRHSVVDP LHDAETNILS TIRIADAARQ HGVRKVVFTS
SGGSIYGEPS EFPVDETVPV DPHSPYAASK VSGEIYLNTF RHLYGLDCSH IAPANVYGPR
QDPHGEAGVV AIFALRLLGG LDTKVFGDGG NTRDYVYVGD VVRAFYLASG EIGGGERFNI
GTSVETSDRQ LHTLVATAAG SKDDPEYAPA RLGDVPRSAL SFGKAKEVLG WEPEVNIEQG
VAKTVEYFRT H

> RXA00871 (1-864, translated) 288 residues
MRWFHKKGEL ARDGWQSVVD ATTPGWEYTG IRIAELGSGE SLELNDTGVE RIFIPLQGSF
DVAHHGQVTH LHGRKSVFDG PTDVLYLPTG QTATLSGQGR VAVAEAPTQE PKEWKYIAPA
ETPVELRGAG RSSRQVHNFG TPEALDAARL IVCEVITPGE NWSSYPPHKH DEHIPGHESK
LEEIYYFESA PSRVGGRAEA AEGAFGMFST YSSPAGEIDI NAMVYSGDIA LVPFGYHGPA
VAAPGYDLYY LNVMAGPDPE RIWLINDDPA HAWVRDTWTG QAFDDRLP

> RXA00872 (1-522, translated) 174 residues
MTNLTSTHEV LAIGRLGVDI YPLQSGVGLA DVQSFGKYLG GSAANVSVAA ARHGHNSALL
SRVGNDPFGE YLLAELERLG VDNQYVATDQ TFKTPVTFCE IFPPDDFPLY FYREPKAPDL
NIESADVSLD DVREADILWF TLTGFSEEPS RGTHREILTT RANRRHTIFD LDYR

> RXA00879 (1-2100, translated) 700 residues
LNELADLYGV ATSYTDYKGA HIEVSDDTLV KILRALGVNL DTSNLPNDDA IQRQIALFHD
REFTRPLPPS VVAVEGDELV FPVHVHDGSP ADVHIELEDG TQRDVSQVEN WTAPREIDGI
RWGEASFKIP GDLPLGWHKL HLKSNERSAE CGLIITPARL STADKYLDSP RSGVMAQIYS
VRSTLSWGMG DFNDLGNLAS VVAQDGADFL LINPMHAAEP LPPTEDSPYL PTTRRFINPI
YIRVEDIPEF NQLEIDLRDD IAEMAAEFRE RNLTSDIIER NDVYAAKLQV LRAIFEMPRS
SEREANFVSF VQREGQGLID FATWCADRET AQSESVHGTE PDRDELTMFY MWLQWLCDEQ
LAAAQKRAVD AGMSIGIMAD LAVGVHPGGA DAQNLSHVLA PDASVGAPPD GYNQQGQDWS
QPPWHPVRLA EEGYIPWRNL LRTVLRHSGG IRVDHVLGLF RLFVMPRMQS PATGTYIRFD
HNALVGILAL EAELAGAVVI GEDLGTFEPW VQDALAQRGI MGTSILWFEH SPSQPGPRRQ
EEYRPLALTT VTTHDLPPTA GYLEGEHIAL RERLGVLNTD PAAELAEDLQ WQAEILDVAA
SANALPAREY VGLERDQRGE LAELLEGLHT FVAKTPSALT CVCLVDMVGE KRAQNQPGTT
RDMYPNWCIP LCDSEGNSVL IESLRENELY HRVAKASKRD

> RXA00909 (1-855, translated) 285 residues
VLILFLALTA AAVVAPILIR TLGRPAFGLL ALVPGIGFFW VLSEFIKGTF KDGGELLLHY
AWMPSAHLNI DFRMDSLAAL FSLIVLGVGA LVLLYCWGYF DSNAGRLSAF GAELVAFAMA
MFGLVISDNI LLMYVFWEIT SVLSFLLVGY YGERASSRRS AGQALMVTTL GGLAMLVGII
LMGTQTGVWR FSEIPAYSSS WADVPYISAA AALILAGALS KSAIAPTHFW LPGAMAAPTP
VSAYLHSAAM VKAGIYLVAR LSPDLNVVGS WYLIIIPLGM LTMLM

> RXA00910 (1-1257, translated) 419 residues
YVGFEVLLVA SYVLLTLGAS PARVRSGVGY VMVSMASSMV FLFGLAMVYA SVGTLNMAHV
GLRMEDVPSG TRSAIFAVLL VAFGIKAAVF PLDSWLPDSY PTAPSLVTAV FAGLLTKVGV
YSIIRARSII FTDGSLDTML MWVALATMLI GILGAMAQND IKRLLSFTLV SHIGYMIFGV

ALGSAQGLSG AIFYAIHHIL VQTSLFLVVG LVERQAGSSS LRRLGSLAYI SPLLAILYFI
PAINLGGIPP FSGFLGKIML IEAGAEDGSW LAWVLIAGAV VTSLLTLYTM VLVWSKAFWR
DRKDAPDGAT ALARPAPLVD VQDEVAVKDR NDVGRMPWGM VFSTALLVSA SLAVSVLAGP
LSSITGRAAE SAQDVNIYRA AVLGPNYLDP SRTLEMERYD ANRDDINHRV DTNGTEDQP

> RXA00913 (1-2118, translated) 706 residues
IISVVGIGTR EALLAGLALT VAHSLFKATL FMTVGAIDHT TGTRDIRKLS GLWRKQPILF
AVAAVSAASM AGIPPLFGFI AKETALDTVL NEQMLHGMPG RLMLAGIVLG SIFTMAYSCY
FLYEAFATKH SKFPEANGVS PAVEAMHPVK FKLWIAPVIL AILTVVFGVF PKPVSEAIVT
HLDNVTPSLD DVHTKLALWH GLNLPLLLSV VIIISGFIIF WERDTVERLR PNTAAFGSAD
TAYDAILDAL RVLSHRLTAS TQRGSLTLNV GVIFFVLTIV PLIALITGEQ SDVRMELWDS
PIQGFIAAII IVVAIVATTM DNRLSALILV GVTGYGIAVI FALHGAPDLA LTQVLVETIV
MVVFMLVLRK MPTEVAWKAE PKQSRVRAWL AGATGLSVVI VTIFAMNART TEPISVYMQD
LAYEIGHGAN TVNVLLVDLR GFDTFGEISV LVIAATGIAS LVYRNRSFRK DSRRPTLATT
GRRWLAAAVD TERAQNRSLM VDVATRILFP AMIMLSVYFF FAGHNAPGGG FAGGLVASLA
FALRYLAGGR EELEEALPID AGRILGTGLF VSATAVLWPM VLLGEPPLTS HIWDLTLPLI
GEIHIASALL FDLGVYLIVI GLTMHILNSL GGQLDRDEEM RKQRARDRAR RLARNQRREA
ATVGARRSNE KSTRQMPTIR PPGADTESVE QNGENQTSIS TKRLKQ

> RXA00945 (1-972, translated) 324 residues
MLERLKRLDP LIVLIVLAVI VAIIIPVRGV AADWFDVAVK IAIALLFFLY GARLSTQEAL
NGLKHWRLHL TILAITFGIF PLIGIGLEPM TAFVSEDIYR GILFLTLVPS TVQSSVAFTS
IAKGNVAGAI VSASLSNLAG VFLTPLLVML IMSAGGGVHV DSQVFLDIAI QLLLPFILGQ
VCRRWVKNFA ANKATKIVDR GSIAMVVYSA FSAGMVAGIW STVSVLEIIY LIVFAILLVM
AMLWFTLFMA TRLGFNRADS IAIQFCGTKK SLATGLPMAA VIFGGANIGL LILPLMIFHQ
VQLMICAWLA ARYGRDAQEQ KANA

> RXA00965 (1-723, translated) 241 residues
MTTFHDLPLE ERLTLARLGT SHYSRQLSLV DNAEFGEHSL LEGWTRSHLI AHVAYNAIAL
CNLMHWANTG EETPMYVSPE ARNEEIAYGS TLNPDALRNL HEHSVARLDV AWRETSEDAW
SHEVLTAQGR TVPASETLWM RSREVWIHAV DLGAVATFGD IPEVILRTLA AEITQKWTSQ
GAGEGLVLLD EPSSTRYPAA PGQDEVVVSG SLAGIVRYAA GRGSDGVTSS TGEVPEPPRW
L

> RXA00999 (1-1437, translated) 479 residues
MTNGDNLAQI GVVGLAVMGS NLARNFARNG NTVAVYNRST DKTDKLIADH GSEGNFIPSA
TVEEFVASLE KPRRAIIMVQ AGNATDAVIN QLADAMDEGD IIIDGGNALY TDTIRREKEI
SARGLHFVGA GISGGEEGAL NGPSIMPGGP AKSYESLGPL LESIAANVDG TPCVTHIGPD
GAGHFVKMVH NGIEYADMQV IGEAYHLLRY AAGMQPAEIA EVFKEWNAGD LDSYLIEITA
EVLSQVDAET GKPLIDVIVD AAGQKGTGRW TVKAALDLGI ATTGIGEAVF ARALSGATSQ
RAAAQGNLPA GVLTDLEALG VDKAQFVEDV RRALYASKLV AYAQGFDEIK AGSDENNWDV
DPRDLATIWR GGCIIRAKFL NRIVEAYDAN AELESLLLDP YFKSELGDLI DSWRRVIVTA
TQLGLPIPVF ASSLSYYDSL RAERLPAALI QGQRDFFGAH TYKRIDKDGS FHTEWSGDR

> RXA01015 (1-342, translated) 114 residues
MRVYLGADHA GFETKNAIAE HLKAHGHEVI DCGAHTYDAE DDYPAFCIEA ASRTVNDPGS
LGIVLGGSGN GEQIAANKVK GARCALAWSV ETARLAREHN NANLIGIGGR MHSE

> RXA01025 (1-915, translated) 305 residues
VVSVSVMGAG SWGTTLAKVF SDAGNAVTLW ARREELASTI RDSHENRDYL PGITLPESLQ
VTSSATEALE GAAIVVLAIP SQALRGNLAE WKETIPQDAT LVSLAKGIEK GTHLRMSEVI
AEVTEADPSR IAVLSGPNLA REIAEGQPAA TVIACPDENR AKLVQAAVAA PYFRPYTNTD
VVGTEIGGAC KNVIALACGI SHGYGLGENT NASLITRGLA EIARLGATLG ADAKTFSGLA
GMGDLVATCS SPLSRNRSFG ERLGQGESLE KAREATNGQV AEGVISSQSI FDLATKLGVE
MPITQ

> RXA01048 (1-288, translated) 96 residues
RSDLPNQINN VLAFPGIFAG ALAAKAKKIT PEMKLAAQRQ SQTSQLRTSR SAASCLPPWI
PALPQQSRQL SRPSPKRKTL KNLLIDASLP VEAPIF

> RXA01049 (1-1011, translated) 337 residues
VVKTEFEKEF NKAKYVMTIG EYVYFKLAGI TGMATSIAAW SGILDAHTGE LDLTILEHIG
VDPALFGEIR NPDEPATDAK VVDKKWKHLE EIPWFHAIPD GWPSNIGPGA VDSKTVAVAA
ATSGAMRVIL PSVPEQIPSG LWCYRVSRDQ CIVGGALNDV GRAVTWLERT IIKPENLDEV
LIREPLEGTP AVLPFFSGER SIGWAASAQA TITNIQEQTG PEHLWRGVFE ALALSYQRVW
EHMGKAGAAP ERVIASGRVS TDHPEFLAML SDALDTPVIP LEMKRATLRG TALIVLEQLE
PGGTRATPPF GTTHQPRFAH HYSKARELFD ALYLKLV

> RXA01050 (1-474, translated) 158 residues
MGSIPTMSIP FDDSRGPYVL AMDIGSTASR GGLYDASGCP IKGTKQRESH EFTTGEGVST
IDADQVVSEI TSVINGILNA ADHHNIKDQI AAVALDSFAS SLILVDGEGN ALTPCITYAD
SRSAQYVEQL RAEIDEKAYH GRTGVCLHTS YHPSRLLW

> RXA01077 (1-1371, translated) 457 residues
MTESQDLAAF VEAAKLNDAS PEAVEQLKIR VLDTVGVAIG ALDAEPIVAI RGLLEDLGGT
EQSTLIGGGK TSPERAAFFN SALSRYLDFM DAYLAKGETN HPSDNFGAVL AAAESVGASG
KDLLTAFAVA YQVHTRLSDV APVRAKGFDH TTQGAFAAGA SAAKALGLPA DQIANALAIA
GTANVALRVT RTGNLSHWKG LAYPHVSKEG TWAALLASRG ITGPEEVFEG NKGFKESVSG
PFEIDWSKED LESVKRTIIK KHNAEIHSQS ALDAAQEIRA QEGFNVDNIE KIHLTTFDVA
YSIIGGGEEG DKQLIRTKEE ADHSLPWMLA VVLLDGQLNP EQYEPSRIVA DDVQTLMKKI
EITPSDEFSD RFPDHMPADL EVTLNDGSVF KASQDSYLGF HDNPLDWDNA RKKFDALVTP
FTGEELREEI ATIIHELDSR QVSELTEALA KVSTTRS

> RXA01089 (1-750, translated) 250 residues
LSRFAANLSL TFTELDFLDR FDAASKHAFS AVEFQYPYDF DVQEIKQRAD SAGLPIELFN
APPGDTFGLA ALASPEDFQQ SIEQAITYAT VLKPKKMHVM AGIADVTSET TARYVENIRW
AAQQLDKLDV VVVIEPINHY SVPGYFLHTL EQAYWLIDSI AHPNVKILFD TFHLQQIHGN
LTRRLREVHG AGLLGHVQVA SVPDRHEPGT GEVNAAYIFQ LLSELGYDGV IAGEYHPAGE
TTAGLGWLEL

> RXA01093 (1-1431, translated) 477 residues
MGVDRRTKIV CTLGPAVASA DGILRLVEDG MDVARLNFSH GDHPDHEQNY KWVREAAEKT
GRAVGILADL QGPKIRLGRF TDGATVWENG ETIRITVDDV EGTHDRVSTT YKNLAKDAKP
GDRLLVDDGK VGLVCVSVEG NDVICEVVEG GPVSNNKGVS LPGMDISVPA LSEKDIRDLR
FALKLGVDFI ALSFVRSPAD AELVHKIMDE EGRRVPVIAK LEKPEAVTSL EPIVLAFDAV
MVARGDLGVE VPLEEVPLVQ KRAIQIAREN AKPVIVATQM LDSMIENSRP TRAEASDVAN
AVLDGADAVM LSGETSVGKD PHNVVRTMSR IVRFAETDGR VPDLTHIPRT KRGVISYSAR
DIAERLNARA LVAFTTSGDT AKRVARLHSH LPLLVFTPNE AVRSELALTW GATTFLCPPV
SDTDDMMREV DRALLAMPEY NKGDMMVVVA GSPPGVTGNT NMIHVHLLGD DTRIAKL

> RXA01099 (1-825, translated) 275 residues
MDARGMLAIA EAVVDDAEAL FMQGFGAAPA HMKSPGDFAT EVDMAIESHM RSMLNMMTGI
AVIGEEGGGA TSGTRWVIDP IDGTANFAAS NPMSAILVSL LVDDQPVLGI TSMPMLGKRL
TAFEGSPLMI NGEPQEPLQE QSSLVSHIGF SSMASPRNTA FPVELRRDLL TELTESYLRP
RITGSVGVDL AFTAQGIFGA CVSFSPHVWD NSAGVMLMRA AGAQVTDTEG HPWAPGRGVV
AGTKRAHDVL LSKIEKVRLM HADAGNDQSL NEEYK

> RXA01111 (1-447, translated) 149 residues
MTSTIEHSYQ VWPGHAYPLG STYDGAGTNF ALFSDVAERV ELCLLDADNN ETRIPLEERD
AHIWHCYLPG VQPGQRYGFR VHGPWNPDEG KRCDANKLLV DPYARAFDGD FDGHPSLFSY
DITNPNDPNG RNTEDSIDHT MKSVVVNPF

> RXA01130 (1-303, translated) 101 residues
VGALTGLERV EKITRINGRG LDLRAEGLNL FLQYTDAPGA LGTVGTKLGA AGINIEAAAL
TQAEKGDGAV LILRVESAVS EELEAEINAE LGATSFQVDL D

> RXA01133 (1-549, translated) 183 residues
VSQNGRPVVL IADKLAQSTV DALGDAVEVR WVDGPNRPEL LDAVKEADAL LVRSATTVDA

EVIAAAPNLK IVGRAGVGLD NVDIPAATEA GVMVANAPTS NIHSACEHAI SLLLSTARQI
LLLMRRCVRA SGSGLLSTVW KFSEKLSVSS VLATLVSCLL SVLLRLRPPL LLTILTLTLL
RAG

> RXA01193 (1-741, translated) 247 residues
MRVALSGLTM AEYFRDVQNQ DVLLFIDNIF RFTQAGSEVS TLLGRMPSAV GYQPTLADEM
GVLQERITST KGRSITSLQA VYVPADDYTD PAPATTFAHL DATTELDRSI ASKGIYPAVN
PLTSTSRILE PAIVGERHYE VSQRVIGILQ KNKELQDIIA ILGMDELSEE DKITVARARR
IERFLGQNFF VAEKFTGLPG SYVPLTDTVD AFERICNGDF DHYPEQAFNG LGGLDDVEAA
YKKLTGK

> RXA01194 (1-372, translated) 124 residues
MAEITVELVS VERMLWAGQA SIVTAQTTEG EIGVLPDHEP LLGQLVENGV VTIQPIDGEK
LIAGVSDGFL SVSKEKVTIL ADFAVWANEV DTASAEADLN SDDELAKAHA EAGLRAVRRS
SEGL

> RXA01200 (1-609, translated) 203 residues
GCLRWKSEPS VLEVLKDAAE QTWSTPREFR AGLVQLGRRA LLRSAEKQGQ LGQVEDELFR
LSRILDRESK LTQLLSDRTQ EIGGRRDLLA KVLYGKVTAV TEALALQAIG RPEHNPIDDI
AALAGAVAEL QGRSVAHVVT AVELNEGQQQ ALAEKLGRIY GRAMSIHSEV DTSLLGGMII
RVGDEVIDGS TSGKLERLRA SFA

> RXA01201 (1-1641, translated) 547 residues
MAELTISSDE IRSAIANYTS SYSAEASREE VGVVISAADG IAQVSGLPSV MANELLEFPG
GVIGVAQNLE ADRVGVVVLG NYELLKEGDQ VRRTGDVLSI PVGEAFLGRV INPLGQPIDG
LGEIASEEDR VLELQAPTVL ERQPVEEPLA TGIKAIDAMT PIGRGQRQLI IGDRKTGKTA
VCVDTILNQK ANWETGDKTK QVRCIYVAIG QKGSTIAALR KTLEEQGALE YTTIVAAPAS
DAAGFKWLAP FAGAALAQHW MYQGNHVLVI YDDLTKQAEA YRAISLLLRR PPGREAYPGD
VFYLHSRLLE RAAKLSDELG AGSITALPII ETKANDVSAF IPTNVISITD GQVFLESDLF
NRGVRPAINV GVSVSRVGGA AQTKGMKKVA GSLRLDLAAF RDLEAFATFA SDLDAASKSQ
LERGQRLVQL LIQSENAPQA VEYQIISLWL AGEGAFDNVP VEDVRRFESE LHEYLGSNAA
QVYEQIAGGA QLSDESKETL LKATEDFKSA FQTTDGTPVI NEPEVEALDA GQVKKDQLTV
SRKVSKK

> RXA01202 (1-975, translated) 325 residues
MATIRELRDR IRSVNSTKKI TKAQELIATS RITKAQGRVA AAAPYAEEIQ RVLERLASAS
SLDHPMLRER EGGKRAAVLV VTSDRGMAGG YNHNVLKKAA ELEKLLAESG YEVVRYVTGK
KGVDYYKFRA EDVAGTWTGF SQDPDWAATH NVRRHLIDGF TASSEGEAAW REGLNLPEGQ
DIQGFDQVHV VYTEFISMLT QNPVVHQLLP VEPVIEDEIF EKGEDLLSSS GEVEPDYEFE
PDADTLLEAL LPQYVSRRLF SIFLEAAAAE SASRRNAMKS ATDNATELVK DLSRVANQAR
QAQITQEITE IVGGAGALAD SGESD

> RXA01203 (1-639, translated) 213 residues
MTTALEEQNA QQAATAGRVV RVIGAVVDVE FPRGELPALY NALTVEVTLE SVKKTVVLEV
AQHLGDNLIR TIAMAPTDGL VRGAAVTDTA RPISVPVGDV VKGHVFNALG DCLDDVSLNN
NPEIERWGIH REPPSFDQLE GKTEILETGI KVIDLLTPYV KGGKIGLFGG AGVGKTVLIQ
EMITRIAREF SGTSVFAGVG KRTREGTDLF LEM

> RXA01204 (1-762, translated) 254 residues
MKGEFHAPDL DKEFFPGHVT DSGEVVNMLF TDFANGWFAM DRIVLIRLLM TAVVVVFFLW
AMRKPKLVPH GVQNFAEYAL DFVGIHIAED ILGKKKGRRF LPILATIFFA ALLMNLATII
PGLNISSNSR IAFPIVMAVA GYIAFIYAGS KRYGFFKYVK SSVVIPNIPP ALHVLVVPIE
FFSTFILRPV TLALRLMANF LAGHIILVLL FFATNFFFFQ FNGWTAMSGV TILMAVLFTV
YEIIVIFLQA YIFA

> RXA01216 (1-1101, translated) 367 residues
TDHTLSALLD AHVEVPTAVT VLTMRLDDPT GYGRIVRNEE GEVTAIVEQK DASAEVQAID
EVNSGVFAFD AAILRSALAE LKSDNAQGEL YLTDVLGIAR GEGHPVRAHT AADARELAGV
NDRVQLAEAG AELNRRTVIA AMRGGATIVD PATTWIDVEV SIGRDVIIHP GTQLKGETVI
GDRVEVGPDT TLTNMTIGDG ASVIRTHGFD STIGENATVG PFTYIRPGTT LGPEGKLGGF

VETKKATIGR GSKVPHLTYV GDATIGEESN IGASSVFVNY DGENKHHTTI GSHVRTGSDT
MFIAPVTVGD GAYSGAGTVI KDDVPPGALA VSGGRQRNIE GWVQKKRPGT AAAQAAEAAQ
NVHNQEG

> RXA01225 (1-1440, translated) 480 residues
MTHNHKDWND RIAVAEEMVP LIGRLHRNNN VVVSVFGRLL VNVSDIDIIK SHRYARHIIS
KELPLESSLD ILRELVDMNL GTASIDLGQL AYSFEESEST DLRAFLEDAL APVIGAETDI
NPTDIVLYGF GRIGRLLARI LVSREALYDG ARLRAIVVRK NGEEDLVKRA SLLRRDSVHG
GFDGTITTDY DNNIIWANGT PIKVIYSNDP ATIDYTEYGI NDAVVVDNTG RWRDREGLSQ
HLKSKGVAKV VLTAPGKGDL KNIVYGINHT DITADDQIVS AASCTTNAIT PVLKVINDRY
GVEFGHVETV HSFTNDQNLI DNFHKGSRRG RAAGLNMVLT ETGAAKAVSK ALPELEGKLT
GNAIRVPTPD VSMAVLNLTL NTEVDRDEVN EFLRRVSLHS DLRQQIDWIR SPEVVSTDFV
GTTHAGIVDG LATIATGRHL VLYVWYDNEF GYSNQVIRIV EEIAGVRPRV YPERRQPAVL

> RXA01227 (1-321, translated) 107 residues
MTYTIAQPCV DVLDRACVEE CPVDCIYEGK RMLYIHPDEC VDCGACEPVC PVEAIFYEDD
VPHEWWDYTG ANAAFFDDLG SPGGAASLGP QDFDAQLVAV LPPQNQN

> RXA01242 (1-777, translated) 259 residues
MYAEERRRQI ASLTAVEGRV NVTELAGRFD VTAETIRRDL AVLDREGIVH RVHGGAVATQ
SFQTTELSLD TRFRSASSAK YSIAKAAMQF LPAEHGGLFL DAGTTVTALA DLISEHPSSK
QWSIVTNCLP IALNLANAGL DDVQLLGGSV RAITQAVVGD TALRTLALMR ADVVFIGTNA
LTLDHGLSTA DSQEAAMKSA MITNAHKVVV LCDSTKMGTD YLVSFGAISD IDVVVTDAGA
PASFVEQLRE RDVEVVIAE

> RXA01243 (1-960, translated) 320 residues
MILTVTASPY LLSTNELDGT IEIGEANKIR QVSTVAGGFG TGVAATLFYG GNETFAVFPA
PEISHYMRLV TFAGLPHEII PVAGPIPMHL TMRDAEGNET KFKDSPMPLD VSQLAILRDL
VVRRAEDAAW VLLGGNLPSI APAAWFVDVV RSLRLYHPHV KVAIAATGAA LRAVIRQLAA
TSPDALIVAA EEIEIATGLE PKTLRGPWVE GDLSPTVAAA RALIDSGVTE VLVTNKRTES
LYVSESESLL ASYDSTPGKQ GVNWRESFTA GFLAASNDGK STEDSVINAV AYANAEGSEW
DNYIPTPDKL RAEHVVIKSL

> RXA01259 (1-858, translated) 286 residues
MGTRFLPATK TIPKELLPVV DTPGIELVAK EAADLGATRL AIITAPNKDG ILKHFEEFPE
LEATLEARGK TDQLNKVRAA RELIATVPVV QEKPLGLGHA VGLAESVLDD DEDVVAVMLP
DDLVLPFGVT ERMAEVRAKF GGSVLAAIEV AEDEVSNYGV FKLGELDAES ESEGIRRVVG
MVEKPAPEDA PSRFAATGRY LLDRAIFDAL RRIEPGAGGE LQLTDAIALL IEEGHPVHIV
VHEGKRHDLG NPAGYIPAVV YFGLRHAEYG SKIHRAVKEI LAEFES

> RXA01262 (1-1161, translated) 387 residues
MKIAVAGLGY VGLSNAALLS KNHKVVAVDI DEERVKLVQE FRSPIVDSDL EEYLSTKPQN
LTATTDAEAA YKGADFIVIA TPTNYDPESN FFDTSSVESV IEIVLKVSPG STIVIKSTIP
VGFTSELRIK HPEASIIFSP EFLREGRAFY DNLYPSRVVV GDRSPLGEEF ATLLAEGAKE
KPPILLTDST EAEAIKLFSN TYLALRVAFF NELDTYASVR SLDTKQIIEG VGLDPRIGSH
YNNPSFGYGG YCLPKDTKQL LANYKDVPQN LISAVVQANK TRKDFIAEDI LSKSPTVVGI
YRLVMKSGSD NFRSSSIQGV MKRIKAKGIE IVVFEPNLGE ETFYNSKILN DIEEFKDYCD
IIIANRPTDE LSDVPEKVYT RDIFQRD

> RXA01311 (1-747, translated) 249 residues
MKLTLEIWRQ AGPTAEGKFE TVQVDDAVAQ MSILELLDHV NNKFIEEGKE PFAFASDCRE
GICGTCGLLV NGRPHGADQN KPACAQRLVS YKEGDTLKIE PLRSAAYPVI KDMVVDRSAL
DRVMEQGGYV TINAGTAPDA DTLHVNHETA ELALDHAACI GCGACVAACP NGAAHLFTGA
KLVHLSLLPL GKEERGLRAR KMVDEMETNF GHCSLYGECA DVCPAGIPLT AVAAVTKERA
RAAFRGKDD

> RXA01312 (1-1077, translated) 359 residues
ESLRNDGRIW SPKEPNDNRD PNTIPEDERD YFLERRYPAF GNLVPRDVAS RAISQQINAG
LGVGPLNNAA YLDFRDATER LGQDTIRERY SNLFTMYEEA IGEDPYSSPM RIAPTCHFTM
GGLWTDFNEM TSLPGLFCAG EASWTYHGAN RLGANSLLSA SVDGWFTLPF TIPNYLGPLL

GSERLSEDAP EAQAAIARAQ ARIDRLMGNR PEWVGDNVHG PEYYHRQLGD ILYFSCGVSR
NVEDLQDGIN KIRALRDDFW KNMRITGSTD EMNQVLEYAA RVADYIDLGE LMCVDALDRD
ESCGAHFRDD HLSEDGEAQR DDQNWCFVSA WEPGENGTFV CHAEPLFFES VPLQTRNYK

> RXA01325 (1-672, translated) 224 residues
MDMTISRSTM AQILDYTLLG PEVTNSELAA FIDSAIELGV GTICVPNSMV NLTAKAQEAG
IRVATVAGFP HGKTPALVKA AEARLAVQSG ASEVDVVLDI AVVKEGDANR LLQEIVAIRE
AVPSPVVLKF ILETAVVSDE AIVTAVNALI AAGADFAKTS TGFHPAGGAT VEAVRVMASA
SRGRVGIKAA GGVKTWEDAV AFVEAGATRI GTSNAGAILE GAPE

> RXA01332 (1-549, translated) 183 residues
AARAAAAAED APGAQAFTRI EDAIAADAVD AVLIAVPGQF HEPVLVPALE AGLPILCEKP
LTPDSESSLR IVELEQKLDK PHIQVGFMRR FDPEYNNLRK LVESGEAGEL LMLRGLHRNP
SVGESYTQSM LITDSVVHEF DVIPWLAGSR VVSVEVKYPK TSSLAHSGLK EPILVIMELE
NGV

> RXA01350 (1-984, translated) 328 residues
MNSPQNVSTK KVTVTGAAGQ ISYSLLWRIA NGEVFGTDTP VELKLLEIPQ ALGGAEGVAM
ELLDSAFPLL RNITITADAN EAFDGANAAF LVGAKPRGKG EERADLLANN GKIFGPQGKA
INDNAADDIR VLVVGNPANT NALIASAAAP DVPASRFNAM MRLDHNRAIS QLATKLGRGS
AEFNNIVVWG NHSATQFPDI TYATVGGEKV TDLVDHDWYV EEFIPRVANR GAEIIEVRGK
SSAASAASSA IDHMRDWVQG TEAWSSAAIP STGAYGIPEG IFVGLPTVSR NGEWEIVEGL
EISDFQRARI DANAQELQAE REAVRDLL

> RXA01365 (1-894, translated) 298 residues
MRTRESVTAV IKAYDVRGVV GVDIDADFIS ETGAAFGRLM RSEGETTVAI GHDMRDSSPE
LAKAFADGVT AQGLDVVHLG LTSTDELYFA SGTLKCAGAM FTASHNPAEY NGIKLCRAGA
RPVGQDSGLA NIIDDLVEGV PAFDGESGSV SEQDLLSAYA EYLNELVDLK NIRPMKVAVD
AANGMGGFTV PEVFKGLPLD VAPLYFELDG NFPNHEANPL EPANLVDLQK FTVETGSDIG
LAFDGDADRC FVVDEKGQPV SPSAICAIVA ERYLEKLPGS TIIHNLITSK AVPEVIAE

> RXA01369 (1-501, translated) 167 residues
NEQCLGDVGV LGALLLNFYK LAPGEALYLD AANLHAYISG LGVEIMANSD NVLRGGLTSK
YVDVPELVRV LDFNSLENAR VDVEEDGATT HYPVPINEFQ LDRVAVQGEA EANHDGPMIV
LCTSGTVSLE AGEKTLEVAA GHAAWVPAND PTIAMRSEDA EVFLARV

> RXA01373 (1-708, translated) 236 residues
MELLEGSLRT YPWGSRTLIA DLKGEESPSS RPEAEVWFGA HPGSPSTIGG NALNEVIAAN
PEEALGTRVA EAFENELPFL LKILAAGAPL SLQAHPSLEQ AREGFARENS AGIDLGAPNR
NYRDPNHKPE LIVALTEFIA MAGFRPLRNT LTIFDALACE PLDRYRSMLT VDNEEESLRA
LFTTWITIPI GKRHELIDAL ISNAHTYLEA SDRDEDIAFV LSHIIELNEQ YPGDVG

> RXA01377 (1-1086, translated) 362 residues
MTLTDNSKNV DAVILVGGKG TRLRPLTVNT PKPMLPTAGH PFLTHLLARI KAAGITHVVL
GTSFKAEVFE EYFGDGSEMG LEIEYVVEDQ PLGTGGGIRN VYDKLRHDTA IVFNGDVLSG
ADLNSILDTH REKDADLTMH LVRVANPRAF GCVPTDEDGR VSEFLEKTED PPTDQINAGC
YVFKKELIEQ IPAGRAVSVE RETFPQLLEE GKRVFGHVDA SYWRDMGTPS DFVRGSADLV
RGIAYSPLLE GKTGESLVDA SAGVRDGVLL LGGTVVGRGT EIGAGCRVDN TVIFDGVTIE
PGAVIENSII SSGARIGANA HISGCIIGEG AQVGARCELN AGMRVFPGVV IPDSGIRFSS
DQ

> RXA01392 (1-1077, translated) 359 residues
VANTSSDWAG APQNASADGE FVRDTNYIDD RIVADVPAGS EPIAQEDGTF HWPVEAGRYR
LVAARACPWA HRTVITRRLL GLENVISLGL TGPTHDVRSW TFDLDPNHLD PVLQIPRLQD
AYFNRFPDYP RGITVPALVE ESSKKVVTND YPSITIDFNL EWKQFHREGA PNLYPAELRE
EMAPVMKRIF TEVNNGVYRT GFAGSQEAHN EAYKRLWVAL DWLEDRLSTR RYLMGDHITE
ADIRLYPTLV RFDAVYHGHF KCGRNKITEM PNLWGYLRDL FQTPGFGDTT DFTEIKQHYY
ITHAEINPTR IVPVGPDLSG FATPHGREKL GGSPFAEGVT LPGPIPAGEE VKNPEPFQK

> RXA01436 (1-1191, translated) 397 residues

MALALVLNSG SSSIKFQLVN PENSAIDEPY VSGLVEQIGE PNGRIVLKIE GEKYTLETPI
ADHSEGLNLA FDLMDQHNCG PSQLEITAVG HRVVHGGILF SAPELITDEI VEMIRDLIPL
APLHNPANVD GIDVARKILP DVPHVAVFDT GFFHSLPPAA ALYAINKDVA AEHGIRRYGF
HGTSHEFVSK RVVEILEKPT EDINTITFHL GNGASMAAVQ GGRAVDTSMG MTPLAGLVMG
TRSGDIDPGI VFHLSRTAGM SIDEIDNLLN KKSGVKGLSG VNDFRELREM IDNNDQDAWS
AYNIYIHQLR RYLGSYMVAL GRVDTIVFTA GVGENAQFVR EDALAGLEMY GIEIDPERNA
LPNDGPRLIS TDASKVKVFV IPTNEELAIA RYAVKFA

> RXA01468 (1-825, translated) 275 residues
MTVNISYLTD MDGVLIKEGE IIPGADRFLQ SLTDNNVEFM VLTNNSIFTP RDLSARLKTS
GLDIPPERIW TSATATAHFL KSQVKEGTAY VVGESGLTTA LHTAGWILTD ANPEFVVLGE
TRTYSFEAIT TAINLILGGA RFICTNPDVT GPSPSGILPA TGSVAALITA ATGAEPYYIG
KPNPVMMRSA LNTIGAHSEH TVMIGDRMDT DVKSGLEAGL STVLVRSGIS DDAEIRRYPF
RPTHVINSIA DLADCWDDPF GDGAFHVPDE QQFTD

> RXA01478 (1-1836, translated) 612 residues
MTIPGASTQT DIPLDTLLED YALLSDTHTG ALLSNMGSLD WLCLPRFDSQ AMFTRLLGDR
EHGHWSLRVP GGEVISQNYL GDSFVVQTVW RSETGTARVV DFMPIHGQEQ PDITDLVRSV
HCVEGEVDVE SILRLRFDYG ESTPYFRTST VDGISIVQAV AGPNAVYVRG PEMPHRPAKD
CHSGTFHLTA GESVEWVLTW APSFEPHPPM PDYTRSLEST LSFWASWVEE LPHQRLYDAE
VRRSMLVLRA LTDLQTGGIV AAPTTSLPED FGGIRNWDYR YVWLRDSALT IEALVEYGFS
QAALQWRTWL LRAIAGDPEN LRIMYGLGGE RHLPERELQH LRGYENSVPV RVGNGAAEQY
QADVVGEVMV ALETIRRAGC LEDEFSWGMQ KAILDFQEAN FDRKDQGIWE MRSEPQYFTH
GRAMMWAGFD RGIKAIEEFN LDGPIERWRE LRAKLREEIM TNGFNEEIQS FTQCYDNTQV
DASLLQLAQI GFIGFDDPKM LSTVARIEQE LLDAHGFLHR YHTDGSDGLA GDEYPFLICS
FWLVEQYASS NRLDEAKEKM NRILAVQSPL GLLAEEYSTH HGRLAGNYPQ AFSHIGLISA
ARAINFEEAR NR

> RXA01482 (1-1875, translated) 625 residues
MRMCGIVGYI GQAGDSRDYF ALDVVVEGLR RLEYRGYDSA GIAIHANGEI SYRKKAGKVA
ALDAEIAKAP LPDSILGIGH TRWATHGGPT DVNAHPHVVS NGKLAVVHNG IIENFAELRS
ELSAKGYNFV SDTDTEVAAS LLAEIYNTQA NGDLTLAMQL TGQRLEGAFT LLAIHADHDD
RIVAARRNSP LVIGVGEGEN FLGSDVSGFI DYTRKAVELA NDQVVTITAD DYAITNFDGS
EAVGKPFDVE WDAAAAEKGG FGSFMEKEIH DQPAAVRDTL MGRLDEDGKL VLDELRIDEA
ILRSVDKIVI VACGTAAYAG QVARYAIEHW CRIPTEVELA HEFRYRDPIL NEKTLVVALS
QSGETMDTLM AVRHAREQGA KVVAICNTVG STLPREADAS LYTYAGPEIA VASTKAFLAQ
ITASYLLGLY LAQLRGNKFA DEVSSILDSL REMPEKIQQV IDAEEQIKKL GQDMADAKSV
LFLGRHVGFP VALEGALKLK EIAYLHAEGF AAGELKHGPI ALVEEGQPIF VIVPSPRGRD
SLHSKVVSNI QEIRARGAVT IVIAEEGDEA VNDYANFIIR IPQAPTLMQP LLSTVPLQIF
ACAVATAKGY NVDQPRNLAK SVTVE

> RXA01534 (1-489, translated) 163 residues
MTSAITTATD LRSVLRNVPT PISFIATHTD QPLGMIVGSF VSISAEPPLV GIFLQKSSSS
WPAIEQALVT GQELGISILG GAHADHVRKL SGPSDQRFEN LGWASTENGA IHLEGADAQL
TTKLHDLQEI GDHFFAVLEV IDASADQDFS SALVYHRSQV SSL

> RXA01535 (1-1407, translated) 469 residues
MTEQEFRIEH DTMGEVKVPA KALWQAQTQR AVENFPISGR GLESAQIRAM GLLKAACAQV
NKDSGALDAE KADAIIAAGK EIASGKHDAE FPIDVFQTGS GTSSNMNTNE VIASIAKANG
VEVHPNDHVN MGQSSNDTFP TATHVAATEA AVNDLIPGLK VLHESLAKKA NEWSEVVKSG
RTHLMDAVPV TLGQEFGGYA RQIQLGIERV EATLPRLGEL AIGGTAAGTG INTSADFGGK
VVAELINLTD VKELKEAENH FEAQAARDAL VEFSGAMRVI AVSLYKIAND IRLMGSGPLT
GLGEIRLPDL QPGSSIMPGK VNPVLCETAT QVSAQVIGND AAVAFSGTQG QFELNVFIPV
MARNVLESAR LLANTSRVFA TRLVDGIEPN EAHMKELAES SPSIVTPLNS AIGYEAAAKV
AKTALAEGKT IRQTVIDLGL VDGEKLTEEE LDKRLDVLAM AHTERENKF

> RXA01550 (1-1344, translated) 448 residues
IFQQLFWRVW EIITEIDRRF RLERAADGLD EETIDRMAPI QRGTVHMAWI ACYAAYSING
VAALHTEIIK AETLADWYAL WPEKFNNKTN GVTPRRWLRM INPGLSDLLT RLSGSDDWVT
DLDELKKLRS YADDKSVLEE LRAIKAANKQ DFAEWILERQ GIEIDPESIF DVQIKRLHEY

KRQLMNALYV LDLYFRIKED GLTDIPARTV IFGAKAAPGY VRAKAIIKLI NSIADLVNND
PEVSPLLKVV FVENYNVSPA EHILPASDVS EQISTAGKEA SGTSNMKFMM NGALTLGTMD
GANVEIVDSV GEENAYIFGA RVEELPALRE SYEPYELYET VPGLKRALDA LDNGTLNDNN
SGLFYDLKHS LIHGYGKDAS DTYYVLGDFA DYRETRDRMA ADYASDPLGW ARMAWINICE
SGRFSSDRTI RDYATEIWKL EPTPAVKK

> RXA01562 (1-1038, translated) 346 residues
EQDLDELMHS TGVIDPLTGA PKSASKPGWT SVFSDELVKI GAQNENVVAI TAAMAGPTGL
SKFEANFPNR FFDVGIAEQH AVTSAAGLAL GGKHPVVAIY STFLNRAFDQ LLMDVGMLNQ
PVTLVLDRSG VTGSDGASHN GVWDMALTSI VPGVQVAAPR DEDSLRELLN EAISIDDGPT
VVRFPKGDLP TPIVAIDTLE DGVDVLAYED ATDVESTDDA PSVLIIAVGE RATVALDVAS
RIKQHGVNVT VVDPRWIVPI PQSLVALSDD HDLVITIEDG VIHGGVGSLL SDALNASEVD
TPRRQIAVPQ KYLDHASRNE VLADYGLDAD GIETTVVGWL DSLFGE

> RXA01569 (1-426, translated) 142 residues
APRHYIVRTS WVIGDGNNFV RTMKSLDERG IAPSVVDDQI GRLSFTEDIA AGIAHLLEVG
AAYGTYNLTN TGEPASWADV ARAVFSDPTK VTGVSTAEYF ANKDAAPRPL NSVLDLGKIE
ATGFSAPTWQ TRLNDYLKEL SK

> RXA01570 (1-855, translated) 285 residues
VKGIILAGGS GTRLYPITKG ISKQLMPIYD KPMVYYPLTT LIQAGIKDIL IITTPEDSAS
FERLLGDGSS WGINLTYAVQ PSPDGLAQAF IIGEEFIGDD DVALVLGDNI FDGAQLGHAL
KQCSNPDGGI VFAYEVSDPE RYGVVEFDAA NKAVSIEEKP TAPKSNFAVV GLYFYDNRVV
DIAKSIKPSS RGELEITSVN DAYLQQGALT VQRLDRGDVW LDTGTIDSMS EASSYVEVLQ
KRTGNIIGSP EVAAYREGFI TAEELTVLGE ELKKSGYGNY LLRAL

> RXA01571 (1-600, translated) 200 residues
VSISVKALQK SGPEAPFEVK IIERRDPRAD DVVIDIKAAG ICHSDIHTIR NEWGEAHFPL
TVGHEIAGVV SAVGSDVTKW KVGDRVGVGC LVNSCGECEQ CVAGFENNCL RGNVGTYNSN
DVDGTITQGG YAEKVVVNER FLCSIPEELN FDVAAPLLCA GITTYSPIAR WNVKEGDKVA
VMGLGGTRTH GCPDRCSQGC

> RXA01572 (1-492, translated) 164 residues
MGVQIAAAKG AEVTVLSRSL RKAELAKELG AARTLATSDE DFFTEHAGEF DFILNTISAS
IPVDKYLSLL KPHGVMAVVG LPPEKQPLSF GALIGGGKVL TGSNIGGIPE TQEMLDFCAK
HGLGAMIETV GVNDVDAAYD RVVAGDVQFR VVIDTASFAE VEAV

> RXA01615 (1-939, translated) 313 residues
MSDSPKNAPR ITDEADVVLI GAGIMSSTLG AMLRQLEPSW TQIVFERLDG PAQESSSPWN
NAGTGHSALC ELNYTPEVKG KVEIAKAVGI NEKFQVSRQF WSHLVEEGVL SDPKEFINPV
PHVSFGQGAD QVAYIKARYE ALKDHPLFQG MTYADDEATF TEKLPLMAKG RDFSDPVAIS
WIDEGTDINY GAQTKQYLDA AEVEGTEIRY GHEVKSIKAD GAKWIVTVKN VHTGDTKTIK
ANFVFVGAGG YALDLLRSAG IPQVKGFAGF PVSGLWLRCT NEELIEQHAA KVYGKASVGA
PPMSVPHLDT RVI

> RXA01626 (1-345, translated) 115 residues
MSKTIIVRTE IEIPGHPTAI HIAEMQELPP SEAQGGVQMC KMQRIIELAG TAEGDVVTGA
GVIGGSNFQL NNEPNEVVPH PDTYADFPDI KAVVISAETF EGLWLEAGAK FPGLN

> RXA01632 (1-1005, translated) 335 residues
MTLRIALFGA GRIGHVHAAN IAANPDLELV VIADPFIEGA QRLAEANGAE AVASPDEVFA
RDDIDGIVIG SPTSTHVDLI TRAVERGIPA LCEKPIDLDI EMVRACKEKI GDGASKVMLG
FNRRFDPSFA AINARVANQE IGNLEQLVII SRDPAPAPKD YIAGSGGIFR DMTIHDLDMA
RFFVPNIVEV TATGANVFSQ EIAEFNDYDQ VIVTLRGSKG ELINIVNSRH CSYGYDQRLE
AFGSKGMLAA DNIRPTTVRK HNAESTEQAD PIFNFFLERY DAAYKAELAT FAQGIRDGQG
FSPNFEDGVI ALELANACLE SAQTGRTVTL NPANV

> RXA01633 (1-1083, translated) 361 residues
MKNITIGMVG VGRIGRMHVA NMLAVAETLK ERDLNIEIVL ADAMPGFAEQ VGADMGVKAA

ASVDKLIEDG VDALFIATST AGHVDVLRKG IAAKLPMFCE KPIASDVPES LNIIREIDAA
GATVQVGHQR RFDLGYQEAK RRLDAGDLGW LHSLKAVSSD AFPPPVSYCA TSGGLFRDVS
LHDFDIIRWL TGQDIVEVYA KGSNNGDPEI GAVGDIDTGA ALLTLADGTL ATAIATRYNG
AGHDVRLDVM GSKDSTIVGL DEKSAFASAE EGIDFPTGES HPTFAERFAD AYKNECIAFV
ELILGERENP CTPADAVAAA IVADAAQLSL VTGEPVKIPT VREILEGSAQ PVEVRALVPS
A

> RXA01695 (1-210, translated) 70 residues
AGLLGASPGA SIAPSAMIEL LERCFGDRMI EWGDKLKDMI PSYGKKLASE PALFEQQWAR
TQKTLKLEEA

> RXA01702 (1-1032, translated) 344 residues
MPIATPEVYN EMLDRAKEGG FAFPAINCTS SETINAALKG FAEAESDGII QFSTGGAEFG
SGLAVKNKVK GAVALAAFAH EAAKSYGINV ALHTDHCQKE VLDEYVRPLL AISQERVDRG
ELPLFQSHMW DGSAVPIDEN LEIAQELLAK AKAANIILEV EIGVVGGEED GVEAKAGANL
YTSPEDFEKT IDAIGTGEKG RYLLAATFGN VHGVYKPGNV KLRPEVLLEG QQVARKKLGL
ADDALPFDFV FHGGSGSEKE KIEEALTYGV IKMNVDTDTQ YAFTRPIVSH MFENYNGVLK
IDGEVGNKKA YDPRSYMKKA EQSMSERIIE SCQDLKSVGK TTSK

> RXA01705 (1-603, translated) 201 residues
MGILNSISTP ADLKALNDED LDALAKEIRT FLVDKVAATG GHLGPNLGVV ELTIGLHRVF
DSPQDPIIFD TSHQSYVHKI LTGRAKDFDS LRQKDGLSGY TCRAESEHDW TESSHASAAL
SYADGLSKAK QLDGDTTHSV VAVVGDGALT GGMCWEALNN IAAGKDRKVV VVVNDNGRSY
SPTIGGFAEN LAGLRMQPFY D

> RXA01743 (1-801, translated) 267 residues
MDLNTFWFIL IAFLFAGYFL LEGFDFGVGI LAPIIGKDSA ARNTVIRTIG PVWDGNEVWL
IVAGGALFAA FPEWYATMFS GMYLPLFLVL VSLIMRVVGL EWRKKVDDPR WQKWSDRAIF
IGSWTPPLMW GFIFANILRG MPLKADHTID AAAALPGMVN VFAILGALAF TALFALHGLA
FIRLKTAGRV RTDAAKAAPV VALLAAVTGG PFVLWAAIAY GRSWSWILAV LIIAAVLGGA
FALIKDRDGL SFLSTSVAVI GVVALLF

> RXA01744 (1-1302, translated) 434 residues
WSEYSRFVGD VFGGPLALEG LIAFFLESVF LGLWIFGWGK IPGWLHTASI WIVAIATNIS
AYFIIVANSF MQHPVGAEYN PETGRAELTD FWALLTNSTA LAAFPHAVAG GFLTAGTFVL
GISGWWIIRA HRQAKKAESE IESKHSMHRP ALWVGWWTTV VSSVALFITG DIQAKLMFVQ
QPMKMASAES LCETATDPNF SILTIGTHNN CDTVTHLIDV PFVLPFLAEG KFTGVTLQGV
NQLQAAAEQA YGPGNYSPNL FVTYWSFRAM IGLMLGSLAI AAIAWLLLRK KRTPTGKIAR
LFQIGSLIAI PFPFLANSAG WIFTEMGRQP WVVHPNPESA GDARTEMIRM TVDMGVSDHA
PWQVWLTLIG FTILYLILFV VWVWLIRRAV LIGPPEEGAP SVEAKTGPAT PIGSDMPMTP
LQFTAAAPTT GEKE

> RXA01745 (1-1494, translated) 498 residues
ILADEDDTVD VGAVIARIGD ANAAAAPAEE EAAPAEEEEP VKEEPKKEAA PEAPAATGAA
TDVEMPELGE SVTEGTITQW LKAVGDTVEV DEPLLEVSTD KVDTEIPSPV AGTIVEILAD
EDDTVDVGAV IARIGDANAA AAPAEEEAAP AEEEEPVKEE PKKEEPKKEE PKKEAATTPA
AASATVSASG DNVPYVTPLV RKLAEKHGVD LNTVTGTGIG GRIRKQDVLA AANGEAAPAE
AAAPVSAWST KSVDPEKAKL RGTTQKVNRI REITAMKTVE ALQISAQLTQ LHEVDMTRVA
ELRKKNKPAF IEKHGVNLTY LPFFVKAVVE ALVSHPNVNA SFNAKTKEMT YHSSVNLSIA
VDTPAGLLTP VIHDAQDLSI PEIAKAIVDL ADRSRNNKLK PNDLSGGTFT ITNIGSEGAL
SDTPILVPPQ AGILGTGAIV KRPVVITEDG IDSIAIRQMV FLPLTYDHQV VDGADAGRFL
TTIKDRLETA NFEGDLQL

> RXA01758 (1-1017, translated) 339 residues
MPKYIAMQVS ESGAPLAANL VQPAPLKSRE VRVEIAASGV CHADIGTAAA SGKHTVFPVT
PGHEIAGTIA EIGENVSRWT VGDRVAIGWF GGNCGDCAFC RAGDPVHCRE RKIPGVSYAG
GWAQNIVVPA EALAAIPDGM DFYEPAPMGC AGVTTFNALR NLKLDPGAAV AVFGIGGLVR
LAIQFAAKMG YRTITIARGL EREELARQLG ANHYIDSNDL HPGQALFELG GADLILSTAS
TTEPLSELST GLSIGGQLTI IGVDGGDITV SAAQLMMNRQ IITGHLTGSA NDTEQTMKFA
HLHGVKPLIE RMPLDQANEA IARISAGKPR FRIVLEPNS

> RXA01814 (1-1662, translated) 554 residues
MAHERAGQLA QPEDLIDVAE LVTAYFTRKP DVNNPDQQVA FGTSGHRGFA LDSAFNEDHI
LATTQAIVDY RNQQPKNWVG PLFIGRDTHA LSEPAMISAL EVLIANDVEV LVDADGRYTP
TPAVSHAILR HNDGIILGTA GPSRPYADGI VITPSHNPPR DGGFKYNPAN GGPADTDATD
WIANRANDIL RGDLADVKRV PVSGVLDERT TAYDFKGIYI ADLPNVVNID AIREAGVRIG
ADPMGGASVD YWGAIAETHG LNLTVVNPHV DSTFRFMTLD TDGKIRMDCS SPHAMASLID
NRDKFDVATG NDADADRHGI VTPDAGLMNP NHYLAVAIEY LFAHRPGWSA DTAVGKTLVS
SSMIDRVVAQ LGRTLVEVPV GFKWFVPGLI SGEIGFGGEE SAGASFLRMD GTTWSTDKDG
LILDLLAAEI IAVTGKTPSQ RYAELAEEFG APAYARTDAE ANREQKAILK ALSPEQVTAT
ELAGEAITAK LTEAPGNGAA IGGLKVTTEN AWFAARPSGT EDKYKIYAES FKGEEHLAQV
QKEAQALVSE VLGQ

> RXA01839 (1-684, translated) 216 residues
MRMNAPVPLG GTSNHLLTGV LKDLGAWDPF NVTEDADLGV RIAAKGYSTA VLDSVTWEEA
NSDTINWLRQ RSRWYKGYLQ TWLVYMRRPK WLVQELGIIP AVRFTFLMAG TPIIAVLNLL
FWYLSLTWIL GQPGTIEQMF PPAVYYPALV CLVVANAATI FMNLIGCREG RDPLLLIAVL
TFPLYWLLMS IAALKGTWQL ITRPSYWEKT AHGLEA

> RXA01851 (1-1686, translated) 562 residues
MTSAHFESRR IGPPLRDNYD VIVIGGGISG VQIARHAQGR GLRTVMFEAR DYSSGTSSTT
SKMIHGGLRY LEQYDFGVVQ EAVKERRYLG IAAPHLVAPR SFMLTAFDWS EPKAPMLGAG
VALYETMAWQ RNQGQSKENH SPRFRWIPKN ALLKEVPWLD PEGLKGAWRH DDTLNLHAER
LLLAVIKAFA ADGGTAINHA KVTRILRNVE EGRVKGVEVT DQVTNTTHEV NAPVVINAAG
PWVAQALGDL AEVTKLKVRQ SKGVHLLTGD LGSQSGVFVR GKNGKHVIVN PWMGRTLIGP
TDTMIDGDAD DAAADESDID LLLETIDSVR ATPLDRKEII STLVGVRPLV DDGTDTYTSS
RRFDISDHAN VGIDGLVSVS GGKWTTSRVM GYKVIEHVVE HQAAVLPPLR HFDSRQMPLS
TSFGAYESVA DSFESALRSH PELDVDDEIR VHLARLYGTE HEKVLDLVAK QPDLGRRLDP
DNLDIAAQAV FAVAEEAAVD LADVLDRRIV LGTLGYVQPA AVRATAEAMA QVTGWSAELI
DAQCQSYLAK QDKIQAVLKP YR

> RXA01859 (1-927, translated) 309 residues
MKKKSFPIAR VIGIGVLGIA GMGILLLWLA VTLSDPASPG AKETEVFDRW KVLFDDYIPP
VRVLVAAIIV ALIFVFIAAT VERTVTNRYR SSVDGERVPL APKIVMAETR GVFHGPITIN
VLVPAHNEAE RITGTIQALK SQHEPPERIV VVADNCTDET TELARAEGVE VLETVNNKFK
KAGGLNQALS RMLPTLGEND IVMIVDADTA LDQGFLKEAR RRFESDRALM AVGGLFYGES
GSGWLGQYQR NEYTRYSRDI YRRRGRVFVL TGTASAFRPR GLRTVAESRG TLIPGRKADV
YDTAGVDRR

> RXA01865 (1-315, translated) 105 residues
MTYTIAQPCV DVLDRACVEE CPVDCIYEGK RMLYIHPDEC VDCGACEPAC PVEAIFYEDD
VPDEWLDYND ANAAFFDDLG SPGGAAKLGP QDFDHPMIAA LPPQA

> RXA01882 (1-990, translated) 330 residues
MIITFTPNPS IDSTLSLGEE LSRGSVQRLD SVTAVAGGKG INVAHAVLLA GFETLAVFPA
GKLDPFVPLV RDIGLPVETV VINKNVRTNT TVTEPDGTTT KLNGPGAPLS EQKLRSLEKV
LIDALRPEVT WVVLAGSLPP GAPVDWYARL TALIHSARPD VRVAVDTSDK PLMALGESLD
TPGAAPNLIK PNGLELGQLA NTDGEELEAR AAQGDYDAII AAADVLVNRG IEQVLVTLGA
AGAVLVNAEG AWTATSPKID VVSTVGAGDC ALAGFVMARS QKKTLEESLL NAVSYGSTAA
SLPGTTIPRP DQLATAGATV TQVKGLKESA

> RXA01884 (1-1473, translated) 491 residues
MHVDGFRFDL ASTLAREFDD VDRLATFFDL VQQDPVVSQV KLIAEPWDVG EGGYQVGNFP
PLWTEWNGKY RDTVRDFWRG EPATLGEFAS RLTGSSDLYA NNGRRPTASI NFVTAHDGFT
LNDLVSYNEK HNMANGEDGR DGESHNRSWN CGVEGPTDDP EIMQLRAQQR RNFLTTLLLS
QGTPMLSHGD EMARTQNGNN NVYCQDNELA WVNWDQAEEN ADLVSFTRRL LRIRANHPVF
RRRQFLAGGP LGADVRDRDI AWLVPNGTLM TQDDWDFAFG KSLQVFFNGD AIEEPDYRGQ
KIHDDSFILM FNAHFEPIDF NLPPEHFGMK WKLLVDTTEA VGHPLEDLTI EAGGTITVPA
RSTMLLRQVE APDYTKLEEK IAAEKREQEL AAEKEAAEKR ELELAAAKEA EDAAEALHLA
AERASTQEAE LAHQHGADAI ADEVAEEPQE LPQDEVAAEV ETEPDTEPDT ESDSEQAEVA

SEEPEADEEE K

> RXA01886 (1-774, translated) 258 residues
MTFKLAACAE MIYQDLPFEE RVKTISDQGF LVEIWDWSTK DIDALVATGA EFSSMTGYLR
GDLITEQGRA ELLATASESL AVAEKLNCPR LNLHGTGLGP QGLPVTPIEV VTPEMWLYAA
ETLRQIAELG ERAGKVFVLE NLNLAVDHPG TPFAKATDTL ALVKAVNHPN LRLNLDLYHA
QIGEGNLIEL LREAQPFIGE IQVADVPGRM EPGTGEINYQ GVAKALAAMG YDGVIGMEAW
ASGDSSDALQ ALKSAFTV

> RXA01887 (1-1011, translated) 337 residues
MSVKLALIGA GRIGSNHARL ITNHVIGSEL VAVVDPTPNA ETLADELGAV AFSNPDDVLT
RDDIDAVLIA TPARTHADLV VKAAAAGKHV FVEKPMAVTL EDADRAINAA REANTVLQVG
FNRRFAAGFA AARARIDAGD IGTPQLLRSV TRDPGPFTAD PNKIPQWTIF LETLIHDFDA
LCYLNPGATP VEVTAHADCL VVPEAAGTGF LDTAVVTVRF DNGAIGTAEA SFSAAYGYDV
RGEVFGSKGM MTAGDARATN MTFYGAEGIA AATSRADTDL LSDAYRAEFQ AFVDSIRTNT
PSKVPGEAAR TALLIALGAI RSVETGATIN LAESIEV

> RXA01888 (1-558, translated) 186 residues
MADVAKAAGV STALVSIVFR DAPGASESTR NHVKEKAAEL GYIPDRRAQK LRQNRSGLIG
VAFEMHQAFH GDIVEHLYPT ARKHGFDLYL SAITPTRTEK DAVNALIRER CEAVILLGSR
MSPSDLETIA QQLPVQVIAR GSGTPKVSSV HVDDAVGAQL ALNHLIELGH EHIIYIDGGD
APGTQE

> RXA01891 (1-819, translated) 273 residues
YYNKDLWAKA GLEDRGPESW EEFSEWGPKL QEAMDSGFAH GWGDATNYLS WTFEGPMWSL
GGNYSEGWES RLTTPETIRA VEWLKSTVDE GFATVSTDVT NEFATGLIGS CIQSTGDLSS
VAGAASFDWG VAALPNPTGE GACPTGGAGL GIPSGISEQR QDNALKFIDF LTNAANTGYW
SRETGYVPVR KDAASDPDHA AFLEENPAYN VAVEQLPDTR SQDNFRVLLP NGDRTIGDAL
EKICLTGADI DVTLAEVETK LNTIYTRDIE PLI

> RXA01895 (1-816, translated) 272 residues
HHLFQPLLYQ VATGILSSGE IAPSTRQILG SQENVNVIKG EVTDINVESQ TVTASLGEFT
RVFEYDSLVV GAGAGQSYFG NDHFAEFAPG MKSIDDALEI RARIIGAFER AEICEDPAER
ERLLTFVVVG AGPTGVELAG QLAEMAHRTL AGEYKNFNTN SAKIILLDGA PQVLPPFGKR
LGRNAQRTLE KMGVNVRLNA MVTNVDATSV TYKTKDGEEH TIESFCKIWS AGVAASPLGK
LVAEQTGVET DRAGRVMVND DLSVGDQKNV FV

> RXA01901 (1-1260, translated) 420 residues
MVKRQLPNPA ELLELMKFKK PELNGKKRRL DSALTIYDLR KIAKRRTPAA AFDYTDGAAE
AELSITRARE AFENIEFHPD ILKPAEHVDT TTQILGGTSS MPFGIAPTGF TRLMQTEGEI
AGAGAAGAAG IPFTLSTLGT TSIEDVKATN PNGRNWFQLY VMRDREISYG LVERAAKAGF
DTLMFTVDTP IAGYRIRDSR NGFSIPPQLT PSTVLNAIPR PWWWIDFLTT PTLEFASLSS
TGGTVGDLLN SAMDPTISYE DLKVIREMWP GKLVVKGVQN VEDSVKLLDQ GVDGLILSNH
GGRQLDRAPV PFHLLPQVRK EVGSEPTIMI DTGIMNGADI VAAVAMGADF TLIGRAYLYG
LMAGGREGVD RTIAILRSEI TRTMALLGVS SLEELEPRHV TQLAKMVPVS DATRSAAAEI

> RXA01915 (1-1008, translated) 336 residues
IDVVSVVVAN FLHREIVEAL LASGKHVLCE KPLSDTIEDA EAMIEAAGRA ATNGTIARIG
LTYRRSPGVA HIRDLVQSGE LGKVLHVTGH YWTDYGSNAQ APISWRYKGP NGSGALADVG
SHLTYLAEFV AGSDFAAVRG GQLSTVITER PKPLGAIVGH EGGAVSDEYE AVENDDIASF
SGSFIGGGTA TLQVSRISQG HPNTLGFEVF CEKGSVLFDF RNSGEFKIFT PATSGDISQE
AGYRTITIGP KHPYWRGGLA MDAPGVGIGQ NEGFVFQARA FLEEIAGISE AESLPRCATL
EEGLHNMQLI DAVSQSAAAG GETVAVPAAA LIPANN

> RXA01919 (1-285, translated) 95 residues
MTTTDHKQLG IMYIIMSFSF FFLGGLMALL IRAELFTPGL QFLSNEQFNQ LFTMHGTVML
LLYGTPIVWG FANYVLPLPT TXQAFSKTRV NSPRE

> RXA01927 (1-1116, translated) 372 residues

NDTRSAQAAL DLNEEIGGDQ AAVDATGSVY VASLTATKMR WMRDHEPENA ARTASVMLPH
DFLTWHLMGR GRKVTDHGDA SGTGYYSTRD RAWRTDLAAL ALGHEVELPE LLAPNAIAGT
TPGGVKVAAG TGDNAAAALG LDLQPGDVSV SIGTSGVAGM TVQHSVHDPS GLVTGFADAT
GAYFPLACTL NGAPVLEFGR RILGVEWEEF DALALAAQPG SGGVTLQPYL EGERTPNRPA
ARGVLAGLNC ATTREDFARA TVEGLLLALD DAVTALVEAT GVPVQRIQLI GGGARSQAVR
EIAPEIFGHE IVVPEPAEYV ALGAARQAAW ALSGEATPPQ WPTPGSDPHR APKNTELSTR
YAKLRAATQG WY

> RXA01952 (1-216, translated) 72 residues
PGLCRQAGRG SQGADDRIQH LLEEHGKKLP AEHNYGRMYK LPESMEEHFK ELDPTNTFNA
GIGGTSPHKD WA

> RXA01955 (1-1599, translated) 533 residues
MTQPGQTTTT SHEAIDAFKR IVGDEHVLTS ERATMPFSKG YRFGGGPVFA VVRPGTLVEM
WRALQVSVDN NLIVIPQASN TGLTGGSGPG FQDYDRPIVI ISTHRIDEVH LINDAREAIS
LAGTPLTHLT DALAKHQREP HSVIGSTSIG ASVIGGIANN SGGSQIRKGP AFTREAIFAR
VNDDGKVELV NHLGISLGDD PEVALDRLQR GEWSPEDVTP APEDSNETEY AEHLRKIVPS
PARYNANPEY LFEASGSAGK LMVFAVRTRT FPREVHPTVF YIGTNNTHEL EEIRRLFLEA
DMPLPISGEY MGRSAFDLAE KYGKDTFVFL KFMSPALQTR MFSFKTWANG LFSKIPGIGP
TFADTVSQAM FSVLPNQLPK RMMEYRNRFE HHLLLTVSES QKAASEKMLK EFFAEPEHTG
EFFICTSDEE KSASLNRFGA ASAATRYAAL KRRHIAGLIP IDVALRRDDW NWLEVLPEEI
DDQLEVKAYY GHFFCHVMHQ DYVAKQGVDL EALHDRIQHL LEERGAKLPA EHN

> RXA01989 (1-630, translated) 210 residues
VKSIHKTIHE GTGAGSDFLG WVDLPVDYDK EEFSRIVEAS KRIKENSDVL VVIGIGGSYL
GARAAIEMLT SSFRNSNEYP EIVFVGNHLS STYTKELVDY LADKDFSVNV ISKSGTTTEP
AVAFRLFKQL VEERYGKEEA QKRIFATTDK EKGALKQLAT NEGYETFIVP DDVGGRYSVL
TAVGLLPIAT AGINIEAMMI GAAKAREELS

> RXA02026 (1-720, translated) 240 residues
PFHIQPETGL LNDPNGLIFY KGKYYVSHQW FPLGAVHGLK YWYNYTSDDL INFKPEGPIL
NPDTKYDSHG VYSGSAFEYN GHLYYMYTGN HRDNHWQRHA SQMIARLKED GSVEKFPKPV
ISQQPEGYTS HFRDPKVFKY GEKYYAIIGA QNNDQQGRLL LYNTEDIINW HYLGEINTEL
DDFGYMWECP DYFNLDNQDV ILICPQGIEP KGNQFKNIYQ SGYILGKFDI EKLTYEHENF

> RXA02028 (1-426, translated) 142 residues
MSLPIDEHVN AVKTVVVPAA GLGTRFLPAT KTVPKELLPV VDTPGIELIA AEAAELGATR
LAIITAPNKA GVLAHFERSS ELEETLMERG KTDQVEIIRR AADLIKAVPV TQDKPLGLGH
AVGLAESVLD DDEDVVAVML PH

> RXA02054 (1-1017, translated) 339 residues
MTSLLVTGGA GFIGANFVRQ TVEQHPEYTH ITVLDKLTYA GNADNLKGLP DSKVTLIEGD
ICDAELVDSL VKDHDITVHF AAESHNDNSL NDPSPFVHTN LIGTFVLLEA VRKHNKRFHH
ISTDEVFGDL ELDDPNRFTE TTAYKPSSPY SATKAGSDHL VHAWIRSFGI QATMSNCSNN
YGPYQHIEKF IPRQITNILA GLTPKLYGTG EQVRDWIHVD DHNDAVHLIL SKGKIGETYI
IGADNDHVNN KQVIELICEL MGLDKNAYEH VADRPGHDMR YAMDSTKLRT ELGWAPKYTD
VDSGMRKGLE QTIDWYRENE AWWRPAKNNV EATYAKQGQ

> RXA02055 (1-921, translated) 307 residues
MEYGKQLTSH TTDIEGLLVF DFPVHGDNRG WFKENWQRTK MTNLGLPDFG PVQNNMSFNA
TAGTTRGMHA EPWDKFVSVA VGSVFGAWVD LRAGSSTYGN VVTQKITPDV GVYVPRGVAN
GFQALEDGTL YTYLVNDHWS PDAHYANVNL NMIDWPLPIT EISEKDKKHP ALIDATPLPA
RKVLVVGAGG QLGTALRAQF PDAEFVTRQE LDITSDLTEA RAWKQYSTII NAAAYTAVDQ
AEHDRAAAWD INAAAVATSR PSRATTTSPS CTCPQIMSST VRANPTMKTH RFPHSACTAN
PKQPATS

> RXA02056 (1-2868, translated) 956 residues
RHSVPRLTKG QGTIIGVGSM DYPAEFQGAS EDRLAELGVG KLVTITSTYD HRVIQGAVSG
EFLRTMSRLL TDDSFWDEIF DAMNVPYTPM RWAQDVPNTG VDKNTRVMQL IEAYRSRGHL
IADTNPLSWV QPGMPVPDHR DLDIETHNLT IWDLDRTFNV GGFGGKETMT LREVLSRLRA

AYTLKVGSEY THILDRDERT WLQDRLEAGM PKPTQAEQKY ILQKLNAAEA FENFLQTKYV
GQKRFSLEGA EALIPLMDSA IDTAAGQGLD EVVIGMPHRG RLNVLFNIVG KPLASIFNEF
EGQMEQGQIG GSGDVKYHLG SEGQHLQMFG DGEIKVSLTA NPSHLEAVNP AMEGIVRAKQ
DYLDKGVDGK TVVPLLLHGD AAFAGLGIVP ETINLAKLRG YDVGGTIHIV VNNQIGFTTT
PDSSRSMHYA TDYAKAFGCP VFHVNGDDPE AVVWVGQLAT EYRRRFGKDV FIDLVCYRLR
GHNEADDPSM TQPKMYELIT GRETVRAQYT EDLLGRGDLS NEDAEAVVRD FHDQMESVFN
EVKEGGKKQA EAQTGITGSQ KLPHGLETNI SREELLELGQ AFANTPEGFN YHPRVAPVAK
KRVSSVTEGG IDWAWGELLA FGSLANSGRL VRLAGEDSRR GTFTQRHAVA IDPATAEEFN
PLHELAQSKG NNGKFLVYNS ALTEYAGMGF EYGYSVGNED SIVAWEAQFG DFANGAQTII
DEYVSSGEAK WGQTSKLILL LPHGYEGQGP DHSSARIERF LQLCAEGSMT VAQPSTPANH
FHLLRRHALS DLKRPLVIFT PKSMLRNKAA ASAPEDFTEV TKFQSVINDP NVADAAKVKK
VMLVSGKLYY ELAKRKEKDG RDDIAIVRIE MLHPIPFNRI SEALAGYPNA EEVLFVQDEP
ANQGPWPFYQ EHLPELIPNM PKMRRVSRRA QSSTATGVAK VHQLEEKQLI DEAFEA

> RXA02061 (1-1494, translated) 498 residues
MTNVSGYHRP ELHITAESGV LFAPAGVLLD DDTWHFFHQY RPSPDHGPRW AHQFAERTPF
VWDICDDVLA PEGDETQVRA GSVVSNNGGV DLYFTSVVGP TSTIQLAHIN NIRGTTELIN
EDELGLDPDV SRIGEVVGNT DGYVKFRSPC VIPGWEDQGN RDEGHSGWLM LAVTGPVEAP
TVVVLDSPDG REWSITGPLS LNGLSGLESD EVLVAPRMIR LRDEVDHEIY DVLIVTIEQD
GIDISGYLVG QLNGSEFDVK TPFTRIDFGH DFSRPRNTNY AETTIGYDFA HIFGLMNGVG
RLDSPTEHLS WKEEGWANAI SFPRIVTLQD GTVFQTPPEG LLDAIHESEA AAGWTGLCEI
PSNSAVEVAL KDQEGEIAAT ITHRHNQLVV DRSMNPNHAG DPHAIAPLTD DETDSLFIVV
DGSTVEVFAD GGYVSMASRV YFNNGPFSEF EVTTTGDASI IRQESHFPVD FSSVSLDIDD
LTALMQFDEN EPHEGPVR

> RXA02063 (1-1227, translated) 409 residues
MVKGVKGRPN VLAIVLAGGE GKRLFPLTED RAKPAVPFGG TYRLIDFVLS NLVNSGFLKI
AVLTQYKSHS LDRHISLSWN VSGPTGQYIA SVPAQQRLGK RWFTGSADAI LQSLNLISDE
KPDYVIVFGA DHVYRMDPSQ MLDEHIASGR AVSVAGIRVP REEATAFGCI QSDVDGNITE
FLEKPADPPG TPDDPDMTYA SMGNYIFTTE ALIQALKDDE NNENSDHDMG GDIIPYFVSR
NDAHVYDFSG NIVPGATERD KGYWRDVGTI DAFYECHMDL ISVHPIFNLY NSEWPIHTTS
EGNLPPAKFV RGGIAQSSMV SSGSIISAGT VRNSVLSNNV VVEEGATVEG AVLMPGVRIG
KGAVVRHAIL DKNVVVRDGE LIGVDQVRDA QRFKVSAGGV VVVGKNQVV

> RXA02100 (1-918, translated) 306 residues
IAGKAHPHDM GGKKLMQEIV HFADQAGVRD RFLFLPDYDI NLASYLISGA DVWLNNPVRP
QEASGTSGMK AVMNGGLTLS ISDGWWDEMP KETTGWTIPT VESQDLECRD HLESQALYDL
LENEVAPLFY KRDKNGIPQD WLDLVRESWT TLSPMVTSTR MVRDYTTQYY RPTKHQAELI
AQPAEAADYA AWLEHIKAEW AGVKVSDLKI SESAITAQEL EVSVRVDSGS LNDDEFQAQA
LFGALGHNGD IEDPEITVLT PRGDGAYAAK VSTDLPGNYG ITARVVPNNR MLVSPAETRL
ITYLEN

> RXA02113 (1-1206, translated) 402 residues
LGRINAEEQN LSEYLSDKLW YQDTADATDA VGDPLVAYFS MEFGIHPSLP IYSGGLGVLA
GENMKSASDL GVPLIGVGLL YTHGYFTQSL SGDGWQQEEY KYHDPAELPI EAVKDKNGEQ
VTVSVTYPGA QEVKIALWVA NVGRIPLLLL DTNIEANPEE LRNVTDRLYG GDNEHRIKQE
LVLGVGGVRA VNAFCEARGL KRSSVAHLNE GHAGFLTLER IRERIAEGME YPAAFEQVRA
SNIFTTHTPV PAGIDRFDME MVRRYLGGGQ PEDQQLCVGV PIEKALELGQ ESDPHRFNMA
HMGLRASQHA NGVAKLHGEV SRDMFAGLYP GYEPREVPIG HVTNGVHLPT WVKPEMKELI
DRVTGGADLA VADSWSNPQA VESEKIWKVR NKFRADLVEV AR

> RXA02122 (1-699, translated) 233 residues
MLHVMKPGSH AAAEKTQSTV VLLIRHGQTP TTGQVLPGQT PGLHLSDKGE EQAREVAQRL
AEVPITAVYS SPMERAQETA APTVSAHGLE LTVEPGLIEC DFGEWTGRKL TELNALEEWK
AVQKTPSTFR FPGGESFVEM QDRMVEAIGN IAQQHPGEIV AAFSHADTIK AAVAHFVGTP
LDSFQRIFID TASISAVEFT GKSSGVSSHM LLTNSRTGSL GYLRDKLPKA PQP

> RXA02140 (1-1077, translated) 359 residues
VEQQNKRGLK RKALLGGVLG LGGLAMAGCE VAPPGGVLGD FLRMGWPDGI TPEAVAMGNF
WSWVWVAAWI IGIIMWGLFL TAIFAWGAKR AEKRGEGEFP KQLQYNVPLE LVLTIVPIII

VMVLFFFTVQ TQDKVTALDK NPEVTVDVTA YQWNWKFGYS EIDGSLAPGG QDYQGSDPER
QAAAEASKKD PSGDNPIHGN SKSDVSYLEF NRIETLGTTD EIPVMVLPVN TPIEFNLASA
DVAHSFWVPE FLFKRDAYAH PEANKSQRVF QIEEITEEGA FVGRCAEMCG TYHAMMNFEL
RVVDRDSFAE YISFRDSNPD ATNAQALEHI GQAPYATSTS PFVSDRTATR DGENTQSNA

> RXA02142 (1-651, translated) 217 residues
VTLANQTAIL DSVTSAVGNT GMAAPQRVAA LNRPNMVSVG TIVFLSQELM FFAGLFAMYF
VSRANGLANG SWGEQTDHLN VPYALLITVI LVSSSVTCQF GVFAAERGDV YGLRKWFLVT
IILGSIFVIG QGYEYITLVG HGLTIQSSVY GSAFFITTGF HALHVIAGVM AFVVVLMRIH
KSKFTPAQAT AAMVVSYYWH FVDVVWIGLF ITIYFIQ

> RXA02143 (1-888, translated) 296 residues
MMETNPQTPE GNSMAKPSAK KVKNRRKVRR TVAGALALTI GLSGAGILAT AITPDAQVAT
AQRDDQALIS EGKDLYDVAC ITCHGVNLQG VEDRGPSLVG VGEGAVYFQV HSGRMPILRN
EAQAERKAPR YTEAQTLAIA AYVAANGGGP GLVYNEDGTL AMEELRGENY DGQITSADVA
RGGDLFRLNC ASCHNFTGRG GALSSGKYAP NLDAANEQEI YQAMLTGPQN MPKFSDRQLS
ADEKKDIIAF IKSTKETPSP GGYSLGSLGP VAEGLFMWVF GILVLVAAAM WIGSRS

> RXA02144 (1-1224, translated) 408 residues
MSNNNDKQYT TQELNAMSNE DLARLGTELD DVTIAYRKER FPIANDPAEK RAARAVTFWL
VLGIIGGLGF LATYIFWPWE YKAHGDEGLL AYTLYTPMLG ITSGLCILSL GFAVVLYVKK
FIPEEIAVQR RHDGPSEEVD RRTIVALLND SWQTSTLGRR KLIMGLAGGG AVLAGLTIIA
PMGGMIKNPW NPKEGPMDVQ GDGTLWTSGW TLVENDVKVY LGRDTAAIAE SHTDATGEHW
STTGVSRLVR MRPEDLAAAS METVFPLPAE MVNDGAEYDP AKDVYEHQMH SVHGPRNAVM
LIRLRTADAE KVIEREGQES FHYGDYYAYS KICTHIGCPT SLYEAQTNRI LCPCHQSQFD
ALHYGKPVFG PAARALPQLP ITVDEEGYLI AAGNFIEPLG PAFWERKS

> RXA02147 (1-1017, translated) 339 residues
MFGRRWVSVV ASCVIASTLI LVPSHSGAEE VDQLIADIEH VSQETSAQNE EVKQLEIDIE
AREVTIKEVQ EQSVSYREAA DQASENVEAY RSEINRIAQA KYRGTVTDPL SIAVSAEDPQ
NVIDRMSYLS TLTKSTSDVV ESLNAETEKS AEAVYQANRT KAEAEFQLGQ LKVRQAELES
EKEALDGRKS EIRDRVDALT PQEREMWVAK NGPLDIDLTD LLGLSAATSG AVDAALSKLG
SPYGWGGIGP NEFDCSGLIY WAYQQMGKTL PRTSQAQMAG GTPVSRDELQ PGDVIGYYPG
ATHVGLYIGD GKIVHASDYG IPVQVVSVDS APFYGARRY

> RXA02149 (1-969, translated) 323 residues
MPQKPASFAV GFDIGGTNMR AGLVDESGRI VTSLSAPSPR TTQAMEQGIF DLVEQLKAEY
PVGAVGLAVA GFLDPECEVV RFAPHLPWRD EPVREKLENL LGLPVRLEHD ANSAAWGEHR
FGAAQGADNW VLLALGTGIG AALIEKGEIY RGAYGTAPEF GHLRVVRGGR ACACGKEGCL
ERYCSGTALV YTARELASHG SFRNSGLFDK IKADPNSING KTITAAARQE DPLALAVLED
FSEWLGETLA IIADVLDPGM IIIGGGLSNA ADLYLDRSVN HYSTRIVGAG YRPLARVATA
QLGADAGMIG VADLARRSVV EAN

> RXA02175 (1-1293, translated) 431 residues
VATDNNKAVL HYPGGEFEMD IIEASEGNNG VVLGKMLSET GLITFDPGYV STGSTESKIT
YIDGDAGILR YRGYDIADLA ENATFNEVSY LLINGELPTP DELHKFNDEI RHHTLLDEDF
KSQFNVFPRD AHPMATLASS VNILSTYYQD QLNPLDEAQL DKATVRLMAK VPMLAAYAHR
ARKGAPYMYP DNSLNARENF LRMMFGYPTE PYEIDPIMVK ALDKLLILHA DHEQNCSTST
VRMIGSAQAN MFVSIAGGIN ALSGPLHGGA NQAVLEMLED IKSNHGGDAT EFMNKVKNKE
DGVRLMGFGH RVYKNYDPRA AIVKETAHEI LEHLGGDDLL DLAIKLEEIA LADDYFISRK
LYPNVDFYTG LIYRAMGFPT DFFTVLFAIG RLPGWIAHYR EQLGAAGNKI NRPRQVYTGN
ESRKLVPREE R

> RXA02196 (1-693, translated) 231 residues
MIKAIFWDMD GTMVDSEPQW GIATYELSEA MGRRLTPELR ELTVGSSLPR TMRLCAEHAG
ITLSDADYER YRAGMFARVH ELFDESLVPN PGVTELLTEL KALEIPMLVT TNTERDLATR
SVAAVGNEFF IGSIAGDEVP TAKPAPDMYL EAARRVGFDP SECLVFEDSY NGMLGAVTAG
CRVIGLHPEE VQAPEGVVPL RSLHGKNSFE GVTAEMVTAW YHQIEPAGVA K

> RXA02209 (1-1659, translated) 553 residues

VVPSIAGPKR PQDRILLSEA KEQFRKDLPT YTDDAVSVDT SIPATRMVNE GGGQPEGGVE
ADNYNASWAG SGESLATGAE GRPSKPVTVA SPQGGEYTID HGMVAIASIT SCTNTSNPSV
MIGAGLIARK AAEKGLKSKP WVKTICAPGS QVVDGYYQRA DLWKDLEAMG FYLSGFGCTT
CIGNSGPLPE EISAAINEHD LTATAVLSGN RNFEGRISPD VKMNYLASPI MVIAYAIAGT
MDFDFENEAL GQDQDGNDVF LKDIWPSTEE IEDTIQQAIS RELYEADYAD VFKGDKQWQE
LDVPTGDTFE WDENSTYIRK APYFDGMPVE PVAVTDIQGA RVLAKLGDSV TTDHISPASS
IKPGTPAAQY LDEHGVERHD YNSLGSRRGN HEVMMRGTFA NIRLQNQLVD IAGGYTRDFT
QEGAPQAFIY DASVNYKAAG IPLVVLGGKE YGTGSSRDWA AKGTNLLGIR AVITESFERI
HRSNLIGMGV VPLQFPAGES HESLGLDGTE TFDITGLTAL NEGETPKTVK VTATKENGDV
VEFDAICPHR HPR

> RXA02213 (1-717, translated) 239 residues
VTESKNSFNA KSTLEVGDKS YDYFALSAVP GMEKLPYSLK VLGENLLRTE DGANITNEHI
EAIANWDASS DPSIEIQFTP ARVLMQDFTG VPCVVDLATM REAVAALGGD PNDVNPLNPA
EMVIDHSVIV EAFGRPDALA KNVEIEYERN EERYQFLRWG SESFSNFRVV PPGTGIVHQV
NIEYLARVVF DNEGLAYPDT CIGTDSHTTM ENGLGILGWG VGGIEAEAAM LGQPVSMLI

> RXA02245 (1-657, translated) 219 residues
MAQRTPLIAP SILAADFSRL GEQVLAVPDA DWIHVDIMDG HFVPNLSFGA DITAAVNRVT
DKELDVHLMI ENPEKWVDNY IDAGADCIVF HVEATEGHVE LAKYIRSKGV RAGFSLRPGT
PIEDYLDDLE HFDEVIVMSV EPGFGGQSFM PEQLEKVRTL RKVIDERGLN TVIEIDGGIS
AKTIKQAADA GVDAFVAGSA VYGAEDPNKA IQELRALAQ

> RXA02256 (1-1002, translated) 334 residues
MTIRVGINGF GRIGRNFFRA VLERSDDLEV VAVNDLTDNK TLSTLLKFDS IMGRLGQEVE
YDDDSITVGG KRIAVYAERD PKNLDWAAHN VDIVIESTGF FTDANAAKAH IEAGAKKVII
SAPASNEDAT FVYGVNHESY DPENHNVISG ASCTTNCLAP MAKVLNDKFG IENGLMTTVH
AYTGDQRLHD APHRDLRRAR AAAVNIVPTS TGAAKAVALV LPELKGKLDG YALRVPVITG
SATDLTFNTK SEVTVESINA AIKEAAVGEF GETLAYSEEP LVSTDIVHDS HGSIFDAGLT
KVSGNTVKVV SWYDNEWGYT CQLLRLTELV ASKL

> RXA02257 (1-1215, translated) 405 residues
MAVKTLKDLL DEGVDGRHVI VRSDFNVPLN DDREITDKGR IIASLPTLKA LSEGGAKVIV
MAHLGRPKGE VNEKYSLAPV AEALSDELGQ YVALAADVVG EDAHERANGL TEGDILLLEN
VRFDPRETSK DEAERTAFAQ ELAALAADNG AFVSDGFGVV HRAQTSVYDI AKLLPHYAGG
LVETEISVLE KIAESPEAPY VVVLGGSKVS DKIGVIEALA AKADKIIVGG GMCYTFLAAQ
GHNVQQSLLQ EEMKATCTDL LARFGDKIVL PVDLVAASEF NKDAEKQIVD LDSIPEGWMS
LDIGPESVKN FGEVLSTAKT IFWNGPMGVF EFAAFSEGTR GIAQAIIDAT AGNDAFSVVG
GGDSAASVRV LGLNEDGFSH ISTGGGASLE YLEGKELPGV AILAQ

> RXA02258 (1-777, translated) 259 residues
MARKPLIAGN WKMNLDHQQA IGTVQKLAFA LPKEYFEKVD VAVTVPFTDI RSVQTLVEGD
KLEVTFGAQD VSQHESGAYT GEVSASMLAK LNCSWVVVGH SERREYHNES DELVAAKAKA
ALSNGISPIV CVGEPLEIRE AGTHVEYVVE QTRKSLAGLD AAELANTVIA YEPVWAIGTG
KVASAADAQE VCKAIRGLIV ELAGDEVAEG LRILYGGSVK AETVAEIVGQ PDVDGGLVGG
ASLDGEAFAK LAANAASVA

> RXA02259 (1-2772, translated) 924 residues
VFKVVMTDFL RDDIRFLGQI LGEVIAEQEG QEVYELVEQA RLTSFDIAKG NAEMDSLVQV
FDGITPAKAT PIARAFSHFA LLANLAEDLY DEELREQALD AGDTPPDSTL DATWLKLNEG
NVGAEAVADV LRNAEVAPVL TAHPTETRRR TVFDAQKWIT THMRERHALQ SAEPTARTQS
KLDEIEKNIR RRITILWQTA LIRVARPRIE DEIEVGLRYY KLSLLEEIPR INRDVAVELR
ERFGEGVPLK PVVKPGSWIG GDHDGNPYVT AETVEYSTHR AAETVLKYYA RQLHSLEHEL
SLSDRMNKVT PQLLALADAG HNDVPSRVDE PYRRAVHGVR GRILATTAEL IGEDAVEGVW
FKVFTPYASP EEFLNDALTI DHSLRESKDV LIADDRLSVL ISAIESFGFN LYALDLRQNS
ESYEDVLTEL FERAQVTANY RELSEAEKLE VLLKELRSPR PLIPHGSDEY SEVTDRELGI
FRTASEAVKK FGPRMVPHCI ISMASSVTDV LEPMVLLKEF GLIAANGDNP RGTVDVIPLF
ETIEDLQAGA GILDELWKID LYRNYLLQRD NVQEVMLGYS DSNKDGGYFS ANWALYDAEL
QLVELCRSAG VKLRLFHGRG GTVGRGGGPS YDAILAQPRG AVQGSVRITE QGEIISAKYG
NPETARRNLE ALVSATLEAS LLDVSELTDH QRAYDIMSEI SELSLKKYAS LVHEDQGFID

YFTQSTPLQE IGSLNIGSRP SSRKQTSSVE DLRAIPWVLS WSQSRVMLPG WFGVGTALEQ
WIGEGEQATQ RIAELQTLNE SWPFFTSVLD NMAQVMSKAE LRLAKLYADL IPDTEVAERV
YSVIREEYFL TKKMFCVITG SDDLLDDNPL LARSVQRRYP YLLPLNVIQV EMMRRYRKGD
QSEQVSRNIQ LTMNGLSTAL RNSG

> RXA02288 (1-846, translated) 282 residues
MSQVIPASSQ EKRRERIVSY VTRHGFARVE ALAELFEVSA MTIHRDLEAL AADNLVERIR
GGARSVSPSM SELAVEQRRH LHRTVKEALC TAAARLIPEG AVVAIDDSTT LESLVEKLPQ
RSPSALITHS LKTMADHRVR AGMSDIRLIA CAGLYFAETD SFLGKATSAQ LNELSADISF
VSTTAVRATG EVPALFHPDM EAADTKRALI GIGSVRVLVV DSSKFGSAGV FKVASIEEFD
HIIIDQQCTR EQRDLLRNSR AQIHVIDHNG DEILDTPTEE DF

> RXA02292 (1-675, translated) 225 residues
MDNDFESIEK MSSGDWYVAT GAEREEVAQK TALLFHEYNQ IGPTDPARTA EILRTVLNPA
SGTCTIKAPA IIEYGFNTTI GEHVFINFGL TILDIAPVRI GARSMLGPNC QLFTAGHPVD
DWEMRSGGWE NGAPISIGED TWLGGNVTVV GGVSIGDRCV IGAGPVVTKD IPDDSIAVGN
PARVVRKRDD SRLERSQLPE GASVDALGIL PTKSPRLSEN IAEKY

> RXA02322 (1-411, translated) 137 residues
MRIHDVYTHL SADNFPKAEH LAWKFSELAT DPVEVTPDVS EMIINRIIDN AAVSAASVLR
RPVTVARQQA QSHPREKGGK VFGISGSYSP EWAAFANGVA VRELDFHDTF LAAEYSHPGD
NIPPLLAVAQ AQRSSGR

> RXA02326 (1-816, translated) 272 residues
MLGRPTKVTP SSKVVGDLAL HLVGAGVDPA DFAADPQKYD IPDSVIAFLR GELGNPPGGW
PEPLRTRALE GRSEGKAPLT EVPEEEQAHL DADDSKERRN SLNRLLFPKP TEEFLEHRRR
FGNTSALDDR EFFYGLVEGR ETLIRLPDVR TPLLVRLDAI SEPDDKGMRN VVANVNGQIR
PMRVRDRSVE SVTATAEKAD SSNKGHVAAP FAGVVTVTVA EGDEVKAGDA VAIIEAMKME
ATITASVDGK IDRVVVPAAT KVEGGDLIVV VS

> RXA02327 (1-960, translated) 320 residues
LLATRVRSFA LKPAAEAVAK LTPELLSVEA WGGATYDVAM RFLFEDPWDR LDELREAMPN
VNIQMLLRGR NTVGYTPYPD SVCRAFVKEA ASSGVDIFRI FDALNDVSQM RPAIDAVLET
NTAVAEVAMA YSGDLSDPNE KLYTLDYYLK MAEEIVKSGA HILAIKDMAG LLRPAAVTKL
VTALRREFDL PVHVHTHDTA GGQLATYFAA AQAGADAVDG ASGTTVWHHL PSHPLSAIVA
AFAHTRRDTG LSLEAVSDLE PYWEAVRGLY LPFESGTPGP TGRVYRHEIP GGQLSNLRAQ
ATALGLADRF ELIEDNYASR

> RXA02328 (1-1383, translated) 461 residues
ASEAVRIGTE GSPVKAYLDI DEIIGAAKKV KADAIYPGYG FLSENAQLAR ECAENGITFI
GPTPEVLDLT GDKSRAVTAA KKAGLPVLAE STPSKNIDEI VKSAEGQTYP IFVKAVAGGG
GRGMRFVASP DELRKLATEA SREAEAAFGD GAVYVERAVI NPQHIEVQIL GDHTGEVVHL
YERDCSLQRR HQKVVEIAPA QHLDPELRDR ICADAVKFCR SIGYQGAGTV EFLVDEKGNH
VFIEMNPRIQ VEHTVTEEVT EVDLVKAQMR LAAGATLKEL GLTQDKIKTH GAALQCRITT
EDPNNGFRPD TGTITAYRSP GGAGVRLDGA AQLGGEITAH FDSMLVKMTC RGSDFETAVA
RAQRALAEFT VSGVATNIGF LRALLREEDF TSKRIATGFI ADHPHLLQAP PADDEQGRIL
DYLADVTVNK PHGVRPKDVA APIDKLPNIK DLPLPRGSRD R

> RXA02329 (1-603, translated) 201 residues
TATRQSRKGE ISSWKAFAPA FAGKMAIEAM DRAMRGEGSP APIWEGEDGV IAWLLSGKDH
VYHVPLPEHG EPKLGILETY TKEHSAEYQS QAPIDLARRM KPLVDAAGGT EHIAEIVLRT
SHHTHYVIGT GANDPQKMDP QASRETLDHS IMYIFAVALQ DGVWHHEFSY TRKRSTRPET
VELWHKIRTV EDPEWTRRYH S

> RXA02332 (1-1143, translated) 381 residues
MSDSQVRKGL NGVISDYTSI SKVMPESNSL TYRGYAVEDL VENCSFEEVI YLLWFGELPT
TEQLRTFNTT GRSYRSLDAG LISLIHSLPN TCHPMDVLRT AVSYMGTFDP DPFTRDADHI
RSIGHNLLAQ LPMVVAMDIR RRSGEEIIAP DHNKGIASNF LSMVFGNDDG SVANSADDIR
DFERSLILYA EHSFNASTFS ARVISSTRSD TYSAITGAIG ALKGPLHGGA NEFVMHTMLD
IDDPNNAADW MGKALDRKER IMGFGHRVYK NGDSRVPSME KSMRSLAARH RGQKWVHMYE

SMQEVMEART GIKPNLDFPA GPAYYMLGFP VDFFTPLFVL ARVSGWTAHI VEQFENNALI
RPLSAYNGVE EREVVPISER T

> RXA02333 (1-219, translated) 73 residues
EIGYNAVIYP VTTLRIAMGQ VEQALAEIKE HGTQEGWLDR MQHRSRLYEL LRYEDYNVFD
QHIFTYRKGE NNE

> RXA02379 (1-705, translated) 235 residues
MRKHRWANAA GLYADTVAES TIGLILAQMH MHATTRLAKS WSVRPEVENN KSWLHDNKTV
AILGAGGIGV RLLEMLKPFN VKTIAVNNSG RPVEGADETF AMDKAEHVWA EADVFVLILP
LTDATYQIVN AETLGKMKPS AVVVNVGRGP LINTDDLVDA LNNGTIAGAA LDVTDPEPLP
DSHPLWEMDN VVITPHTANT NERIRALTGE LTLRNIELFE AGEQMATEVD VVAGY

> RXA02399 (1-1296, translated) 432 residues
MSNVGKPRTA QEIQQDWDTN PRWNGITRDY TADQVADLQG SVIEEHTLAR RGSEILWDAV
TQEGDGYINA LGALTGNQAV QQVRAGLKAV YLSGWQVAGD ANLSGHTYPD QSLYPANSVP
SVVRRINNAL LRSDEIARTE GDTSVDNWVV PIVADGEAGF GGALNVYELQ KAMIAAGAAG
THWEDQLASE KKCGHLGGKV LIPTQQHIRT LNSARLAADV ANTPTVVIAR TDAEAATLIT
SDVDERDQPF ITGERTAEGY YHVKNGLEPC IARAKSYAPY ADMIWMETGT PDLELAKKFA
EGVRSEFPDQ LLSYNCSPSF NWSAHLEADE IAKFQKELGA MGFKFQFITL AGFHSLNYGM
FDLAYGYARE GMTSFVDLQN REFKAAEERG FTAVKHQREV GAGYFDQIAT TVDPNSSTTA
LKGSTEEGQF HN

> RXA02404 (1-2136, translated) 712 residues
MQVAKVLYDF VTEAVLPRVG VDAEKFWSGF AAIARDLTPR NRELLARRDE LQMLIDDYHR
NNSGTIDQEA YEDFLKEIGY LVEEPEAAEI RTQNVDTEIS STAGPQLVVP ILNARFALNA
ANARWGSLYD ALYGTNAIPE TDGAEKGKEY NPVRGQKVIE WGREFLDSVV PLDGASHADV
EKYNITDGKL AAHIGDSVYR LKNRESYRGF TGNFLDPEAI LLETNGLHIE LQIDPVHPIG
KADKTGLKDI VLESAITTIM DFEDSVAAVD AEDKTLGYSN WFGLNTGELK EEMSKNGRIF
TRELNKDRVY IGRNGTELVL HGRSLLFVRN VGHLMQNPSI LIDGEEIFEG IMDAVLTTVC
AIPGIAPQNK MRNSRKGSIY IVKPKQHGPE EVAFTNELFG RVEDLLDLPR HTLKVGVMDE
ERRTSVNLDA SIMEVADRLA FINTGFLDRT GDEIHTSMEA GAMVRKADMQ TAPWKQAYEN
NNVDAGIQRG LPGKAQIGKG MWAMTELMAE MLEKKIGQPR EGANTAWVPS PTGATLHATH
YHLVDVFKVQ DELRAAGRRD SLRNILTIST APNTNWSEEE KKEEMDNNCQ SILGYVVRWV
EHGVGCSKVP DIHDIDLMED RATLRISSQM LANWIRHDVV SKEQVLESLE RMAVVVDKQN
AGDEAYRDMA PKYDASLAFQ AAKDLIFEGT KSPSGYTEPI LHARRREFKA KN

> RXA02414 (1-747, translated) 249 residues
MSYNSPYNNT NFSTTGAFQP AGGPVKPWNK PDASLNQQLK NKSRVRTGLT IAIGYVVVIW
AVHLASIVIA LLTGFNLTNF GIHPLDTSAL WGIFTSPLLH GSFSHLIGNT VPGFIFSFLI
GMSGKRVFWE VTIIAGLIGG LGTWIFGGIG TNHIGASGLI YGWLGYLIVR GIFNKDIKQF
LLGIVLAFIY SGLFWGLLPT QIGVSWQGHL FGALGGIGAG AFIASDDPAA LKAKKQQKKL
EKQQRQRGL

> RXA02435 (1-558, translated) 186 residues
VTDNLGSTSI GDAWILYAPL MDDGGFGPLR AIGGMFLHIG PGHMLLNLVL LWLLGREIER
DFGSALFTAM YFVGGIGASA AVIWMDPYSP TAGASGAIYA MMAILVGLFV LRSADIRAPL
ILIAINIAYT LMSTNVSLWG HLGGLITGAL ITWPMVKAKT QRTRWIIVLI GFAVVVAAVI
LGIDRV

> RXA02440 (1-840, translated) 280 residues
MVSHGAPGDT FWDLVRKGAE DAAQKDNVEL RYSSNPEIPE QSNLVQNAID SRVDGIAMTM
PNAQSLGPVA QKAVDAGIPV VGLNAGMNEY QDYGMTGFFG QDESVAGASA GARLAEENAQ
KVLCVIHEQG NSSQEARCGG VSEGLGKQVE TLYVNGMDLT SVNSTLQAKL AQDRSIDWVV
GLQAGVSMAI SDAADAANSE VKIATFDTNA QLMTAIRDGK IQFAIDQQPY LQGYMAVDSL
WLAHRNGTTV GGGRPVYTGP AIVDATNVDV IAEAVGEGLR

> RXA02453 (1-753, translated) 251 residues
MKSIFISGAA NGIGKAVALK FLHEGWLVGA YDLAEITYSH PNLRWGYLNV RQSESWDKAL

EDFATHTGGT IDVVDNNAGV IIEGPLQDAE EGSVDKLLAI NVNGVTLGAR AAHPYLARTP
GAQLLNMSSA SAVYGQPQIA VYSASKFYVA GLTEALNLEW RKDDIRVVDV WPLWAKTDLV
NGVKAKSLKR LGVRITPEQV AQAVWDAVHP KSRWAKGKVH HGVSKLDKAL YLMKSLSPDR
VAMCFARLIA G

> RXA02474 (1-774, translated) 258 residues
MSKVAMVTGG AQGIGRGISE KLAADGFDIA VADLPQQEEQ AAETIKLIEA AGQKAVFVGL
DVTDKANFDS AIDEAAEKLG GFDVLVNNAG IAQIKPLLEV TEEDLKQIYS VNVFSVFFGI
QAASRKFDEL GVKGKIINAA SIAAIQGFPI LSAYSTTKFA VRGLTQAAAQ ELAPKGHTVN
AYAPGIVGTG MWEQIDAELS KINGKPIGEN FKEYSSSIAL GRPSVPEDVA GLVSFLASEN
SNYITGQVML VDGGMLYN

> RXA02480 (1-849, translated) 283 residues
LSIGALSMAV WAHHMFVTGA VLLPFFSFMT FLISVPTGVK FFNWVGTMWK GHITWETPMI
WSVGFMATFL FGGLTGIMLA SPPLDFHLAD SYFLIAHFHY TLFGTVVFAS CAGVYFWFPK
MTGRMMDERL GKIHFWLTFV GFHGTFLIQH WVGNMGMPRR YADYLDSDGF TIYNQISTVF
YFLLGLSVIP FIWNVFKSWR YGELVTVDDP WGYGNSLEWA TSCPPPRHNF ASLPRIRSER
PAFELHYPHM IERMRAEAHT GHHDDINAPE LGTAPALASD SSR

> RXA02481 (1-612, translated) 204 residues
MLTGFLTPGG AADLGGPCTP HCLTQFTPQA LVLTCGLSGV GATGIGSVAS AINMLTTILC
LRAPGMTMFR MPIFTWNIFV VSVLALLIFP LLLAAALGVL YDRKLGGHLY DPANGGSLLW
QHLFWFFGHP EVYVLALPFF GIVSEIIPVF SRKPMFGLRR PDLRNLVHWC TVHGCVGSPH
VRYWRSFASV LLLHDVPDFG SYRR

> RXA02485 (1-1101, translated) 367 residues
LDSSLAQEIA AIDGVELDSE VTFADLTTLR IGGKPRSAVR CQTTEALVSA IKLLDDASLP
LLIVGGGSNL VVADGDLDVI AVIIETDDVS INLTDGLLTA DAGAVWDDVV HLSVDAGLGG
IECLSGIPGS AGATPVQNVG AYGTEVSDVL TRVQLLDRTT HQVSWVDASE LDLSYRYSNL
KFTNRAVVLA IELQLLTDGL SAPLRFGELG RRLAISEAEP HPRRPVRMVR DAVLELRRAK
GMVVEHTDHD TWSAGSFFTN PIVDPALADA VFEKVGEPTM PRFPAGDGKE KLSAAWLIER
AGFKKGHPGA GAKASLSTKH TLALTNRGDA RASDLVALAK EIRDGVLETF GVTLVPEPVW
IGISIDD

> RXA02492 (1-717, translated) 239 residues
MTNGKLILLR HGQSEWNASN QFTGWVDVNL TEQGEAEAKG VLPGVVYTSL LRRAIRTANI
ALNAADRHWI PVIRDWRLNE RHYGALQGLD KAATKEKYGD DQFMEWRRSY DTPPPELADD
AEYSQANDPR YADLDVVPRT ECLKDVVVRF VPYFEEEILP RAKKGETVLI AAHGNSLRAL
VKHLDGISDA DIAELNIPTG IPLVYEIAED GSVVNPGGTY LDPEAAAAGA AAVANQGNK

> RXA02528 (1-975, translated) 325 residues
MSAKSSLKEV AELAGVGYAT ASRALSGKGY VSPQTREKVQ AAAKELNYVP NQLAKALREH
RSALVGVIVP DLSNEYYSES LQTIQQDLKA AGYQMLVAEA NSVQAQDVVM ESLISIQAAG
IIHVPVVGSI APEGIPMVQL TRGELGPGFP RVLCDDEAGF FQLTESVLGG SGMNIAALVG
EESLSTTQER MRGISHAASI YGAEVTFHFG HYSVESGEEM AQVVFNNGLP DALIVASPRL
MAGVMRAFTR LNVRVPHDVV IGGYDDPEWY SFVGAGITTF VPPHEEMGKE AVRLLVDLIE
NPELPTGDVV LQGQVILRGS STHSG

> RXA02539 (1-1518, translated) 506 residues
MTVYANPGTE GSIVNYEKRY ENYIGGKWVP PVEGQYLENI SPVTGEVFCE VARGTAADVE
LALDAAHAAA DAWGKTSVAE RALILHRIAD RMEEHLEEIA VAETWENGKA VRETLAADIP
LAIDHFRYFA GAIRAQEDRS SQIDHNTVAY HFNEPIGVVG QIIPWNFPIL MATWKLAPAL
AAGNAIVMKP AEQTPASILY LINIIGDLIP EGVLNIVNGL GGEAGAALSG SNRIGKIAFT
GSTEVGKLIN RAASDKIIPV TLELGGKSPS IFFSDVLSQD DAFAEKAVEG FAMFALNQGE
VCTCPSRALV HESIADEFLE LGVKRVQNIK LGNPLDTETM MGAQASQEQM DKISSYLKIG
PEEGAQTLTG GKVNKVDGME NGYYIEPTVF RGTNDMRIFR EEIFGPVLSV ATFSDFDEAI
RIANDTNYGL GAGVWSRDQN TIYRAGRAIQ AGRVWVNQYH NYPAHSAFGG YKESGIGREN
HLMMLNHYQQ TKNLLVSYDP NPTGLF

> RXA02551 (1-360, translated) 120 residues
MSVCEAHNPE NYSTGGGNII GGVVSPTLAA SEWGWQVDPL GLRIVLNNYW ERWQKPLFIV
ENGLGAKDVL IDGPSGPTVN DDYRIKYLDD GGSGILKRYK KKSFDWCRDI IATNGESLES

> RXA02556 (1-1158, translated) 386 residues
LIVSTQPITD RSALSAEHAE VIKATLPLVG GKINEITPVF YNKMFAAHPE LIANTFNGGN
QKQGDQQKAL AASIATFATM LVTPDAPDPV QLLSRIGHKH VSLGITADQY DIVHEHLFAA
IVEVLGAETV TAPVAEAWDA VYWIMANVLI GFENNLYASN DLEPGDVFRE VTVTAKKQLS
ATVWEYTLAG ELVAPEPGQY TSIGVVLDDG ARQLRQYSLL GGSDTEYRIA VEDNGEVSGF
LRDRVSVGDK IEATIAAGDL VLNKDTNPVV LISQGIGSTP MVGMLAGMNP ERDVVVLHAD
QAESTYAQVE EVQGLVEKLP KAAFEIFYRD NDQWLEVAGR IPSGASVYLC GGVEFLKNVR
EQIEALDEQP RDVNFELFAP NDWLIS

> RXA02560 (1-822, translated) 274 residues
MQGNSLNLAD NSERKKPMPS PGELLAARYG QPATWTPPQW NETLDVIHQH RSVRRWLDKP
VDDDTIRTII SAAQSAGTSS NKQVISVIVV KDPELRKGLA GITRQMFPHL EQVPAVLIWL
IDYSRISAVA AREDLPTGAL DYLDEAAWGF LDAGIAAQNA AIAAESLGLG TLYLGSVRND
AEAVHKLLGL PPEIVPVVGL EMGHADPPEP AGIKPPLPQE AIVHWDTYTE KNLELIDSYD
RALDTYYSRY GQHQLWSKQT AHRAASKRCY KNQE

> RXA02572 (1-645, translated) 215 residues
AVAEICEPTG ADAVALVDAI GHDDRIGRKF LGAGLGFGGG CLPKDIRAFM ARAGELGADQ
ALTFLREVDS INMRRRDRVV QLAKEMCGGS LLGKRVTVLG AAFKPNSDDV RDSPALSVAG
SLSLQGAAVS VYDPEAMDNA RRVFPTLSYA SSTKEALIDA HLVVLATEWQ EFRDLDPEVA
GGVVEKRAII DGRNVLDVAK WKAAGWEMEA LGRNL

> RXA02596 (1-489, translated) 163 residues
PVVYTGPLDL YFNYAEGKLG WRTLDFETEV VETGDFQGTP VMNYNDADVP FTRIHEFRHF
HPERDDSYPK DKTVIMREFS RFADNEDEPY YPINTPDDRD MLKQYRLLAA EEAANNKVLF
GGRLGTYQYL DMHMAIGSAL SMFDNKLVPF FEEGTPLEQE RGH

> RXA02611 (1-1752, translated) 584 residues
DAWSDPMATW RHAITTKIEA GQGSDELYND FEHGAQLFER AAENLSKEDR TALFDVASSL
RRGGDVRARL APALTASVTH LLELNPLREL VTMGENLQVR VERRAALVNS WYELFPRSTG
GWDESGTPVH GTFATTAQAL ERVAKMGFDT VYFPPIHPIG EVNRKGRNNT LTPEPHDVGS
PWAIGSKDGG HDATHPRLGT IEDFQALLAR ARELNLEVAL DLALQAAPDH PWAQEHREFF
TVLADGTIAY AENPPKKYQD IYPINFDNDA PKIYEEVYRV VKFWVDLGVT TFRVDNPHTK
PANFWQWLIS AIHKSNPEVI FLAEASTRPA RLYFLSKIGF SQSYTYFTWK VTNEELTEFA
TEIAPMADIS RPNLFVNTPD ILHASLQHGG RAMFAIRAAL AATMSPVWGV YSGYELFEHE
AVKPGSEEYL DSEKYELRPR DFEGALERGD SLEDYIALLN QIRRANPALQ QLRNIHFHEA
DNDQIIAYSK VDALTGNTVL IVVNLDPRSA REATVRLDLG ALGLEAGAQF EVRDAITGSR
YLWSETNFVR LEPLRDVAHI FVLPELPASR RERLAWREIK TYRA

> RXA02612 (1-2193, translated) 731 residues
MTVDPASHIT IPEADLARLR HCNHHDPHGF YGWHETEAGS VIRTRQVGAT QVNLLIDDTS
HVMTPIGDDI FAIDLGHRER ADYRLEVTWP DQEPQVKADP YYFLPTVGEM DIYLFSEGRH
ERLWEILGAN IKTYQTALGT VRGTAFTVWA PNAIGCAVVG GFNGWNASQH PMRSMGGSGL
WELFIPGIEE GEVYKFAVQT REGQRRDKAD PMARRAELAP ATGSIVASSE YQWQDSEWLR
ERSQTDLASK PMSVYEVHLG SWRWGKNYED LATELVDYVA DLGYTHVEFL PVAEHPFGGS
WGYQVTGYYA PTSRWGTPDQ FRALVDAFHA RGIGVIMDWV PAHFPKDDWA LARFDGEALY
EHPDWRRGEQ KDWGTLVFDF GRNEVRNFLV ANALYWIEEF HIDGLRVDAV ASMLYLDYSR
EHGEWEPNIY GGRENLEAVQ FLQEMNATVL RLHPGALTIA EESTSWPGVT APTWDGGLGF
SLKWNMGWMH DTLEYFSKNP VHRAFHHSEL TFSLVYAFSE RFVLPISHDE VVHGKGSLWD
RMPGDTWNKA AGLRTFLAYM WSHPGKKLLF MGQEFGQREE WAEGQGLPWD IVDGWQGEYH
EAIRTLTRSL NGVYSDSPAL HTQDFTGEGF TWNKGDDATN NILAFTRFGS DGSQMLCVFN
LSGTSQPEYQ LGVAAGGEWK LVLNTDDAEF LGAENDIATS VQAAATPRDN FAYSLSLHVP
AMSAQFYSLQ K

> RXA02621 (1-819, translated) 273 residues
MSELICGPAI LFAPAGRAEI IPKAASKADM VIIDLEDGAG EVDREVAYRN IRESGLDPKR

TIVRTVGPSD PHFLADVEMV KSTDFTLVMV PKLLGSVPEE LDGLNIIAMI ETPQAATSIP
QIAADPKVVG MFWGAEDLTH LLGGTHSRFL GDESNEGSYR DTMRLTRALM HLHAAANGKF
TIDAIHADFH DEEGLYLEAV DAARTGFAGT ACIHPKQIEI VRRAYRPEAN QLEWAKKVVE
EAENHPGAFK LDGQMIDAPL ISQARMVISR QPA

> RXA02640 (1-1527, translated) 509 residues
MRISKANAYV AAIDQGTTST RCIFIDAQGK VVSSASKEHR QIFPQQGWVE HDPEEIWDNI
RSVVSQAMVS IDITPHEVAS LGVTNQRETT VVWDKHTGEP VYNAIVWQDT RTSDICLEIA
GEEGQEKWLD RTGLLINSYP SGPKIKWILD NVEGARERAE KGDLLFGTMD TWVLWNLTGG
VRGDDGDDAI HVTDVTNASR TLLMDLRTQQ WDPELCEALD IPMSMLPEIR PSVGEFRSVR
HRGTLADVPI TGVLGDQQAA LFGQGGFHEG AAKNTYGTGL FLLMNTGTSL KISEHGLLST
IAYQREGSAP VYALEGSVSM GGSLVQWLRD NLQLIPNAPA IENLAREVED NGGVHVVPAF
TGLFAPRWRP DARGVITGLT RFANRKHIAR AVLEANAFQT REVVDAMAKD AGKALESLRV
DGAMVENDLL MQMQADFLGI DVQRLEDVET TAVGVAFAAG LGSGFFKTTD EIEKLIAVKK
VWNPDMSEEE RERRYAEWNR AVEHSYDQA

> RXA02642 (1-498, translated) 166 residues
MTESKNYDLI VVGSGLFGLT VAERAASQLG KKVLIVERRS HLGGNAYSEA EPETGIEIHK
YGAHLFHTSN TRVWEYVNQF TSFTGYQHRV FAMHNGTAYQ FPMGLGLINQ FFGKYYSPDE
ARELIKEQSA EIDSSDATNL EEKAISLIGR PLYEAFIRDY TAKQWQ

> RXA02654 (1-885, translated) 295 residues
MISLLNDPRT LFPKVDPPKQ SQPEPGLDIK LSPQADIGLS SYQGSGRLKG RKALITGGDS
GIGAAVAIAY AREGADVAIA YLPEEQADAD RVLQAIEETG QKAFSFPGDL RDPEYCRSLV
QETVNALGGL DILVNNASRQ VWAPGLTEIT DENFDQTLQV NLYGSFRVTK AAIPHLKPGS
SIIFTSSIQA YQPSETLLDY AMTKAALNNL SKGLASSLIG DGIRVNSVAP GPFWTPLQPS
HGQPQEKIEG FGQHAPIGRA GHPVELAGAY VFLASDEASY VVGETLGVTG GTPTP

> RXA02666 (1-768, translated) 256 residues
MSSTRIPVIA LLAAAGRGTR LGGPIPKAFV TLRERTLLER SLQAMLTSES VDEIIILVSP
DMETYARDLL RKRGLLNDPE GVRVRLVHGG GERADSVWAG LQAISLDDAT PDAIVLIHDS
ARALTPPGMI ARVVRKVHEG ATAVIPVLPV SDTIKRVSPD GGVVVDTPNR AELRAVQTPQ
GFLLSELVAA NEKFFADPNP GFIPTDDASL MEWYGADVVC VQGDPMAFKV TTPIDMMLAQ
RITDEAEPTI FEVPGD

> RXA02675 (1-363, translated) 121 residues
ILMTGMRHEN FGIMIARGDL AVELGFDRMA EVPQLIMALA EAAHVPTILA TQVLENMAKN
GLPSRAEITD AAMALRAECV MLNKGPHIND AIKVLTEMSR KLGASQRKSR LLLRKVKSWE
E

> RXA02694 (1-942, translated) 314 residues
MKETVGNKIV LIGAGDVGVA YAYALINQGM ADHLAIIDID EKKLEGNVMD LNHGVVWADS
RTRVTKGTYA DCEDAAMVVI CAGAAQKPGE TRLQLVDKNV KIMKSIVGDV MDSGFDGIFL
VASNPVDILT YAVWKFSGLE WNRVIGSGTV LDSARFRYML GELYEVAPSS VHAYIIGEHG
DTELPVLSSA TIAGVSLSRM LDKDPELEGR LEKIFEDTRD AAYHIIDAKG STSYGIGMGL
ARITRAILQN QDVAVPVSAL LHGEYGEEDI YIGTPAVVNR RGIRRVVELE ITDHEMERFK
HSANTLREIQ KQFF

> RXA02695 (1-1422, translated) 474 residues
MNEFDQDILQ EIKTELDELI LELDEVTQTH SEAIGQVSPT HYVGARNLMH YAHLRTKDLR
GLQQRLSSVG ATRLTTTEPA VQARLKAARN VIGAFAGEGP LYPPSDVVDA FEDADEILDE
HAEILLGEPL PDTPSCIMVT LPTEAATDIE LVRGFAKSGM NLARINCAHD DETVWKQMID
NVHTVAEEVG REIRVSMDLA GPKVRTGEIA PGAEVGRARV TRDETGKVLT PAKLWITAHG
SEPVPAPESL PGRPALPIEV TPEWFDKLEI GSVINVPDTR GSRRAFTVTR VFDGAVLAEG
PQKAYISNGT LLEHNYDRSR VYGIPAVVQR INLKVGDRLI LTDEELTYDP SLGSGRTPRI
SCTLPQAVDA IKVGHRVLFD DGAIAAVCID KTSTADGHND VELEVTHARP QGVNLAAYKG
INLPDSELPL PSLTEEDLQH LRFVVKYADI AAISFIRNVA DVEYLLQALA DIGD

> RXA02729 (1-744, translated) 248 residues

MDSPMSNSTG TDIVVVGSIN ADLTAKVQRH PEPGETLLGS GGTVSAGGKG ANQAVAAAQL
GAKVTMIGAV GTDQMAGEAL THLRQSGADM SAIATVDGPT GLAIITVSDD GENTIIVIPG
ANASVTAEFV DKHSQLIENA GIVLLQGEIP ADGFERAVDL SQGRVVINLA PVVPVGHDQL
RRADPLLVNE HEGALVLDML GTPATTSDPQ SLVTELLEQG FTSVVMTLGA EGALVGTPGQ
LTAIPTPK

> RXA02730 (1-1038, translated) 346 residues
MATEKFRPTL KDVARQAGVS IATASRALAD NPAVAASTRE RIQQLASDLG YRANAQARAL
RSSRSNTIGV IVPSLINHYF AAMVTEIQST ASKAGLATII TNSNEDATTM SGSLEFLTSH
GVDGIICVPN EECANQLEDL QKQGMPVVLV DRELPGDSTI PTATSNPQPG IAAAVELLAH
NNALPIGYLS GPMDTSTGRE RLEDFKAACA NSKIGEQLVF LGGYEQSVGF EGATKLLDQG
AKTLFAGDSM MTIGVIEACH KAGLVIGKDV SVIGFDTHPL FALQPHPLTV IDQNVEQLAQ
RAVSILTELI AGTVPSVTKT TIPTALIHRE SIINSTLRKK DGLPNE

> RXA02737 (1-1542, translated) 514 residues
VSTNTTPSSW TNPLRDPQDK RLPRIAGPSG MVIFGVTGDL ARKKLLPAIY DLANRGLLPP
GFSLVGYGRR EWSKEDFEKY VRDAASAGAR TEFRENVWER LAEGMEFVRG NFDDDAAFDN
LAATLKRIDK TRGTAGNWAY YLSIPPDSFT AVCHQLERSG MAESTEEAWR RVIIEKPFGH
NLESAHELNQ LVNAVFPESS VFRIDHYLGK ETVQNILALR FANQLFEPLW NSNYVDHVQI
TMAEDIGLGG RAGYYDGIGA ARDVIQNHLI QLLALVAMEE PISFVPAQLQ AEKIKVLSAT
KPCYPLDKTS ARGQYAAGWQ GSELVKGLRE EDGFNPESTT ETFAACTLEI TSRRWAGVPF
YLRTGKRLGR RVTEIAVVFK DAPHQPFDGD MTVSLGQNAI VIRVQPDEGV LIRFGSKVPG
SAMEVRDVNM DFSYSESFTE ESPEAYERLI LDALLDESSL FPTNEEVELS WKILDPILEA
WDADGEPEDY PAGTWGPKSA DEMLSRNGHT WRRP

> RXA02738 (1-1080, translated) 360 residues
MSHIDDLAQL GTSTWLDDLS RERITSGNLS QVIEEKSVVG VTTNPAIFAA AMSKGDSYDA
QIAELKAAGA SVDQAVYAMS IDDVRNACDL FTGIFESSNG YDGRVSIEVD PRISADRDAT
LAQAKELWAK VDRPNVMIKI PATPGSLPAI TDALAEGISV NVTLIFSVAR YREVIAAFIE
GIKQAAANGH DVSKIHSVAS FFVSRVDVEI DKRLEAIGSD EALALRGKAG VANAQRAYAV
YKELFDAAEL PEGANTQRPL WASTGVKNPA YAATLYVSEL AGPNTVNTMP EGTIDAVLEQ
GNLHGDTLSN SAAEADAVFS QLEALGVDLA DVFQVLETEG VDKFVASWSE LLESMEARLK

> RXA02739 (1-2100, translated) 700 residues
LTTLTLSPEL QALTVRNYPS DWSDVDTKAV DTVRVLAADA VENCGSGHPG TAMSLAPLAY
TLYQRVMNVD PQDTNWAGRD RFVLSCGHSS LTQYIQLYLG GFGLEMDDLK ALRTWDSLTP
GHPEYRHTKG VEITTGPLGQ GLASAVGMAM AARRERGLFD PTAAEGESPF DHHIYVIASD
GDLQEGVTSE ASSIAGTQQL GNLIVFWDDN RISIEDNTEI AFNEDVVARY KAYGWQTIEV
EAGEDVAAIE AAVAEAKKDT KRPTFIRVRT IIGFPAPTMM NTGAVHGAAL GAAEVAATKT
ELGFDPEAHF AIDDEVIAHT RSLAERAAQK KAAWQVKFDE WAAANPENKA LFDRLNSREL
PAGYADELPT WDADEKGVAT RKASEAALQA LGKTLPELWG GSADLAGSNN TVIKGSPSFG
PESISTETWS AEPYGRNLHF GIREHAMGSI LNGISLHGGT RPYGGTFLIF SDYMRPAVRL
AALMETDAYY VWTHDSIGLG EDGPTHQPVE TLAALRAIPG LSVLRPADAN ETAQAWAAAL
EYKEGPKGLA LTRQNVPVLE GTKEKAAEGV RRGGYVLVEG SKETPDVILM GSGSEVQLAV
NAAKALEAEG VAARVVSVPC MDWFQEQDAE YIESVLPAAV TARVSVEAGI AMPWYRFLGT
QGRAVSLEHF GASADYQTLF EKFGITTDAV VAAAKDSING

> RXA02740 (1-930, translated) 310 residues
LDTIKAYIAL TKPRVIELLL VATIPTMLQA ERGENNIVLI LLTVFGGWMG AAAANTFNMV
ADSDIDQRMG RTRARPLVRH TVSNRDASIF AWVLTVASFL WLWLLCDSML AGIFVLITIF
FYIFVYTKWL KRRTHMNIVW GGAAGCMPVL VGWAVIVDQF EPGVPQQWWQ AIVLFMVIFF
WTPPHTWALA MKYREDYKAA GVPMLPVVRT PVQVTAQIVW YSVATVLTTF LLIPATGWIY
AAIAVISGVT FLFMAIKLHL GIKNGGKVKP LKLFILSNNY LAVLFVALSV DAVLGLETIG
EMLGWTTTFF

> RXA02741 (1-966, translated) 322 residues
MKAILVSRTG GPEVLEFTDT DAPKPTDDQV LVEVDMAGVN FIDTYYRQGE YHARLPFIPG
FEGTGRVLED PQGLIAAGTK VAWCDAMGSY AQQVCVPRDR LVAVPEGVSS EVAASMLMQG
ITAHYLTNGV YELEEGDSCL ITAGAGGVGL LATQMAAAKG VRVYSVVSTD EKAELALDAG
AYEVFRYSDN LAEQVRRHNG GRGVDVVYDG VGQSTFNESL EAVRPRGTVC LFGAASGPVE

PFDPQLLNTH GSIFLTRPSI GAWTSEEGEF AKRAQAVTQA IVEGTLRVRV TGTYSLADAY
IAHRDLQARS TSGSLVLEIP KD

> RXA02743 (1-1038, translated) 346 residues
VSTSDAPSNN PVELKPITFW APTIKVQRIL ALLLLIFQGG ITVTGSIVRV TGSGLGCDTW
PLCHEGSLVP VAGAAPWIHQ AVEFGNRMLT FVLAAAALAL FIAVLGAKRR REILVHSFIQ
GLGIILQAVI GGITVLVDLH WYAVALHFLP SMILVFMAAI LYTRIGEPDD GEITTTFPTW
IRNVAVIGAV ALSVVLITGT MTTGAGVHSG DASITMDDRL DVSIDLMAHI HGYSMYIYLF
FTLIVVAGLY KAKTTKHNKQ LGLMLILFIL IQAGIGILQY RMGVPRWSIP FHIAMSSVVV
AFTSLLWAQG RIRVGGKATV TGSVDGDIKN EIITNPFEKK SKQPVK

> RXA02797 (1-903, translated) 301 residues
MNNRIVVVGS INADLNVLVD RHPAPGETLL GSGGHITAGG KGANQAVAAA LQGADVAFVG
AVGKDPYAAP ALEFLRSSGV DLTAVSEVDD TTGLAVITVA KDGENNIVVI PGANSLVNCD
YVSSQSALLA EAGILLLQGE IPADGFKEAI HHTMGRVVVN LAPVIEVEKS ALLEADPIIA
NEHEAGLILD QFGAGIDSMD PHELAQALLD AGFASVVLTL GSAGALVADA TGITDIATPT
VQAVDTTGAG DAFAGAFCAR LIKGDSLIDA ATHAARVGAY SVQTAGAQAS YPDASVSLPS
V

> RXA02803 (1-399, translated) 133 residues
SGEMLAAALS AGMASQGVDV IRVGVIPTPA VAFLTDDYGA DMGVMISASH NPMPDNGIKF
FSAGGHKLPD HVEDEIERVM DSLPAEGPTG HGVGRVIEEA TDAQDRYLEH LKEAVPTSLE
GIKIVVDAAN GAA

> RXA02807 (1-465, translated) 155 residues
MAHSYAEQLI DTLEAQGVKR IYGLVGDSLN PIVDAVRQSD IEWVHVRNEE AAAFAAGAES
LITGELAVCA ASCGPGNTHL IQGLYDSHRN GAKVLAIASH IPSAQIGSTF FQETHPEILF
KECSGYCEMV NGGEQGERIL HHAIQSTMAG KGVSV

> RXA02821 (1-180, translated) 60 residues
VGYGIATIGP GLGIGILVGK ALEGMARQPE MAGQLRTTMF LGIAFVEALA LIGLVAGFLF

> RXA02829 (1-276, translated) 92 residues
MQKNILKSGI EISELGLGCM SLGTDYKKAQ PIIESAIDNG ITYFDTADIY DQGVNEEIVG
KALKKYQNRD DIVIGTKVGN RLTDDGHMTW GS

> RXA02852 (1-279, translated) 93 residues
VAVSDFSTDL PNQIREWVPG DYTVLGADGF GFSDTRPAAR RFFNIDAESI VVAVLNSLAR
EGKIDVSVAA QAAEKFKLDD PTSVSVDPNA PEE

> RXA02853 (1-1407, translated) 469 residues
MAKRIVIIGG GPAGYEAALA GAKYGAEVTV IEDVGVGGSA VTMDCVPSKS FIAGTGIKTD
LRRADDMGLN RGLGKAHLEI DALNIRVKDL AKAQSEDILG QLQRSDVRMI NGVGRFDDYN
TKQTTHYIKV THSDGSEETV ECDLVLVATG ATPRILKGAE PDGERILTWR QVYDIEELPT
HLIVVGSGVT GAEFVSAFAE LGVKVTMVAS RDRILPHDDA DAADVLETVL AERGVSLEKH
ARVESVTRTE DGGVCVRTAD GREIYGSHAL MTVGSIPNTA DLGLENIGVE LAPSGHIKVD
XVSRTNIPGV YAAGDCTDLF PLASVAAMQG RIAMYHALGE GVSPIRLKTV ATAVFTRPEI
AAVGITHAQV DSGEVSARVI VLPLATNPRA KMRSLRHGFV KLFCRRNSGL IIGGVVVAPT
ASELILPIAV AVTNRLTVAD LADTFAVYPS LSGSITEAAR QLVQHDDLG

> RXA02854 (1-1584, translated) 528 residues
MDESRQLSFG TAGLRAPVGP ARHQMNVLQV TRTTAGVASW LAERAALNPV PHLVPEDETG
IGRALYPQDG PLRVVVGYDA RYGSHTFAAT TAEVFAGAGF EVTLLPTPSP TPLIPWLVNK
HGLDAGVQIT ASHNGAADNG YKVFLSNGRQ LYSELEPELE AHINAVEDPI RVPRVTVRPT
ADQLRRYVDE MVSLVTPDQA DLLRVNSERG NLRVVYTALH GVGGRAMANA FQFAGFPHTH
GVKAQQYPDP TFPTVAFPNP EEPSAIELLL ERAKEKNADI LFALDPDADR CAVGIRTADG
GHRMLSGDEV GTLLATRLVP EYSGEGPRPV VATTVVSSQL LGIIAEDKGW DYSETLTGFK
NLSRAADGLD GPLAFAYEEA VGTCPVPDVV PDKDGISTAL FMASWAAELK AQGASLQQKL
NELYRRYGYF ASSQIAVRTS SPRELVDHWI AHPQQELIGV SVTPHILPEK QGIALHGQVG

HVHIRAIGRV SGTEAKAKLY LEVGQASSHD EAAQLLHQLE DEVQSWLS

> RXA02872 (1-672, translated) 224 residues
AREAWRIFMS HWDLYAGTAT GYWVEQEFEH VFGINAERLN VGTPEHADAI FDELTDILAK
PDFRPRALAE QFNLEVLATT DDPLDDLADH KALADDPTFS PRVLPTFRPD AYTKMYNAGW
AEKTTKLIDT AGDGKAGWEG YLQAMRNRRQ YFINHGATSA DHGLHDTDTT PLSHKDAQKI
LDKGLAGTAT LAEMHAFEAN TTYRFAEMSQ EDGLVMTIHP GVYR

> RXA02873 (1-510, translated) 170 residues
FGENKDLISD SSFNRWLRTV SLGSTQDADM AAASNLAANS KMARQNTRDI LDAVSDGGVM
LGRNGALVLG PVVGTLHIKF IAPLNKRVER VMYKTGLSEA AAAEQCALED RLREEMAHAL
YQWNPGRDEN YDLVINTGSM TYEQIVDLVV ETYARKYPLH VRIIPNGKDQ

> RXA02887 (1-408, translated) 136 residues
MADQAKLGGK PSDDSNFAMI RDGVASYLND SDPEETNEWM DSLDGLLQES SPERARYLML
RLLERASAKR VSLPPMTSTD YVNTIPTSME PEFPGDEEME KRYRRWIRWN AAIMVHRAQR
PGIGVGGHIS TYAGAA

> RXA02897 (1-1287, translated) 429 residues
DLDGFRQEVS REQGGIPSYP HPHGMKDFWE FPTVSMGLGP MDAIYQARFN RYLENRGIKD
TSDQHVWAFL GDGEMDEPES RGLIQQAALN NLDNLTFVVN CNLQRLDGPV RGNTKIIQEL
ESFFRGAGWS VIKVVWGREW DELLEKDQDG ALVEIMNNTS DGDYQTFKAN DGAYVREHFF
GRDPRTAKLV ENMTDEEIWK LPRGGHDYRK VYAAYKRALE TKDRPTVILA HTIKGYGLGH
NFEGRNATHQ MKKLTLDDLK LFRDKQGIPI TDEQLEKDPY LPPYYHPGED APEIKYMKER
RAALGGYLPE RRENYDPIQV PPLDKLRSVR KGSGKQQIAT TMATVRTFKE LMRDKGLADR
LVPIIPDEAR TFGLDSWFPT LKIYNPHGQN YVPVDHDLML SYREAPEGQI LHEGINEAGS
VASFIAAGT

> RXA02902 (1-672, translated) 224 residues
LASDLGIKFV AVVDKDLETA EKFATGLGAA GDSSESSVKA HGSLPALFSK KKIDVLHITT
PHDQHIGLAL EALHHGVNVI LEKPLANELD QAQRLIDYLD ENPDGPKIAV CYQNRYNVSS
QELRRLLDSG DLGAINGAYS SVVWTRTPGY YTQKPWRGQQ AHSGGGLLMN QAIHTLDLLQ
WFLGKATEVK GTVSTDKYAD VIDVEDTAHA YIGHESGVHT SEVS

>RXN00013 TRANSLATE of: rxn00013.seq check: 4426 from: 1 to: 873
MEGMTNPEQTHPAASLEDMIKTITKTFVIAHDQDSDEHLAQALVYNAGRLAWRMRENGVD
TDYKTSVSDVVTDADRAAEAFVAGVLEALRPEDGVLGEEGADRASKSGKTWVIDPVDGTY
NFTQGSDYWCSALALVEGDPSAPSRVLFGAVHRPAMGYTWFGGPGIRTTLDGKELDLLVD
APLNQISLATYIHPSRIAEPDIQKAWMSVATHPATLRMFGAGSIDLANIADGSMGAWVQH
SVADWDWLPGRALIEGVGGACIKVTAGGVEWSVAGNAEAVSEISETLSALD

>RXN00014 TRANSLATE of: rxn00014.seq check: 1159 from: 1 to: 780
MSKYADDLALALELAELADSITLDRFEASDLEVSSKPDMTPVSDADLATEEALREKIATA
RPADSILGEEFGGDVEFSGRQWIIDPIDGTKNYVRGVPVWATLIALLDNGKPVAGVISAP
ALARRWWASEGAGAWRTFNGSSPRKLSVSQVSKLDDASLSFSSLSGWAERDLRDQFVSLT
DTTWRLRGYGDFFSYCLVAEGAVDIAAEPEVSLWDLAPLSILVTEAGGKFTSLAGVDGPH
GGDAVATNGILHDETLDRLK

>RXN00043 TRANSLATE of: rxn00043.seq check: 5115 from: 1 to: 1164
MAEVVHYQENAGQAVKKIEGRIVTPHGVIDGFLQLENGIITELSGEPAPKNAGFHPELPT
IVPSFIDLHNHGGNGGAFPTGTQDQARNAAQYHREHGTTVMLASMVSAPADALAAQVENL
IPLCEEGLLCGIHLEGPFINACRCGAQNPDFIFPGNPTDLAQVIHAGKGWIKSITVAPET
DNLTELLDLCAAHHIIASFGHTDADFDTTTSAIALAKEKNVTVTATHLFNAMPPLHHRDP
GSVGALLAAARAGDAYVELIADGVHLADGTVDLARSNNAFFITDAMEAAGMPDGEYILGV
LNVTVTDGVARLRDGGAIAGGTSTLASQFVHHVRRGMTLIDATLHTSTVAAKILGLSDHE
IVKSNPVNFVVFDSNGQLQQVHLDHQVI

>RXN00148 TRANSLATE of: rxn00148.seq check: 5482 from: 1 to: 2211
MTSIPNFSDIPLTAETRASESHNVDAGKVWNTPEGIDVKRVFTQADRDEAQAAGHPVDSL
PGQKPFMRGPYPTMYTNQPWTIRQYAGFSTAAESNAFYRRNLAAGQKGLSVAFDLATHRG

YDSDNERVVGDVGMAGVAIDSILDMRQLFDGIDLSSVSVSMTMNGAVLPILAFYIVAAEE
QGVGPEQLAGTIQNDILKEFMVRNTYIYPPKPSMRIISNIFEYTSLKMPRFNSISISGYH
IQEAGATADLELAYTLADGIEYIRAGKEVGLDVDKFAPRLSFFWGISMYTFMEIAKLRAG
RLLWSELVAKFDPKNAKSQSLRTHSQTSGWSLTAQDVYNNVARTAIEAMAATQGHTQSLH
TNALDEALALPTDFSARIARNTQLLLQQESGTVRPVDPWAGSYYVEWLTNELANRARKHI
DEVEEAGGMAQATAQGIPKLRIEESAARTQARIDSGRQALIGVNRYVAEEDEEIEVLKVD
NTKVRAEQLAKLAQLKAERNDAEVKAALDALTAAARNEHKEPGDLDQNLLKLAVDAARAK
ATIGEISDALEVVFGRHEAEIRTLSGVYKDEVGKEGTVSNVERAIALADAFEAEEGRRPR
IFIAKMGQDGHDRGQKVVASAYADLGMDVDVGPLFQTPAEAARAAVDADVHVVGMSSLAA
GHLTLLPELKKELAALGRDDILVTVGGVIPPGDFQDLYDMGAAAIYPSGTVIAESAIDLI
TRLAAHLGFDLDVDVNE

>RXN00200 TRANSLATE of: rxn00200.seq check: 5263 from: 1 to: 3438
MRQVGGNGGHQLDSINVSDVVESKKLKGSAQEPPQVAPGWLKKLAISSGLLGLLMFVLLP
FLPVNQVQSSLSWPQNGELSSVNAPLISYAPQSMDASIPVSALDSLNDNQSLVMGTLPLD
STDATNRGLFVRTIDGNLDVIVRGEVLLDLSPTEVNRLPDDAILEISSTEETTSAEITGT
AFSGETEGDERPQVTGVYTELVDDPSTASALASAGLNVDIEINSRFTSSPSLLKYAAIFI
GLASVLVSLWTLHRMDILDGRKAHRFLPANWYKLKPLDGVVVAILVFWHFLGANTSDDGF
IMTMARVSQNADYMANYYRWFGVPESPFGAPYYDLLALMAYISTSSIWLRLPALLAGLIM
WFVITREVMPRFGSLVNGRRVAHWSAAMVFLAFWLPYNNGTRPEPIIAMGALLAWVSFER
AIATSRLLPAAIGVIIATISLASGPTGLMAVAALLVSLSALIRILYRRLPLIGASRGASK
SKVFGASMAMLAPFLASGTAILIAVFGDQTLSTVMESISVRSAKGPALTWYHEYVRYQTV
MEQTVDGSFTRRFAVLMLMACLAIVVIAILRYGRIPGAAKGPSLRLMMVIFGTMFFMMFT
PTKWTHHFGVYAGLAGALAGLAAVGLSYVAVKSPRMRTISIGAFLFLLALALAGVNGFWY
TSSYAVPWWDKTIQIKGIEASTVVLVIAVIVLIIGVIQSFVHDVKTAQAETNHSMGELVA
EDEAKRERASRFTGLAASPIAGVSALVVLITCASMGKGFVDQYPAYSVGLGNLRSLTGNT
CGLASDAMLETNSNDSFLTPVNSTLGESLESEDIRGFSAAGIPPSISQDQADLSAVGAIA
NTDDSTETGGSDESSGQSTGNTGGVRGSEGINGSNARLPFNLDYTQVPVVGSWSAGTQNP
ANITTDWYEIPEATEEAPIIVVSAAGRIEHYDINGVRQSGQSVMLEYGRLRDNGDVEDLG
EAMMYDIGPEPSWRNLRYPLDQLPEEADVVRIVATDVNLDEDQWVALTPPRVPNLDSLNN
VIGSETPGLLDWAVGLQFPCQRTFDHYAGVTEIPEYRISPDHGGKSTLSPFQDWAGGGSM
GTAEAVNNAYEIPSYLRNDWGRDWGSIERYSLRTNSNGDAPKVADINLETIQRSGLWNPG
HMKVDE

>RXN00231 TRANSLATE of: rxn00231.seq check: 1223 from: 1 to: 1470
MTINVFELLVKSPTGLLIGDSWVEASDGGTFDVENPATGETIATLASATSEDALAALDAA
CAVQAEWARMPARERSNILRRGFELVAERAEEFATLMTLEMGKPLAEARGEVTYGNEFLR
WFSEEAVRLYGRYGTTPEGNLRMLTALKPVGPCLLITPWNFPLAMATRKVAPAIAAGCVM
VLKPARLTPLTSQYFAQTMLDAGLPAGVLNVVSGASASAISNPIMEDDRLRKVSFTGSTP
VGQQLLKKAADKVLRTSMELGGNAPFIVFEDADLDLAIEGAMGAKMRNIGEACTAANRFL
VHESVADEFGRRFAARLEEQVLGNGLDEGVTVGPLVEEKARDSVASLVDAAVAEGATVLT
GGKAGTGAGYFYEPTVLTGVSTDAAILNEEIFGPVAPIVTFQTEEEALRLANSTEYGLAS
YVFTQDTSRIFRVSDGLEFGLVGVNSGVISNAAAPFGGVKQSGMGREGGLEGIEEYTSVQ
YIGIRDPYAG

>RXN00296 TRANSLATE of: rxn00296.seq check: 2905 from: 1 to: 2844
MTHTIKFNRLDPEVFSQHSRAKLRTDMTTRAAYSSDAGIFRRVPAAVAEPENVEQIRDAI
AVAVARGWSVVGRGGGSSVAGNAIGEGLIIDTSRYFNRILDIDPVAQTAVVEPGVVCDAL
RDAAAEFGLTYGPDPSTHSRCTIGGMVANNACGSHSVAFGTAAENLVDVTLMLSDGREVT
VTKDGCDDAEINQKLTDLASKNQDLISKELGRFPRQVSGYGLHYLAHDMAKAMAGTEGTI
GIITRLTVKLVPTPKVKALAVLAFDTVFDAARAAAKLRLPGVATIEGMGGDLLAALRSKQ
GQSEAGQNLPGNRIGIEAGGWLYCETGSDTLQAAVQAAEEVATAVDTIDYVVVSEPSEMR
ELWRIRESSAGIVTRLADGGEAWPNWEDSAVPPENLADYLRDLYALMDKFDYQGIPFGHF
GEGCVHVRISFDFSTKEGLKKFEAFMNEASTLVASYGGSLSGEHGDGRARSSFLDRMYSA
EMRALFEEFKLIFDPQRIFNPGVLVWADPVMQGLRMDPGQRALDITPVHKFSKDKGSMIN
AVNRCVGVSACRSESDAMCPSFQITGDEVHSTRGRARLLSEMFRGESIADGYRSEEVNEA
LDLCLSCKACASECPVNVDMSTYKAEFLDKHYAGRLRPMAHYVMGWLPLLGHVAHKIPLL
PTLIDATMQSALTAPVVRKVGGLADRPLISFAHRSLRKYKPKKNSGETVVLWPDSFNTNL
DTGPAHAAIKTLEALGYNVVIPDGFVCCGLTWHSTGQLSMTKKVLEQTAKVMKPYLDQGL
TVVGLEPSCTVMLQDEATELSDNPDLARLAALTKPFAEVIAPKITELVESGSLQLTESTA
LTQVHCHERSLGDPQQSALVLEALGVKDEQIATGCCGLAGNWGFEKDHAEMSFALGEREL

FPKVRKAEGHVIADGFSCRTQIEQGTGKQATHLAEVVLSILEQNNMAQ

>RXN00310 TRANSLATE of: rxn00310.seq check: 2380 from: 1 to: 435
MSDKIWKVGIIGCGAISRNHIEAVQAIPGAEVSAVCDVDGAKASETAAKYGISPSFTSVD
EILASGVDIVAVCTPHPTHETVVLAAAAAGVHVLCEKPIAIELDSAQRMIDACESAGVQL
GVLFQRRFWPAAQKMKKEPSWANAR

>RXN00316 TRANSLATE of: rxn00316.seq check: 4820 from: 1 to: 1146
MGQCTVALYREHSYYTATPWRGTWAADGGGVLMTQAIHYIDLLYWLLGEPVEVFGYTNSF
KHGDNIEVEDSAVATVRFESGALATISATTAAEPALGAQVQVMGTKGATMTILEFPEGTD
GRLIVRSENDTRRNHPIPPRGSLSQCRSFHHQRCFDPVSHRPDRRLYRCAQRRPPTTDHR
PRCHQSSESSPWCLRISSHPPAGLFDLTEAFKTSRQIGLAPLSSLSTPPDQLVRLAAATG
FSFVGLRVIAVTPNERVYDLSPGSPLLAATQQALKETALYVLDTEFLQVNADTTREAWLP
ALEAAGALGAKTFTIAAGDDNIAPLTDTIGAMVDDARDFGVTPALEPISYRSVHSIPQAA
AIARDSGGKVVADTLHMARFGA

>RXN00317 TRANSLATE of: rxn00317.seq check: 4403 from: 1 to: 654
VTTPSKKTLLFDLDGTLVDSFPGIRTSFLHTLHEKNWEIPSEERISQVPGPPMEWTFQDL
GMTPEQAQDALQTYLEHYGQVGWDLSEAFPGMRDLLIRLKYEGFRLCTATSKGEFFAEKV
LRKFEMFDLFEFMGAATDSGNRRSKSAVIKHVLDSVGLDEPNDILMIGDRSHDIEGSSEF
GIDCVAVTWGYGSKTEWDAARYTVSTAEELERIIHDWA

>RXN00337 TRANSLATE of: rxn00337.seq check: 9748 from: 1 to: 1050
MLLTYAFVDVEGGVEKHSLSTADIAARAHAHMKSHDVLGRQTTPPQPEGGVAARLGGIAW
TMIHKQMLSRDTKGLDITVLSTIPEGVGLGENSAMDVALALALYRENIEEAPTKARIAEI
CSQSAFMFSETSVLRARHTVALRGETGQISVVDYADGSVTQAPHPVSRSAGLSAFVVAAQ
TETDPSIYREIYARHAFIDEAARAFSVESLRLLPDASTRVVDWLQAVIEVTGREDLPSIE
QAQRWLNLWENETRRAQRTANALRSRRLSEFSELLMESQDDLSDTFDFPPADLALARLCV
ERGATAARSTSARGVIALVDAHHAHNFAADLSEDGLLVVPLGHGDVAEQG

>RXN00387 TRANSLATE of: rxn00387.seq check: 3252 from: 1 to: 855
MFRSNISYAVGDDIQNDPETWEDYELRVNHPLRIEGDRVYLQGHGFAPTFTVTWPNGETR
TQTVQWRPDDPTFFLSSGVVRFDPPAGMYPDLYERRQNQLAIQGLFAPTAEWEGDNNELL
TSSYPAMRDPAVAIDIYRGDNGLDTGIGQSLFSLDSSLMHSGVLQKIERVNLQIGDTVTL
DDGTTVSFDGASEFANYQISRDPTQNWVLVTTVISLVSLVGSLMIRRRRIWVRFYPQENG
TTRVETGGLARTDRAGWGGEYEKFHRELLGLKEEDEDEEYFDHDD

>RXN00388 TRANSLATE of: rxn00388.seq check: 9749 from: 1 to: 1011
MLPVNQTYAQFSDTAFVSAYIIYVLALILSLVYYVKQQGIIDARREQTRVSELVGAGGSA
DVDTDLPDDIADGVLADEDLAKREETARKLANMTQSLMWLGVMVHLVSVVMRALSASRFP
FGNLYEYILMVTLFAMIGAVLILQRPQFRVVWPWILTPMLALLFYGGTQLYSDAAPVVPA
LQSFWFPIHVSSVSIGASIGIVSGIASLLYILRMWQPKGKEKGFFGAVAKPLPSGKTLDN
LAYKTAIWTVPIFGLGIILGAIWAEAAWGRFWGWDPKETVSFITWVLYAGYLHARATAGW
RNTNAAWINILALVTMIFNLFFINMVVSGLHSYAGLN

>RXN00389 TRANSLATE of: rxn00389.seq check: 9029 from: 1 to: 1560
MITATALHGCSLIDGEWVAGKNGEITGFDPRTNASLNPSYSLANSAQLRAATTSAKRAFE
SYRLTTPEVRADFLDSIADNIDALSGEIVQRASLETGLGTTRLTGEVARTSNQLRLFAET
VRSGQFHRVRIERGPRIDLRQRQVPLGPVAVFGASNFPVAFSTAGGDTASALAAGCPVVF
KAHNAHPGTAELVGQAVRGAVEKHEFDAGVFNLVYGRGVEIGQELAADPNITAIGFTGSR
QGGLALSQTAFSRPVPVPVFAEMSATNPVFVFPGALADLDASSSLAEAFTASVTGSSGQL
CTKPGLVFIPRGVVGDAFVALVAAKFKETTGQTMLTQGIAQAWQRGVDNLAAQPSVKILA
QGTPGDGENAPGPVVFESDVQALLNNVVLQEEIFGAASLVVRYDSPDQLHQVANSLEGQL
TATIHASQDDFQEVSKLIPLLEDLAGRVLYGGWPTGVEVGHTVIHGGPYPATSNAQSTSV
GTLAIERFMRPVSYQTFPAELLPDPVSEANKWAVPREIDR

>RXN00401 TRANSLATE of: rxn00401.seq check: 9893 from: 1 to: 939
MARFSPQDLADHLKDGLLSFPATAFQDDLEVDEAAYVEHIEWQSSYPVAGLFAAGGTGEG
FSLTVEENHRVTQLAVQASSPEVPVLGSATGSTKSAIANAQGAEAAGAEGVLLLPPYLTE
CDAEGLYNHAAAVCESTSLGVIVYNRANAIYSPEVIARLSERYPNFIGFKDGTGNIEHLA
KITTLCGDRLFYLGGLPTAETFALPLLQMGMSTYSSAMFNFIPDFALSFYADVRAQDSAA

VKQKLSDFVLPYLDIRDRAQGYGVSIGKGGLKAVGRNAGGVRPPLRNLSEQDIADLSDLL
ATSGAGSYRLQLR

>RXN00427 TRANSLATE of: rxn00427.seq check: 2014 from: 1 to: 786
MGRILVFYSVTLEVAGDRPVYTPSRTNLGDGGGFAFGFLTALALGANAVWCTDDDGRPEG
PGVLKTLIDAASRHNLEEVSPVVCNADDPERLAFPLRRGLEWRRMRSELIDPANPEDDLL
PGIASLFNGALISAYAMERIGVPDYRLFIRGDEVEYHRRLVRSGLPFGTCLTTAYLHPDG
SDEFKPILGGRMHTQYPDNDFKRFFTYRNRGYLMSQPGMRKLLPQEYARFAWFFLVQKRD
VKGFREWLRLHKLGRDEKFNRP

>RXN00483 TRANSLATE of: rxn00483.seq check: 5018 from: 1 to: 1464
VLVTGATGYIGGRLITELLAAGFQVRATSRKKTSLQRFDWYEDVEAVEADLTDATELDTL
FKDVDVVYYLVHSMGGKNVDFEEQEQRTAENVIQAADQAGIKQIVYLSGLHPRNRKIEEL
SKHMRSREKVAQILLAGQTPALILRAATIIGSGSASFEIIRHLTERLPRMIAPQWITNQI
EPLAIRDVLHYLISAADLKDPVNRSCDIGCGKSYEFADLLRIYADVRGLKRHVNSVPLNL
PMDKLSGLWISLVTPVPFQLSFPLAQSMAEDAVTEEHSIKDIISDPPDGFIEYREAVELA
LAAEFDRGVPTSWDRSWTVQQPWAGQPTDPEWAGKAVYEDVRTEDTDLRAAQVWPIIEGL
GGVNGWYSAPLLWRLRGIADRLIGGPGLGGRRDPRHLKLGDRIDWWRVTEIDPPHRLVLT
AEMKVDGGAWLILEVADKENGGCTYTQRAIFEPKGLPGYLYWWVVSPFHAIIFPYMRSNI
LKAARKLT

>RXN00519 TRANSLATE of: rxn00519.seq check: 5871 from: 1 to: 2214
MAKIIWTRTDEAPLLATYSLKPVVEAFAATAGIEVETRDISLAGRILAQFPERLTEDQKV
GNALAELGELAKTPEANIIKLPNISASVPQLKAAIKELQDQGYDIPELPDNATTDEEKDI
LARYNAVKGSAVNPVLREGNSDRRAPIAVKNFVKKFPHRMGEWSADSKTNVATMDANDFR
HNEKSIILDAADEVQIKHIAADGTETILKDSLKLLEGEVLDGTVLSAKALDAFLLEQVAR
AKAEGILFSAHLKATMMKVSDPIIFGHVVRAYFADVFAQYGEQLLAAGLNGENGLAAILS
GLESLDNGEEIKAAFEKGLEDGPDLAMVNSARGITNLHVPSDVIVDASMPAMIRTSGHMW
NKDDQEQDTLAIIPDSSYAGVYQTVIEDCRKNGAFDPTTMGTVPNVGLMAQKAEEYGSHD
KTFRIEADGVVQVVSSNGDVLIEHDVEANDIWRACQVKDAPIQDWVKLAVTRSRLSGMPA
VFWLDPERAHDRNLASLVEKYLADHDTEGLDIQILSPVEATQLSIDRIRRGEDTISVTGN
VLRDYNTDLFPILELGTSAKMLSVVPLMAGGGLFETGAGGSAPKHVQQVQEENHLRWDSL
GEFLALAESFRHELNNNGNTKAGVLADALDKATEKLLNEEKSPSRKVGEIDNRGSHFWLT
KFWADELAAQTEDADLAATFAPVAEALNTGAADIDAALLAVQGGATDLGGYYSPNEEKLT
NIMRPVAQFNEIVDALKK

>RXN00528 TRANSLATE of: rxn00528.seq check: 9827 from: 1 to: 1089
MSTSTIRVAIAGVGNCATSLIQGVEYYRNADPSETVPGLMHVKFGDYHVGDIEFVAAFDV
DAEKVGIDLADATEASQNCTIKIADVPQTGINVLRGPTLDGLGDHYRATIDESTAEPVDV
VQALIDAKADVLVSYLPVGSEEADKFYAQAAIDAGCAFVNALPVFIASDPEWAKKFTDAG
IPIVGDDIKSQIGATITHRVLARLFEERGVRVDRTMQLNVGGNMDFKNMLDRNRLESKKV
SKTQAVTSNIPDGPLSGKVEDRNVHIGPSDHVQWLDDRKWAYVRLEGTAFGGVPLNLEYK
LEVWDSPNSAGIIIDAVRAAKIALDRGIGGPIMPASSYLMKSPPEQLPDDVACERLEAFI
IEA

>RXN00595 TRANSLATE of: rxn00595.seq check: 7949 from: 1 to: 1530
MAMDVLLPIFVAVPLAASAIAVLLPWRLIRDILHIIVPFAGIFAGIWLFAHTAEHGPIAH
NVGLYVGGVAIPFAADTFSAIMLITTSIVAVAANWFATIVGETRARFYPALTLMLITGVN
GALLTADLFNFFVFIEVMLLPSYGLIAMTGTWARLASGRIFVLVNLSASTLLVAGVGIVY
GVIGSVNIAALQDVVEGNPLVASAMGIVVIAIAVKAGVFPVHTWLPRTYPGTSAAVMGLF
SGLHTKVAVYMLYRIWVHIFNMDPTWNWLIVAFMVISMLVGGFAGLAENSIRRVLAYQMV
NGMPFILIMMAFTSDDPQRALAAGLLYTLHHMITIAALVLTSGAIEETYGTGMLSKLSGL
ARREPVVAAVFAAGAFSVVGFPPFSGMWGKALILLEIARVGNIAAWIAIAAIIIASLGAL
LSMIRVWREVFWGGAMHQRGVSPQLRISPAKIAPALSLIILSVGMFIFAGPLIDATLTAT
DGLLNTDAYQQAVLGENAIGVPSPSYQGGN

>RXN00606 TRANSLATE of: rxn00606.seq check: 8402 from: 1 to: 2274
VLTGVIAVLIAMSAFTKSAQFPFHFWLPEAMAAATPVSAFLHAAAVVKAGIYLLLRFSIV
FHDVAVWNWLLIIVGMGTAIMSAYFAVQKTDLKKLTAYSTVSHLGWIVATIGVGTPFALG
AAIVHTLSHALFKSSLFMLIGVIDHQTGTRDIRRLGFLVKKMPFTFVSVLIGALSMASVP

PLLGFVSKEGMITAFMDAPIGNSYVVLLLVGAAIGAVLTFTYSAKLVLGAFVDGPRDMSH
VKEAPVSLWLPAALPGLMSLPLVLVLSLFDAPVSAAATSAAGEAAHMHLALWHGINTPLL
ISLGVLVAGILGVLFRKELWKIAETSPFPIATGNDILSMLVYRANLLGKFFGRMADSMSP
RRHLVSLIVLLWALAAFATIHPSVQLAPKQPGIDRWIDLIPLAIIALSVFGLLTTRNRLS
AAVLVGTVGVGVSFQMLLLGAPDVALTQFLVEGLVVVIIMMVVRHQPANFKRIKPSRRRS
TVLVAVLAAFAAFMAVWGLLGRHERSELAMWYLNQGPEITSGANVVNTILVEFRALDTLG
ELSVLGMAAVVIGAMVASMPRHPFAKGTHPRPFGQSQLNSIPLRMLLKVLVPALCFLSFM
VFMRGHNDPGGGFIAALIAGGALMLLYLSKAKDGRIFRPNVPFILTGAGILMAVFSGVLG
LTHGSFLYAIHFNFVGQHWTTSMIFDLGVYLAVLGMVSMAINGLGGYLRPGTDNADLDYA
RRSGPLPATPTVEPEPEGDEDWPEPINPAGDNKEEANR

>RXN00635 TRANSLATE of: rxn00635.seq check: 3133 from: 1 to: 1737
MAHSYAEQLIDTLEAQGVKRIYGLVGDSLNPIVDAVRQSDIEWVHVRNEEAAAFAAGAES
LITGELAVCAASCGPGNTHLIQGLYDSHRNGAKVLAIASHIPSAQIGSTFFQETHPEILF
KECSGYCEMVNGGEQGERILHHAIQSTMAGKGVSVVVIPGDIAKEDAGDGTYSNSTISSG
TPVVFPDPTEAAALVEAINNAKSVTLFCGAGVKNARAQVLELAEKIKSPIGHALGGKQYI
QHENPFEVGMSGLLGYGACVDASNEADLLILLGTDFPYSDFLPKDNVAQVDINGAHIGRR
TTVKYPVTGDVAATIENILPHVKEKTDRSFLDRMLKAHERKLSSVVETYTHNVEKHVPIH
PEYVASILNELADKDAVFTVDTGMCNVWHARYIENPEGTRDFVGSFRHGTMANALPHAIG
AQSVDRNRQVIAMCGDGGLGMLLGELLTVKLHQLPLKAVVFNNSSLGMVKLEMLVEGQPE
FGTDHEEVNFAEIAAAAGIKSVRITDPKKVREQLAEALAYPGPVLIDIVTDPNALSIPPT
ITWEQVMGFSKAATRTVFGGGVGAMIDLARSNIRNIPTP

>RXN00684 TRANSLATE of: rxn00684.seq check: 631 from: 1 to: 1284
MTSQTSQQSTSTGGCPFGHTSESTSHHGYQPFDMHNPFPAYKELRQEEPVMFDERIGYWV
VTKYDDIKTTFDDWETFSSENAQAPVRKRGPQATQIMTDGGFTAYSGLSARIPPEHTRIR
AIAQKAFTPRRYKALEPDIRAMVIDRVEKMLANDQHVGDMVSDLAYDIPTITILTLIGAD
IFMVVTYKRWSDSRAAMTWGDLSDEEQIPHAHNLVEYWQECQRMVADAHAHGGDNLTADL
VRAQQEGQEITDHEIASLLYSLLFAGHETTTTLISNCFRVLLDHPEQWQAILENPKLIPA
AVDEVLRYSGSIVGWRRKALKDTEIGGVAIKEGDGVLLLMGSANRDEARFENGEEFDISR
ANAREHLSFGFGIHYCLGNMLAKLQAKICLEEVTRLVPSLHLVADKAIGFRENLSFRVPT
SVPVTWNA

>RXN00705 TRANSLATE of: rxn00705.seq check: 1372 from: 1 to: 915
MGRITQNLQVPRVVSTDEQVFVNTRPDTVAVEEPLEIRVNGTALTTTMRTPGHDIELVHG
LLLSEGLITDASEVFTARYCAGAVGPDNQNTYNVLELDVIPKDNPARDPVQNPSHNPEGS
QHEALHIPTFQPVRELNLVAAQRNVLTTSACGVCGTTSIEQLMNKKGWPITPITPDPRMI
VSLPDKLKSKQKIFDKTGGVHAAGLATLDGEMLIIREDVGRHNAADKVIGNMLMAGKLPL
ENTILVMSSRASFELVQKAAMAGISGVIAVGAATSLAIEAAQDSGIFLAGFVRGNKFNHY
AGELG

>RXN00799 TRANSLATE of: rxn00799.seq check: 3114 from: 1 to: 1644
MSQERPQIGSRLSRVIEQDGLQFRDLDGDGVLAPYEDWRLTPAERAADLVKRMNVEEKAG
LMIIGSHYPGYSPLAPESEGKDAEKCEPLLNPVDMWREDNPITGVPFTEPVLATSSTENA
INLRNQRYLIVRDNLPARGLATWTNAVQEVAERSRLGIPVAFASNPRNHVALVAQFGVNE
SAGVFSEWPGELGLAALRDAELMETFGTEAAKEWRAGGVHKLYGYMADLASEPRWSRFNG
TFGEDPELISDYIAAVVRGLQGPELSKNSVSTTIKHFPGGGVRLDGHDPHFHWGQTNEYP
TEDALGKYHLPPFQAAIDAGCASIMPYYARPMNNSANQLDQQLWQNPTTQFEEVAFAYNR
TFIQDLLRDAMGHRGYVNSDSGVIDAMMWGVEELSEPERFAAAVRAGTDIFSDMANPRRL
LEAVAEGHLDESELNQPVQRLLEEIFQLGLFENPYVSEDEAEKIIGAPEVSALGNKAQLD
SVTLLRNNPIRAATGSCSKPEDLPIGYWPYQDRRGSTTAGSSHSRRTPRGNLGVFRVRSR
SCNRVGSP

>RXN00868 TRANSLATE of: rxn00868.seq check: 5375 from: 1 to: 1911
MAETKRMTVSQALVEFLGHQWTVDGDIRERTIPGMFGIFGHGNVAGIGQALKQYNVEQPE
LMPYYQARNEQAMVHQSVGYARMHRRRGTYASAASVGPGATNLLTGAALATTNRLPALLL
PSDTFATRVADPVLQQLEQPWDIGLTVNDAFRPVSKFFDRVQRPEQLFSIALAAMRVLTD
PAETGAVTIALPEDVQAEMLDVPVEFLQDREWHIRRPRPERAALARAIEVIKNAKNPMII
AGGGVLYSDAETQLQALVEQTGIPVGTSQAGGGVLAWDHAQNLGGVGATGTLAANRIAGD
ADVIIGIGTRYSDFTTASRTAFQNPDVTFININVASFDAYKHGTQLPVIADAREAIVELA
EALQGFTVAEDYAQRIAKEKAAWDAEVDKSFAPSGLALPGQPEIIGAVQASTSEKDVIVQ

AAGSLPGDLHKLWRVRDALGYHVEYAFSCMGYEIAGGIGAKRGLDAAGDDRDVVIMVGDG
SYLMLNTELVTAVAEGIKVIVVLIQNHGYASIGHLSETVGSQRFGTWYREYDAEAKNFQG
EQILPVDLAMNARSYGMDVIEVEPSANAIEDLKAAMATAKASEKSTFIHINSDPLIYAPD
GAGWWDVPVSETSTLDSTNAAREDYLKNQALQRPLLG

>RXN00871 TRANSLATE of: rxn00871.seq check: 1232 from: 1 to: 888
MRWFHKKGELARDGWQSVVDATTPGWEYTGIRIAELGSGESLELNDTGVERIFIPLQGSF
DVAHHGQVTHLHGRKSVFDGPTDVLYLPTGQTATLSGQGRVAVAEAPTQEPKEWKYIAPA
ETPVELRGAGRSSRQVHNFGTPEALDAARLIVCEVITPGENWSSYPPHKHDEHIPGHESK
LEEIYYFESAPSRVGGRAEAAEGAFGMFSTYSSPAGEIDINAMVYSGDIALVPFGYHGPA
VAAPGYDLYYLNVMAGPDPERIWLINDDPAHAWVRDTWTGQAFDDRLPYENANKEG

>RXN00872 TRANSLATE of: rxn00872.seq check: 2930 from: 1 to: 954
MTNLTSTHEVLAIGRLGVDIYPLQSGVGLADVQSFGKYLGGSAANVSVAAARHGHNSALL
SRVGNDPFGEYLLAELERLGVDNQYVATDQTFKTPVTFCEIFPPDDFPLYFYREPKAPDL
NIESADVSLDDVREADILWFTLTGFSEEPSRGTHREILTTRANRRHTIFDLDYRPMFWES
PEEATKQAEWALQHSTVAVGNKEECEIAVGETEPERAGRALLERGVELAIVKQGPKGVMA
MTKDETVEVPPFFVDVINGLGAGDAFGGALCHGLLSEWPLEKVLRFANTAGALVASRLEC
STAMPTTDEVEASLNQKV

>RXN00879 TRANSLATE of: rxn00879.seq check: 6977 from: 1 to: 2118
VTARRFLNELADLYGVATSYTDYKGAHIEVSDDTLVKILRALGVNLDTSNLPNDDAIQRQ
IALFHDREFTRPLPPSVVAVEGDELVFPVHVHDGSPADVHIELEDGTQRDVSQVENWTAP
REIDGIRWGEASFKIPGDLPLGWHKLHLKSNERSAECGLIITPARLSTADKYLDSPRSGV
MAQIYSVRSTLSWGMGDFNDLGNLASVVAQDGADFLLINPMHAAEPLPPTEDSPYLPTTR
RFINPIYIRVEDIPEFNQLEIDLRDDIAEMAAEFRERNLTSDIIERNDVYAAKLQVLRAI
FEMPRSSEREANFVSFVQREGQGLIDFATWCADRETAQSESVHGTEPDRDELTMFYMWLQ
WLCDEQLAAAQKRAVDAGMSIGIMADLAVGVHPGGADAQNLSHVLAPDASVGAPPDGYNQ
QGQDWSQPPWHPVRLAEEGYIPWRNLLRTVLRHSGGIRVDHVLGLFRLFVMPRMQSPATG
TYIRFDHNALVGILALEAELAGAVVIGEDLGTFEPWVQDALAQRGIMGTSILWFEHSPSQ
PGPRRQEEYRPLALTTVTTHDLPPTAGYLEGEHIALRERLGVLNTDPAAELAEDLQWQAE
ILDVAASANALPAREYVGLERDQRGELAELLEGLHTFVAKTPSALTCVCLVDMVGEKRAQ
NQPGTTRDMYPNWCIPLCDSEGNSVLIESLRENELYHRVAKASKRD

>RXN00999 TRANSLATE of: rxn00999.seq check: 9801 from: 1 to: 1452
MTNGDNLAQIGVVGLAVMGSNLARNFARNGNTVAVYNRSTDKTDKLIADHGSEGNFIPSA
TVEEFVASLEKPRRAIIMVQAGNATDAVINQLADAMDEGDIIIDGGNALYTDTIRREKEI
SARGLHFVGAGISGGEEGALNGPSIMPGGPAKSYESLGPLLESIAANVDGTPCVTHIGPD
GAGHFVKMVHNGIEYADMQVIGEAYHLLRYAAGMQPAEIAEVFKEWNAGDLDSYLIEITA
EVLSQVDAETGKPLIDVIVDAAGQKGTGRWTVKAALDLGIATTGIGEAVFARALSGATSQ
RAAAQGNLPAGVLTDLEALGVDKAQFVEDVRRALYASKLVAYAQGFDEIKAGSDENNWDV
DPRDLATIWRGGCIIRAKFLNRIVEAYDANAELESLLLDPYFKSELGDLIDSWRRVIVTA
TQLGLPIPVFASSLSYYDSLRAERLPAALIQGQRDFFGAHTYKRIDKDGSFHTEWSGDRS
EVEA

>RXN01025 TRANSLATE of: rxn01025.seq check: 6040 from: 1 to: 996
VVSVSVMGAGSWGTTLAKVFSDAGNAVTLWARREELASTIRDSHENRDYLPGITLPESLQ
VTSSATEALEGAAIVVLAIPSQALRGNLAEWKETIPQDATLVSLAKGIEKGTHLRMSEVI
AEVTEADPSRIAVLSGPNLAREIAEGQPAATVIACPDENRAKLVQAAVAAPYFRPYTNTD
VVGTEIGGACKNVIALACGISHGYGLGENTNASLITRGLAEIARLGATLGADAKTFSGLA
GMGDLVATCSSPLSRNRSFGERLGQGESLEKAREATNGQVAEGVISSQSIFDLATKLGVE
MPITQAVYGVCHRDMKVTDMIVALMGRSKKAE

>RXN01048 TRANSLATE of: rxn01048.seq check: 6923 from: 1 to: 1224
MTIDLQRSTQNLTHEEIFEAHEGGKLSISSTRPLRDMRDLSLAYTPGVAQVCEAIKEDPE
VARTHTGIGNTVAVISDGTAVLGLGDIGPQASLPVMEGKAQLFSSFAGLKAIPIVLDVHD
VDALVETIAAIAPSFGAINLEDISAPRCFEVERRLIERLDIPVMHDDQHGTAVVILAALR
NSLKLLDRKIEDLKIVISGAGAAGVAAVDMLTNAGATDIVVLDSRGIIHDSREDLSPVKA
ALAEKTNPRGISGGINEAFTGADLFIGVSGGNIGEDALKLMAPEPILFTLANPTPEIDPE
LSQKYGAIVATGRSDLPNQINNVLAFPGIFAGALAAKAKKITPEMKLAAQRQSQTSQLRT
SRSAASCLPPWIPALPQQSRQLSRPSPKRKTLKNLLIDASLPVEAPIF

>RXN01049 TRANSLATE of: rxn01049.seq check: 4562 from: 1 to: 1482
MGSIPTMSIPFDDSRGPYVLAMDIGSTASRGGLYDASGCPIKGTKQRESHEFTTGEGVST
IDADQVVSEITSVINGILNAADHHNIKDQIAAVALDSFASSLILVDGEGNALTPCITYAD
SRSAQYVEQLRAEIDEKAYHGRTGVCLHTSYHPSRLLWLKTEFEKEFNKAKYVMTIGEYV
YFKLAGITGMATSIAAWSGILDAHTGELDLTILEHIGVDPALFGEIRNPDEPATDAKVVD
KKWKHLEEIPWFHAIPDGWPSNIGPGAVDSKTVAVAAATSGAMRVILPSVPEQIPSGLWC
YRVSRDQCIVGGALNDVGRAVTWLERTIIKPENLDEVLIREPLEGTPAVLPFFSGERSIG
WAASAQATITNIQEQTGPEHLWRGVFEALALSYQRVWEHMGKAGAAPERVIASGRVSTDH
PEFLAMLSDALDTPVIPLEMKRATLRGTALIVLEQLEPGGTRATPPFGTTHQPRFAHHYS
KARELFDALYLKLV

>RXN01130 TRANSLATE of: rxn01130.seq check: 121 from: 1 to: 603
MDLARKLGLLAGKLVDAAPVSIEVEARGELSSEQVNALGLSAVRGLFSGIIEESVTFVNA
PRIAEERGLDISVKTNSESVTHRSVLQVKVITGSGASATVVGALTGLERVEKITRINGRG
LDLRAEGLNLFLQYTDAPGALGTVGTKLGAAGINIEAAALTQAEKGDGAVLILRVESAVS
EELEAEINAELGATSFQVDLD

>RXN01143 TRANSLATE of: rxn01143.seq check: 3222 from: 1 to: 1119
IPVVTTLMALGTFPESHELHMGMPGMHGTVSAVGALQRSDLLIAIGSRFDDRVTGDVDTF
APDAKIIHADIDPAEIGKIKQVEVPIVGDAREVLARLLETTKASKAETEDISEWVDYLKG
LKARFPRGYDEQPGDLLAPQFVIETLSKEVGPDAIYCAGVGQHQMWAAQFVDFEKPRTWL
NSGGLGTMGYAVPAALGAKAGAPDKEVWAIDGDGCFQMTNQELTTAAVEGFPIKIALINN
GKPGAWVRQWQTLFYEGRYSNTKLRNQGEYMPDFVTLSEGLGCVAIRVTKAEEVLPAIQK
AREINDRPVVIDFIVGEDAQVWPMVSAGSSNSDIQYALGLRPFFDGDESAAEDPADIHEA
VSDIDAAVESTEA

>RXN01144 TRANSLATE of: rxn01144.seq check: 6367 from: 1 to: 516
MANSDVTRHILSVLVQDVDGIISRVSGMFTRRAFNLVFLVSAKTETHGINRITVVVDADE
LNIEQITKQLNKLIPVLKVVRLDEETTIARAIMLVKVSADSTNRPQIVDAANIFRARVVD
VAPDSVVIESTGTPGKLRALLDVMEPFGIRELIQSGQIALNRGPKTMAPAKI

>RXN01146 TRANSLATE of: rxn01146.seq check: 6296 from: 1 to: 693
MTGAKAIVRSLEELNADIVFGIPGGAVLPVYDPLYSSTKVRHVLVRHEQGAGHAATGYAQ
VTGRVGVCIATSGPGATNLVTPIADANLDSVPMVAITGQVGSGLLGTDAFQEADIRGITM
PVTKHNFMVTNPNDIPQALAEAFHLAITGRPGPVLVDIPKDVQNAELDFVWPPKIDLPGY
RPVSTPHARQIEQAVKLIGEAKKPVLYVGGGVIKADAHEELRAFAEYTGIP

>RXN01175 TRANSLATE of: rxn01175.seq check: 3032 from: 1 to: 1386
VSWTVDIPKEVLPDLPPLPEGMQQQFEDTISRDAKQQPTWDRAQAENVRKILESVPPIVV
APEVLELKQKLADVANGKAFLLQGGDCAETFESNTEPHIRANVKTLLQMAVVLTYGASTP
VIKMARIAGQYAKPRSSDLDGNGLPNYRGDIVNGVEATPEARRHDPARMIRAYANASAAM
NLVRALTSSGTADLYRLSEWNREFVANSPAGARYEALAREIDSGLRFMEACGVSDESLRA
ADIYCSHEALLVDYERSMLRLATDEEGNEELYDLSAHQLWIGERTRGMDDFHVNFASMIS
NPIGIKIGPGITPEEAVAYADKLDPNFEPGRLTIVARMGHDKVRSVLPGVIQAVEASGHK
VIWQSDPMHGNTFTASNGYKTRHFDKVIDEVQGFFEVHRALGTHPGGIHIEFTGEDVTEC
LGGAEDITDVDLPGRYESACDPRLNTQQSLELAFLVAEMLRN

>RXN01193 TRANSLATE of: rxn01193.seq check: 6139 from: 1 to: 1449
MTTALEEQNAQQAATAGRVVRVIGAVVDVEFPRGELPALYNALTVEVTLESVKKTVVLEV
AQHLGDNLIRTIAMAPTDGLVRGAAVTDTARPISVPVGDVVKGHVFNALGDCLDDVSLNN
NPEIERWGIHREPPSFDQLEGKTEILETGIKVIDLLTPYVKGGKIGLFGGAGVGKTVLIQ
EMITRIAREFSGTSVFAGVGERTREGTDLFLEMEEMGVLQDTALVFGQMDEPPGVGMRVA
LSGLTMAEYFRDVQNQDVLLFIDNIFRFTQAGSEVSTLLGRMPSAVGYQPTLADEMGVLQ
ERITSTKGRSITSLQAVYVPADDYTDPAPATTFAHLDATTELDRSIASKGIYPAVNPLTS
TSRILEPAIVGERHYEVSQRVIGILQKNKELQDIIAILGMDELSEEDKITVARARRIERF
LGQNFFVAEKFTGLPGSYVPLTDTVDAFERICNGDFDHYPEQAFNGLGGLDDVEAAYKKL
TGK

>RXN01204 TRANSLATE of: rxn01204.seq check: 374 from: 1 to: 810
MKGEFHAPDLDKEFFPGHVTDSGEVVNMLFTDFANGWFAMDRIVLIRLLMTAVVVVFFLW

AMRKPKLVPHGVQNFAEYALDFVGIHIAEDILGKKKGRRFLPILATIFFAALLMNLATII
PGLNISSNSRIAFPIVMAVAGYIAFIYAGSKRYGFFKYVKSSVVIPNIPPALHVLVVPIE
FFSTFILRPVTLALRLMANFLAGHIILVLLFSATNFFFFQFNGWTAMSGVTILMAVLFTV
YEIIVIFLQAYIFALLVAVYIELSLHADSH

>RXN01225 TRANSLATE of: rxn01225.seq check: 1629 from: 1 to: 1440
MTHNHKDWNDRIAVAEEMVPLIGRLHRNNNVVVSVFGRLLVNVSDIDIIKSHRYARHIIS
KELPLESSLDILRELVDMNLGTASIDLGQLAYSFEESESTDLRAFLEDALAPVIGAETDI
NPTDIVLYGFGRIGRLLARILVSREALYDGARLRAIVVRKNGEEDLVKRASLLRRDSVHG
GFDGTITTDYDNNIIWANGTPIKVIYSNDPATIDYTEYGINDAVVVDNTGRWRDREGLSQ
HLKSKGVAKVVLTAPGKGDLKNIVYGINHTDITADDQIVSAASCTTNAITPVLKVINDRY
GVEFGHVETVHSFTNDQNLIDNFHKGSRRGRAAGLNMVLTETGAAKAVSKALPELEGKLT
GNAIRVPTPDVSMAVLNLTLNTEVDRDEVNEFLRRVSLHSDLRQQIDWIRSPEVVSTDFV
GTTHAGIVDGLATIATGRHLVLYVWYDNEFGYSNQVIRIVEEIAGVRPRVYPERRQPAVL

>RXN01312 TRANSLATE of: rxn01312.seq check: 2455 from: 1 to: 2019
MSTHSETTRPEFIHPVSVLPEVSAGTVLDAAEPAGVPTKDMWEYQKDHMNLVSPLNRRKF
RVLVVGTGLSGGAAAAALGELGYDVKAFTYHDAPRRAHSIAAQGGVNSARGKKVDNDGAY
RHVKDTVKGGDYRGRESDCWRLAVESVRVIDHMNAIGAPFAREYGGALATRSFGGVQVSR
TYYTRGQTGQQLQFSTASALQRQIHLGSVEIFTHNEMVDVIVTERNGEKRCEGLIMRNLI
TGELTAHTGHAVILATGGYGNVYHMSTLAKNSNASAIMRAYEAGAYFASPSFIQFHPTGL
PVNSTWQSKTILMSESLRNDGRIWSPKEPNDNRDPNTIPEDERDYFLERRYPAFGNLVPR
DVASRAISQQINAGLGVGPLNNAAYLDFRDATERLGQDTIRERYSNLFTMYEEAIGEDPY
SSPMRIAPTCHFTMGGLWTDFNEMTSLPGLFCAGEASWTYHGANRLGANSLLSASVDGWF
TLPFTIPNYLGPLLGSERLSEDAPEAQAAIARAQARIDRLMGNRPEWVGDNVHGPEYYHR
QLGDILYFSCGVSRNVEDLQDGINKIRALRDDFWKNMRITGSTDEMNQVLEYAARVADYI
DLGELMCVDALDRDESCGAHFRDDHLSEDGEAQRDDQNWCFVSAWEPGENGTFVCHAEPL
FFESVPLQTRNYK

>RXN01332 TRANSLATE of: rxn01332.seq check: 4448 from: 1 to: 576
HISAIIEPDAARAAAAAEDAPGAQAFTRIEDAIAADAVDAVLIAVPGQFHEPVLVPALEA
GLPILCEKPLTPDSESSLRIVELEQKLDKPHIQVGFMRRFDPEYNNLRKLVESGEAGELL
MLRGLHRNPSVGESYTQSMLITDSVVHEFDVIPWLAGSRVVSVEVKYPKTSSLAHSGLKE
PILVIMELENGV

>RXN01340 TRANSLATE of: rxn01340.seq check: 5971 from: 1 to: 858
KVGEIIASVFDTFNIPQGLVSIITTTRDAELSAELMADPRLAKVTFTGSTNVGRILVRQS
ADRLLRTSMELGGNAAFVIDEAADLDEAVSGAIAAKLRNAGQVCIAANRFLVHESRAAEF
TSKLATAMQNTPIGPVISARQRDRIAALVDEAITDGARLIIGGEVPDGSGFFYPATILAD
VPAQSRIVHEEIFGPVATIATFTDLAEGVAQANSTEFGLAAYGFSNNVKATQYMAEHLEA
GMVGINRGAISDPAAPFGGIGQSGFGREGGTEGIEEYLSVRYLALP

>RXN01365 TRANSLATE of: rxn01365.seq check: 6665 from: 1 to: 1374
MRTRESVTAVIKAYDVRGVVGVDIDADFISETGAAFGRLMRSEGETTVAIGHDMRDSSPE
LAKAFADGVTAQGLDVVHLGLTSTDELYFASGTLKCAGAMFTASHNPAEYNGIKLCRAGA
RPVGQDSGLANIIDDLVEGVPAFDGESGSVSEQDLLSAYAEYLNELVDLKNIRPMKVAVD
AANGMGGFTVPEVFKGLPLDVAPLYFELDGNFPNHEANPLEPANLVDLQKFTVETGSDIG
LAFDGDADRCFVVDEKGQPVSPSAICAIVAERYLEKLPGSTIIHNLITSKAVPEVIAENG
GTAVRTRVGHSFIKAKMAETGAAFGGEHSAHYYFTEFFNADSGILAAMHVLAALGSQDQP
LSEMMARYNRYVASGELNSRLANAEAQQERTQAVLDAFADRTESVDTLDGVTVELKDTSA
WFNVRASNTEPLLRLNVEAASKEEVDALVAEILGIIRA

>RXN01369 TRANSLATE of: rxn01369.seq check: 8434 from: 1 to: 1182
MELLEGSLRTYPWGSRTLIADLKGEESPSSRPEAEVWFGAHPGSPSTIGGNALNEVIAAN
PEEALGTRVAEAFENELPFLLKILAAGAPLSLQAHPSLEQAREGFARENSAGIDLGAPNR
NYRDPNHKPELIVALTEFIAMAGFRPLRNTLTIFDALACEPLDRYRSMLTVDNEEESLRA
LFTTWITIPIGKRHELIDALISNAHTYLEASDRDEDIAFVLSHIIELNEQYPGDVGVLGA
LLLNFYKLAPGEALYLDAANLHAYISGLGVEIMANSDNVLRGGLTSKYVDVPELVRVLDF
NSLENARVDVEEDGATTHYPVPINEFQLDRVAVQGEAEANHDGPMIVLCTSGTVSLEAGE
KTLEVAAGHAAWVPANDPTIAMRSEDAEVFLARV

>RXN01376 TRANSLATE of: rxn01376.seq check: 9104 from: 1 to: 861
VTYSPGKYLASFLDSLPGATSRDTHVVMADNGSVDGVPEQAAASRSNVEFLSTGGNLGYG
TAINIAARSLRARREAGEIDGEFFLVSNPDVVFDEDSIDQLLECAKRHPEAGAVGPLIRE
ADGSAYPSARAVPTLANGIGHALLGAVWKSNPWSAAYRDDEDMDTERTAGWLSGSCLLLR
WDAFDRVGGFDERYFMYMEDVDLGDRLVRAGFTNVFCPSAQIIHAKGHVAGKNPENMLPA
HHESAYRFQADRLAKPWQAPIRLALRIGLKLRAGVAVGVSKMRTKAS

>RXN01406 TRANSLATE of: rxn01406.seq check: 5966 from: 1 to: 1023
MTIRIGLVGYGVGGRLFHTPYIQASTHCELVGVVARSEGTKAAVAEDLPDVAIVGSLTEL
LELGVDAVVISTPPATRRELALEAINAGVAVVADKPFAPSAADAMELVEAAEKAGVLLNV
FHNRRNDTHIVTALGIQEELGAMRGLDLRLDLIEPDSLEAGPEGGLLRDLGSHVVDQTLV
LMGPATSVTAQLGSIDLPEGPTNARFRIVLEHESGAVSHISASKIDRLESWEIRLVGERG
SYVSNYTDVQTVAIKQGLRPTNDREHWGYESEERWGTLVTDEGSKVIPSAQGDYTRFYDA
FALAVENGGAGPVPAREGVAVLKVLDAVAQSAAEKRTIELS

>RXN01468 TRANSLATE of: rxn01468.seq check: 6994 from: 1 to: 825
MTVNISYLTDMDGVLIKEGEIIPGADRFLQSLTDNNVEFMVLTNNSIFTPRDLSARLKTS
GLDIPPERIWTSATATAHFLKSQVKEGTAYVVGESGLTTALHTAGWILTDANPEFVVLGE
TRTYSFEAITTAINLILGGARFICTNPDVTGPSPSGILPATGSVAALITAATGAEPYYIG
KPNPVMMRSALNTIGAHSEHTVMIGDRMDTDVKSGLEAGLSTVLVRSGISDDAEIRRYPF
RPTHVINSIADLADCWDDPFGDGAFHVPDEQQFTD

>RXN01498 TRANSLATE of: rxn01498.seq check: 692 from: 1 to: 1563
MIKRLPLGPLPKELHQTLLDLTANAQDAAKVEVIAPFTGETLGFGFDGDEQDVEHAFALS
RAAQKKWVHTTAVERKKIFLKVHDLVLKNRELLMDIVQLETGKNRASAADEVLDVAITTR
FYANNAGKFLNDKKRPGALPIITKNTQQYVPKGVVGQITPWNYPLTLGVSDAVPALLAGN
AVVAKPDLATPFSCLIMVHLLIEAGLPRDLMQVVTGPGDIVGGAIAAQCDFLMFTGSTAT
GRILGRTMGERLVGFSAELGGKNPLIVAKDADLDKVEAELPQACFSNSGQLCVSTERIYV
EEDVYEEVIARFSKAAKAMSIGAGFEWKYEMGSLINHAQLDRVSTFVDQAKAAGATVLCG
GKSRPDIGPFFYEPTVLADVPEGTPLLTEEVFGPVVFIEKVATLEEAVDKANGTPYGLNA
SVFGSSETGNLVAGQLEAGGIGINDGYAATWASVSTPLGGMKQSGLGHRHGAEGITKYAE
IRNIAEQRWMSMRGPAKMPRKVYSDTVATALKLGKIFKVLP

>RXN01550 TRANSLATE of: rxn01550.seq check: 138 from: 1 to: 1512
VQLNDTHPVLAIPELMRLLMDEHDMGWEESWAIVFKTFAYTNHTVLTEALEQWDQQIFQQ
LFWRVWEIITEIDRRFRLERAADGLDEETIDRMAPIQHGTVHMAWIACYAAYSINGVAAL
HTEIIKAETLADWYALWPEKFNNKTNGVTPRRWLRMINPGLSDLLTRLSGSDDWVTDLDE
LKKLRSYADDKSVLEELRAIKAANKQDFAEWILERQGIEIDPESIFDVQIKRLHEYKRQL
MNALYVLDLYFRIKEDGLTDIPARTVIFGAKAAPGYVRAKAIIKLINSIADLVNNDPEVS
PLLKVVFVENYNVSPAEHILPASDVSEQISTAGKEASGTSNMKFMMNGALTLGTMDGANV
EIVDSVGEENAYIFGARVEELPALRESYEPYELYETVPGLKRALDALDNGTLNDNNSGLF
YDLKHSLIHGYGKDASDTYYVLGDFADYRETRDRMAADYASDPLGWARMAWINICESGRF
SSDRTIRDYATEIWKLEPTPAVKK

>RXN01554 TRANSLATE of: rxn01554.seq check: 7857 from: 1 to: 2142
LKKHVTSAVTAVVTAFSTAALGLSIAVSPAVAQVANPAPDLSAPYTWVEEFDSEDALKGW
NIFRQPDYGSDKVLYTEDALSIEDGKLTITTQRHCVDEDFAISDPVNRGKLNDSTAQVEP
CAPGQFEKFTSARIVTPKIARGEFDLSVTATLNTGGVEGVRSAIWMQNGEQACSSATNNG
LYGELDLVEHFSYDLRSPWSPSNTHLGCDPESVNGTNRAPRELKLDESLDGVEHTWTVST
TRDGVEYFIDDEAINRQSWRNDVTLGHAEIDDFGISAQTFDEIVDREWTLTLNQKVESAD
WAKPRSSEEDFPVRSMVIDRIEVTGSPAVSEDTPMPDTTQLLTQDTLEYLGRMPVLERYE
PASADFADGRRPSWNYFNLKESWQNPELEQRPEAVEFVDGRMDIVTRRHCLATTDDIATP
ENAQEEPCAPGEVTRYSSARVHLPEIPAGNFRLTVRARAQSEELVDGVRPAIWMQNNTNF
CADNDGRPYGELDITEFYSSRVNTQYSAVHLGCAGNRPEMKLRQMEMEESMFGDWHDWGV
EVFDGQIVFTIDGKAVTSSGKDVFGNSVTPAAAPLRPAHFKLSEEEYREVIGQPWHLILN
TMVEQSGKDSWITAVDNNEAFPEHRFQIDHVAVDIESDSVDNVWPDAANEIPDNVGIEDS
DDGSDLEVGSTGSSTAETVSWISLFTALSSLVFTLALNQEALQNLINQFMRQFK

>RXN01562 TRANSLATE of: rxn01562.seq check: 4942 from: 1 to: 1908
MGILNSISTPADLKALNDEDLDALAKEIRTFLVDKVAATGGHLGPNLGVVELTIGLHRVF
DSPQDPIIFDTSHQSYVHKILTGRAKDFDSLRQKDGLSGYTCRAESEHDWTESSHASAAL
SYADGLSKAKQLDGDTTHSVVAVVGDGALTGGMCWEALNNIAAGKDRKVVVVVNDNGRSY
SPTIGGFAENLAGLRMQPFYDRFMEKGKTSLKSMGWVGERTFEALHAFKEGVKSTVIPTE
MFPELGMKYVGPVDGHNQKAVDNALKYAHDYDGPIIVHMVTEKGRGYAPAEQDLDELMHS
TGVIDPLTGAPKSASKPGWTSVFSDELVKIGAQNENVVAITAAMAGPTGLSKFEANFPNR
FFDVGIAEQHAVTSAAGLALGGKHPVVAIYSTFLNRAFDQLLMDVGMLNQPVTLVLDRSG
VTGSDGASHNGVWDMALTSIVPGVQVAAPRDEDSLRELLNEAISIDDGPTVVRFPKGDLP
TPIVAIDTLEDGVDVLAYEDATDVESTDDAPSVLIIAVGERATVALDVASRIKQHGVNVT
VVDPRWIVPIPQSLVALSDDHDLVITIEDGVIHGGVGSLLSDALNASEVDTPRRQIAVPQ
KYLDHASRNEVLADYGLDADGIETTVVGWLDSLFGE

>RXN01569 TRANSLATE of: rxn01569.seq check: 9598 from: 1 to: 1359
MEYGKQLTSHTTDIEGLLVFDFPVHGDNRGWFKENWQRTKMTNLGLPDFGPVQNNMSFNA
TAGTTRGMHAEPWDKFVSVAVGSVFGAWVDLRAGSSTYGNVVTQKITPDVGVYVPRGVAN
GFQALEDGTLYTYLVNDHWSPDAHYANVNLNMIDWPLPITEISEKDKKHPALIDATPLPA
RKVLVVGAGGQLGTALRAQFPDAEFVTRQELDITSDLTEARAWKQYSTIINAAAYTAVDQ
AEHDRAAAWDINAAAVANLATIARDNNLTLVHVSSDYVFDGAAESYDENAPFSPLGVYGQ
SKAAGDIGDTTAPRHYIVRTSWVIGDGNNFVRTMKSLDERGIAPSVVDDQIGRLSFTEDI
AAGIAHLLEVGAAYGTYNLTNTGEPASWADVARAVFSDPTKVTGVSTAEYFANKDAAPRP
LNSVLDLGKIEATGFSAPTWQTRLNDYLKELSK

>RXN01580 TRANSLATE of: rxn01580.seq check: 9660 from: 1 to: 717
MYKNMHIVAHRGAEDLHLENTMTAFQAAAPADAFELDIHATADNQVVVIHDRTAARVAAP
DSLHRDTPVARLSAAQIKEITLIDGSPVPTLEEVLLQTSLPIQVEIKSAGAVPAAAALLQ
KYPEHLERLLFISFIDAALVEIVDRLPEARVGILRDASMDDLRILDYIPLKNVGAILPSW
KALNVASIADLHTKGIKVGCWTIRDENAFGIAQQAGVDYATVSDPSRFLAPSPAGELHW

>RXN01593 TRANSLATE of: rxn01593.seq check: 9774 from: 1 to: 867
MYVTNNASRAPEVVAAQLREIGLADTTADNVMTSAQAACKMAAEKIPAGSKVYVLGSESF
RELATEAGFVVVDSADDKPVAVLHGHNPETGWAQLSEAALSINAGAQYFASNLDSTLPME
RGRHIGNGSMVAAVVNATGVKPLSAGKPGPAMFYAGAETLNSSKPLAVGDRLDTDIAGGN
AAGMDTFQVLTGVSGYYDLVRAIPRAAPHLYRHLDAGSLQRSGRAQARCPGRFFSAYRRR
HPGHFRRRCRRNSGCSTPHCVGCGLGGHRAVTEVRADSEVAATALQSWW

>RXN01630 TRANSLATE of: rxn01630.seq check: 5194 from: 1 to: 1077
MSDQKIVVGLLGITHPHASARVRALREIDGVEVVAAADTDSRLQYFTDKYDVEPREIDDV
LNDDRINAIMVHSKSKDMVPHAKRALAAGKSVVVEKPGGGTVADLEELLALKEAADPQRI
VQVGYNVRLSESVQRLKELLDAGLIGEVVSVQARGAAKVGEHITEHLNQPADMGGVLWIL
GCHMLDALVEVFGAPESVNARVHKTAKLSDDTSREDSASALLYYPDFSVSFSFDGHDDLE
WFESSRLTVYGTKGMIEAGILPQTLRVYLNESRQGWPQGWTEWTQSYFTPPFARTESNKF
SELPELENISNFRTEMQGWVNSIRTGSRNVAPVEDALTVARIVSACYESDNNQGISVNI

>RXN01631 TRANSLATE of: rxn01631.seq check: 4404 from: 1 to: 879
MKPQLIASCWTSAGDAAPDRDDLSSPVAIDERIALVAETGWAGIGLVHADLIKARDTIGY
EELRRRIHAAGIEIIEVEFLNGWWATGAERQESDAVRADLFAAAQALGSPHIKVGAGEGT
NGVVPIAHMASAFTDLAAEAEAHGVKLALEATPFSHLKTIYDALEVVSHSDSPSAGLMVD
IWHTAKIGIPNDELWRNIPLSKVNAVEVDDGFIDTPIDLFDDSTNRRAYCGEGEFDPASF
IRGAIDAGWTGAYGVEIISAEHRSLPVKEGLQRAFDTTIAAFEQAARLAPSTN

>RXN01695 TRANSLATE of: rxn01695.seq check: 9144 from: 1 to: 1500
MSDSPKNAPRITDEADVVLIGAGIMSSTLGAMLRQLEPSWTQIVFERLDGPAQESSSPWN
NAGTGHSALCELNYTPEVKGKVEIAKAVGINEKFQVSRQFWSHLVEEGVLSDPKEFINPV
PHVSFGQGADQVAYIKARYEALKDHPLFQGMTYADDEATFTEKLPLMAKGRDFSDPVAIS
WIDEGTDINYGAQTKQYLDAAEVEGTEIRYGHEVKSIKADGAKWIVTVKNVHTGDTKTIK

ANFVFVGAGGYALDLLRSAGIPQVKGFAGFPVSGLWLRCTNEELIEQHAAKVYGKASVGA
PPMSVPHLDTRVIEGEKGLLFGPYGGWTPKFLKEGSYLDLFKSIRPDNIPSYLGVAAQEF
DLTKYLVTEVLKDQDKRMDALREYMPEAQNGDWETIVAGQRVQVIKPAGFPKFGSLEFGT
TLINNSEGTIAGLLGASPGASIAPSAMIELLERCFGDRMIEWGDKLKDMIPSYGKKLASE
PALFEQQWARTQKTLKLEEA

>RXN01744 TRANSLATE of: rxn01744.seq check: 8546 from: 1 to: 1539
VDVVDIARWQFGITTVYHFIFVPLTIGLAPLVAIMQTFWQVTGKEHWYRATRFFGTVLLI
NFAVGVATGIVQEFQFGMNWSEYSRFVGDVFGGPLALEGLIAFFLESVFLGLWIFGWGKI
PGWLHTASIWIVAIATNISAYFIIVANSFMQHPVGAEYNPETGRAELTDFWALLTNSTAL
AAFPHAVAGGFLTAGTFVLGISGWWIIRAHRQAKKAESEIESKHSMHRPALWVGWWTTVV
SSVALFITGDIQAKLMFVQQPMKMASAESLCETATDPNFSILTIGTHNNCDTVTHLIDVP
FVLPFLAEGKFTGVTLQGVNQLQAAAEQAYGPGNYSPNLFVTYWSFRAMIGLMLGSLAIA
AIAWLLLRKKRTPTGKIARLFQIGSLIAIPFPFLANSAGWIFTEMGRQPWVVHPNPESAG
DARTEMIRMTVDMGVSDHAPWQVWLTLIGFTILYLILFVVWVWLIRRAVLIGPPEEGAPS
VEAKTGPATPIGSDMPMTPLQFTAAAPTTGEKE

>RXN01752 TRANSLATE of: rxn01752.seq check: 3364 from: 1 to: 1461
MMEQDLSYREILPLNASEEKKKAALIDAIEGLRVRDPLLSASIAFTRGQKVAFIAVVVGF
ILMLIFARQAALIGLSATCTFMYLITLLDRFIMFSRGIRAESIIQVSDEDALAFPEDKLK
TYTVLVPAYGEPEVIAQLLASMHAFDYPKHLLQVLLMLEEDDLPTIAAAEAAGVDQVATI
IKVPPAQPRTKPKACNYGLHFATGEIVTIFDAEDMPDPLQLRRVVVAFERSASNTVCVQS
RLSYRNARQNLLTAWFTIEYDVWFNFLLPGVMRMNAPVPLGGTSNHLLTGVLKDLGAWDP
FNVTENADLGVPIAAKGYSTAVLDSVTWEEANSDTINWLRQRSRWYKGYLQTWLVYMRRP
KWLVQELGIIPAVRFTFLMAGTPIIAVLNLLFWYLSLTWILGQPGTIEQMFPPAVYYPAL
VCLVVANAATIFMNLIGCREGRDPLLLIAVLTFPLYWLLMSIAALKGTWQLITRPSYWEK
TAHGLEA

>RXN01884 TRANSLATE of: rxn01884.seq check: 9417 from: 1 to: 1890
VTAIELMPVHQFLQDDRLRDLGMRNYWGYNSFGFFAPYNDYAANKNPGGAVAEFKGLVRS
YHEAGLEVILDVVYNHTAEGNHMGPTIAFRGIDNEAYYRLVEGDRRHYMDYTGTGNSLNV
RDPHSLQLIMDSLRYWVTEMHVDGFRFDLASTLAREFDDVDRLATFFDLVQQDPVVSQVK
LIAEPWDVGEGGYQVGNFPPLWTEWNGKYRDTVRDFWRGEPATLGEFASRLTGSSDLYAN
NGRRPTASINFVTAHDGFTLNDLVSYNEKHNMANGEDGRDGESHNRSWNCGVEGPTDDPE
IMQLRAQQRRNFLTTLLLSQGTPMLSHGDEMARTQNGNNNVYCQDNELAWVNWDQAEENA
DLVSFTRRLLRIRANHPVFRRRQFLAGGPLGADVRDRDIAWLVPNGTLMTQDDWDFAFGK
SLQVFFNGDAIEEPDYRGQKIHDDSFILMFNAHFEPIDFNLPPEHFGMKWKLLVDTTEAV
GHPLEDLTIEAGGTITVPARSTMLLRQVEAPDYTKLEEKIAAEKREQELAAEKEAAEKRE
LELAAAKEAEDAAEALHLAAERASTQEAELAHQHGADAIADEVAEEPQELPQDEVAAEVE
TEPDTEPDTESDSEQAEVASEEPEADEEEK

>RXN01891 TRANSLATE of: rxn01891.seq check: 8435 from: 1 to: 864
GGHYGLPFARSTVLFYYNKDLWAKAGLEDRGPESWEEFSEWGPKLQEAMDSGFAHGWGDA
TNYLSWTFEGPMWSLGGNYSEGWESRLTTPETIRAVEWLKSTVDEGFATVSTDVTNEFAT
GLIGSCIQSTGDLSSVAGAASFDWGVAALPNPTGEGACPTGGAGLGIPSGISEQRQDNAL
KFIDFLTNAANTGYWSRETGYVPVRKDAASDPDHAAFLEENPAYNVAVEQLPDTRSQDNF
RVLLPNGDRTIGDALEKICLTGADIDVTLAEVETKLNTIYTRDIEPLI

>RXN01895 TRANSLATE of: rxn01895.seq check: 607 from: 1 to: 951
MSVNPTRPEGGRHHVVVIGSGFGGLFAAKNLAKADVDVTLIDRTNHHLFQPLLYQVATGI
LSSGEIAPSTRQILGSQENVNVIKGEVTDINVESQTVTASLGEFTRVFEYDSLVVGAGAG
QSYFGNDHFAEFAPGMKSIDDALEIRARIIGAFERAEICEDPAERERLLTFVVVGAGPTG
VELAGQLAEMAHRTLAGEYKNFNTNSAKIILLDGAPQVLPPFGKRLGRNAQRTLEKMGVN
VRLNAMVTNVDATSVTYKTKDGEEHTIESFCKIWSAGVAASPLGKLVAEQTGVETDRAGR
VMVNDDLSVGDQKNVFV

>RXN01927 TRANSLATE of: rxn01927.seq check: 8048 from: 1 to: 1380
MALVLGIDSSTQSCKALLVDAATGQVIDEGRASHPSGSEVDPRAWIAALDQATEGLLERA
DAVSIAGQQHGMVALDENDEIVRPALLWNDTRSAQAALDLNEEIGGDQAAVDATGSVYVA
SLTATKMRWMRDHEPENAARTASVMLPHDFLTWHLMGRGRKVTDHGDASGTGYYSTRDRA

WRTDLAALALGHEVELPELLAPNAIAGTTPGGVKVAAGTGDNAAAALGLDLQPGDVSVSI
GTSGVAGMTVQHSVHDPSGLVTGFADATGAYFPLACTLNGAPVLEFGRRILGVEWEEFDA
LALAAQPGSGGVTLQPYLEGERTPNRPAARGVLAGLNCATTREDFARATVEGLLLALDDA
VTALVEATGVPVQRIQLIGGGARSQAVREIAPEIFGHEIVVPEPAEYVALGAARQAAWAL
SGEATPPQWPTPGSDPHRAPKNTELSTRYAKLRAATQGWY

>RXN01952 TRANSLATE of: rxn01952.seq check: 6335 from: 1 to: 1713
MTQPGQTTTTSHEAIDAFKRIVGDEHVLTSERATMPFSKGYRFGGGPVFAVVRPGTLVEM
WRALQVSVDNNLIVIPQASNTGLTGGSGPGFQDYDRPIVIISTHRIDEVHLINDAREAIS
LAGTPLTHLTDALAKHQREPHSVIGSTSIGASVIGGIANNSGGSQIRKGPAFTREAIFAR
VNDDGKVELVNHLGISLGDDPEVALDRLQRGEWSPEDVTPAPEDSNETEYAEHLRKIVPS
PARYNANPEYLFEASGSAGKLMVFAVRTRTFPREVHPTVFYIGTNNTHELEEIRRLFLEA
DMPLPISGEYMGRSAFDLAEKYGKDTFVFLKFMSPALQTRMFSFKTWANGLFSKIPGIGP
TFADTVSQAMFSVLPNQLPKRMMEYRNRFEHHLLLTVSESQKAASEKMLKEFFAEPEHTG
EFFICTSDEEKSASLNRFGAASAATRYAALKRRHIAGLIPIDVALRRDDWNWLEVLPEEI
DDQLEVKAYYGHFFCHVMHQDYVAKQGVDLEALHDRIQHLLEERGAKLPAEHNYGRMYKL
PESMEEHFKELDPTNTFNAGIGGTSPHKDWA

>RXN02036 TRANSLATE of: rxn02036.seq check: 338 from: 1 to: 381
VHIPFGHLADTVSWDCGGGSCATNDLVSLFMPAAFMSTLAACVFGAWAIGLIAPALFIAV
TAWAFRSGVQAAIADGYTSATSVGFEMTVSLILFIIAGLCFLGWIPMFINNRQVARKVRE
RAAGLSN

>RXN02046 TRANSLATE of: rxn02046.seq check: 7831 from: 1 to: 417
MKETLTTGLTHQMTYIVPANRTVPHLLPEAAEFETMPDVLATGYMVGIIEWACMELLRPH
LDDGEISLGTHVNFSHAAPTVPGSTVTIDVEVTEINRRAVTFNITAADEFATISTGTHQR
GVVNREKFVSRLPEAPKEN

>RXN02100 TRANSLATE of: rxn02100.seq check: 3527 from: 1 to: 2325
LGRINAEEQNLSEYLSDKLWYQDTADATDAVGDPLVAYFSMEFGIHPSLPIYSGGLGVLA
GENMKSASDLGVPLIGVGLLYTHGYFTQSLSGDGWQQEEYKYHDPAELPIEAVKDKNGEQ
VTVSVTYPGAQEVKIALWVANVGRIPLLLLDTNIEANPEELRNVTDRLYGGDNEHRIKQE
LVLGVGGVRAVNAFCEARGLKRSSVAHLNEGHAGFLTLERIRERIAEGMEYPAAFEQVRA
SNIFTTHTPVPAGIDRFDMEMVRRYLGGGQPEDQQLCVGVPIEKALELGQESDPHRFNMA
HMGLRASQHANGVAKLHGEVSRDMFAGLYPGYEPREVPIGHVTNGVHLPTWVKPEMKELI
DRVTGGADLAVADSWSNPQAVESEKIWKVRNKFRADLVEVARAATAKSWSHRGHTEAELA
WTSRVLDPNVLTIGFARRVSTYKRLTLMLRNPERLRSILLNEERPVQFVIAGKAHPHDMG
GKKLMQEIVHFADQAGVRDRFLFLPDYDINLASYLISGADVWLNNPVRPQEASGTSGMKA
VMNGGLTLSISDGWWDEMPKETTGWTIPTVESQDLECRDHLESQALYDLLENEVAPLFYK
RDKNGIPQDWLDLVRESWTTLSPMVTSTRMVRDYTTQYYRPTKHQAELIAQPAEAADYAA
WLEHIKAEWAGVKVSDLKISESAITAQELEVSVRVDSGSLNDDEFQAQALFGALGHNGDI
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>RXN02125 TRANSLATE of: rxn02125.seq check: 5612 from: 1 to: 801
MVATSQFIDDSEAAQAVRAAIVAGYRNIDTALAYGNERGVGEGIRTAGVPREELFISTKL
AAEIKDYDGAVAAIDESLAKIGLDYVDLMLIHSPQPWSDFRGGDYSEGNREAWRALEDAY
KAGKIRSIGVSNFLEADLENILDSATVAPHVNQLLVHVGNTPSELISFCDSKGILVEAYS
PIAHGEMLKNQQVKAIADKYNVSIPQLCIRYTIQLGTVSLPKTANPDHMSSNAQIDFEIS
EEDMAALQEVTARDYGEHSGFPVYSGK

>RXN02206 TRANSLATE of: rxn02206.seq check: 8771 from: 1 to: 936
MVGSSGLRVSRLGLGTSTWGSGTELAEAGDIFKAFINSGGTLIDVSPNYTTGVAEEMLGT
MLDAEVSRSAVVISSSAGVNPALPLGRRVDCSRRNLIAQLDVTLRALNTDYLDLWSVGYW
DEGTPPHEVADTLDYAVRTGRVRYAGVRGYSGWQLAVTHAASNHAAASARPVVVAQNEYS
LLERRAEQELLPATQHLGVGFFAGAPLGQGVLTAKYRSEIPHDSRAASTGRDAEVQSYLD
NRGRIIVDALDTAAKGLGISPAVTATTWVRDRPGVTAVIVGARTHEQLSHLLKAESVTLP
TPITQALDDVSL

>RXN02209 TRANSLATE of: rxn02209.seq check: 8467 from: 1 to: 1671
TESTVVPSIAGPKRPQDRILLSEAKEQFRKDLPTYTDDAVSVDTSIPATRMVNEGGGQPE

GGVEADNYNASWAGSGESLATGAEGRPSKPVTVASPQGGEYTIDHGMVAIASITSCTNTS
NPSVMIGAGLIARKAAEKGLKSKPWVKTICAPGSQVVDGYYQRADLWKDLEAMGFYLSGF
GCTTCIGNSGPLPEEISAAINEHDLTATAVLSGNRNFEGRISPDVKMNYLASPIMVIAYA
IAGTMDFDFENEALGQDQDGNDVFLKDIWPSTEEIEDTIQQAISRELYEADYADVFKGDK
QWQELDVPTGDTFEWDENSTYIRKAPYFDGMPVEPVAVTDIQGARVLAKLGDSVTTDHIS
PASSIKPGTPAAQYLDEHGVERHDYNSLGSRRGNHEVMMRGTFANIRLQNQLVDIAGGYT
RDFTQEGAPQAFIYDASVNYKAAGIPLVVLGGKEYGTGSSRDWAAKGTNLLGIRAVITES
FERIHRSNLIGMGVVPLQFPAGESHESLGLDGTETFDITGLTALNEGETPKTVKVTATKE
NGDVVEFDAICPHRHPR

>RXN02213 TRANSLATE of: rxn02213.seq check: 8081 from: 1 to: 774
VTESKNSFNAKSTLEVGDKSYDYFALSAVPGMEKLPYSLKVLGENLLRTEDGANITNEHI
EAIANWDASSDPSIEIQFTPARVLMQDFTGVPCVVDLATMREAVAALGGDPNDVNPLNPA
EMVIDHSVIVEAFGRPDALAKNVEIEYERNEERYQFLRWGSESFSNFRVVPPGTGIVHQV
NIEYLARVVFDNEGLAYPDTCIGTDSHTTMENGLGILGWGVGGIEAEAAMLGQPVSMLIP
RVVGFKLTGEIPVGVTAT

>RXN02326 TRANSLATE of: rxn02326.seq check: 550 from: 1 to: 816
MLGRPTKVTPSSKVVGDLALHLVGAGVDPADFAADPQKYDIPDSVIAFLRGELGNPPGGW
PEPLRTRALEGRSEGKAPLTEVPEEEQAHLDADDSKERRNSLNRLLFPKPTEEFLEHRRR
FGNTSALDDREFFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMRNVVANVNGQIR
PMRVRDRSVESVTATAEKADSSNKGHVAAPFAGVVTVTVAEGDEVKAGDAVAIIEAMKME
ATITASVDGKIDRVVVPAATKVEGGDLIVVVS

>RXN02327 TRANSLATE of: rxn02327.seq check: 173 from: 1 to: 960
LLATRVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWDRLDELREAMPN
VNIQMLLRGRNTVGYTPYPDSVCRAFVKEAASSGVDIFRIFDALNDVSQMRPAIDAVLET
NTAVAEVAMAYSGDLSDPNEKLYTLDYYLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKL
VTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDGASGTTVWHHLPSHPLSAIVA
AFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQLSNLRAQ
ATALGLADRFELIEDNYASR

>RXN02328 TRANSLATE of: rxn02328.seq check: 5494 from: 1 to: 1596
VTAITLGGLLLKGIITLVSTHTSSTLPAFKKILVANRGEIAVRAFRAALETGAATVAIYP
REDRGSFHRSFASEAVRIGTEGSPVKAYLDIDEIIGAAKKVKADAIYPGYGFLSENAQLA
RECAENGITFIGPTPEVLDLTGDKSRAVTAAKKAGLPVLAESTPSKNIDEIVKSAEGQTY
PIFVKAVAGGGGRGMRFVASPDELRKLATEASREAEAAFGDGAVYVERAVINPQHIEVQI
LGDHTGEVVHLYERDCSLQRRHQKVVEIAPAQHLDPELRDRICADAVKFCRSIGYQGAGT
VEFLVDEKGNHVFIEMNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKELGLTQDKIKT
HGAALQCRITTEDPNNGFRPDTGTITAYRSPGGAGVRLDGAAQLGGEITAHFDSMLVKMT
CRGSDFETAVARAQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQA
PPADDEQGRILDYLADVTVNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDR

>RXN02333 TRANSLATE of: rxn02333.seq check: 9284 from: 1 to: 915
MNLFSNGVDVGRRRQAFKAALAAPHIARLPGAFSPLIARSIEEAGFEGVYVSGAVIAADL
ALPDIGLTTLTEVAHRARQIARVTDLGVLVDADTGFGEPMSAARTVAELEDAGVAGCHLE
DQVNPKRCGHLDGKEVVRTDVMVRRIAAAVSARRDPNFVICARTDAAGVEGIDAAIERAK
AYLDAGADMIFTEALHSEADFRYFRHAIPDALLLANMTEFGKTTLLSADVLEEIGYNAVI
YPVTTLRIAMGQVEQALAEIKEHGTQEGWLDRMQHRSRLYELLRYEDYNVFDQHIFTYRK
GENNE

>RXN02399 TRANSLATE of: rxn02399.seq check: 7887 from: 1 to: 1344
VVGTAHCESALKEVTLMSNVGKPRTAQEIQQDWDTNPRWNGITRDYTADQVADLQGSVIE
EHTLARRGSEILWDAVTQEGDGYINALGALTGNQAVQQVRAGLKAVYLSGWQVAGDANLS
GHTYPDQSLYPANSVPSVVRRINNALLRSDEIARTEGDTSVDNWVVPIVADGEAGFGGAL
NVYELQKAMIAAGAAGTHWEDQLASEKKCGHLGGKVLIPTQQHIRTLNSARLAADVANTP
TVVIARTDAEAATLITSDVDERDQPFITGERTAEGYYHVKNGLEPCIARAKSYAPYADMI
WMETGTPDLELAKKFAEGVRSEFPDQLLSYNCSPSFNWSAHLEADEIAKFQKELGAMGFK
FQFITLAGFHSLNYGMFDLAYGYAREGMTSFVDLQNREFKAAEERGFTAVKHQREVGAGY
FDQIATTVDPNSSTTALKGSTEEGQFHN

>RXN02404 TRANSLATE of: rxn02404.seq check: 8768 from: 1 to: 2217
MTEQELLSAQTADNAGTDSTERVDAGGMQVAKVLYDFVTEAVLPRVGVDAEKFWSGFAAI
ARDLTPRNRELLARRDELQMLIDDYHRNNSGTIDQEAYEDFLKEIGYLVEEPEAAEIRTQ
NVDTEISSTAGPQLVVPILNARFALNAANARWGSLYDALYGTNAIPETDGAEKGKEYNPV
RGQKVIEWGREFLDSVVPLDGASHADVEKYNITDGKLAAHIGDSVYRLKNRESYRGFTGN
FLDPEAILLETNGLHIELQIDPVHPIGKADKTGLKDIVLESAITTIMDFEDSVAAVDAED
KTLGYSNWFGLNTGELKEEMSKNGRIFTRELNKDRVYIGRNGTELVLHGRSLLFVRNVGH
LMQNPSILIDGEEIFEGIMDAVLTTVCAIPGIAPQNKMRNSRKGSIYIVKPKQHGPEEVA
FTNELFGRVEDLLDLPRHTLKVGVMDEERRTSVNLDASIMEVADRLAFINTGFLDRTGDE
IHTSMEAGAMVRKADMQTAPWKQAYENNNVDAGIQRGLPGKAQIGKGMWAMTELMAEMLE
KKIGQPREGANTAWVPSPTGATLHATHYHLVDVFKVQDELRAAGRRDSLRNILTISTAPN
TNWSEEEKKEEMDNNCQSILGYVVRWVEHGVGCSKVPDIHDIDLMEDRATLRISSQMLAN
WIRHDVVSKEQVLESLERMAVVVDKQNAGDEAYRDMAPKYDASLAFQAAKDLIFEGTKSP
SGYTEPILHARRREFKAKN

>RXN02434 TRANSLATE of: rxn02434.seq check: 219 from: 1 to: 1650
MRTFAAYIAIDGLSFSYPNTHVLSDISLTVANGDIAGLIGENGAGKSTLLSLIAGVMEPD
QGRIYLPERTGFIAQETDLPFEQPVQSLIDAAVAPVRAVDAAITDLSTKLGDASLSAEEQ
AQVATDFDAALGAAEELGLWELDARIETIVAGLGLAEVDRSTPIGELSGGQRRRFALAAL
LLEPHDALIFDEPTNHLDDTAVDFLISEISRFKGPVLIASHDRFFLDSVCTELIDLDPAL
GPEGGSGEEVKQAVSFGGGFSEYIKERETRRTRWAQLYTAQETEREKLEETTGTTESDIF
HSSVSKSEAKITAKFYADRAAKTQGNRVRSAKNRLKELERYEIPAPPKPLEFQGIPEASG
NGHGETLEVRAIAVENRLQPLTFHIDPGDHILVEGPNGVGKSTLLSVLEGVLEPTEGELI
VPEGLKVARLKQDDQWTEKQLNTPVDELFAALSKGPVGLNLVEMGLLRETSQSSPLRALS
LGQRRRVSLGLILASPPDLLLLDEPTNHLSLALSEELESAIEKFPGRVILASHDRWIRKR
WTGKKISLSR

>RXN02461 TRANSLATE of: rxn02461.seq check: 9219 from: 1 to: 408
MRGLIVDYAGVLDGTDEDQRRWRNLLAAAKKNGVGTVILSNDPGGLGAAPIRELETNGVV
DKVLLSGELGVEKPEEAAFQAAADAIDLPMRDCVLVDDSILNVRGAVEAGLVGVYYQQFD
RAVVEIVGLFGLEGEF

>RXN02480 TRANSLATE of: rxn02480.seq check: 3686 from: 1 to: 1656
MTTTDHKQLGIMYIIMSFSFFFLGGLMALLIRAELFTPGLQFLSNEQFNQLFTMHGTVML
LLYGTPIVWGFANYVLPLQIGAPDVAFPRLNAFGFWITTVGGVAMLTGFLTPGGAADFGW
TMYSPLSDAIHSPGLGSDMWIVGVGATGIGSVASAINMLTTILCLRAPGMTMFRMPIFTW
NIFVVSVLALLIFPLLLAAALGVLYDRKLGGHLYDPANGGSLLWQHLFWFFGHPEVYVLA
LPFFGIVSEIIPVFSRKPMFGYVGLIFATLSIGALSMAVWAHHMFVTGAVLLPFFSFMTF
LISVPTGVKFFNWVGTMWKGHITWETPMIWSVGFMATFLFGGLTGIMLASPPLDFHLADS
YFLIAHFHYTLFGTVVFASCAGVYFWFPKMTGRMMDERLGKIHFWLTFVGFHGTFLIQHW
VGNMGMPRRYADYLDSDGFTIYNQISTVFYFLLGLSVIPFIWNVFKSWRYGELVTVDDPW
GYGNSLEWATSCPPPRHNFASLPRIRSERPAFELHYPHMIERMRAEAHTGHHDDINAPEL
GTAPALASDSSR

>RXN02554 TRANSLATE of: rxn02554.seq check: 9544 from: 1 to: 624
MSHTKPSIAILGAGRVGSSLARSAVAAGYEVKVAGSGAVDKIALTAEILMPGAVPSTADQ
AVKDADIVFLAVPLHKFRSVNPATLEGKIVIDTMNHWVPVNGELEEIDQDPRSTSEIIAE
FFAGSTMVKSFNHIGYHEIEQDAGTGRAIAYATDDVDAGAQVAQLIKSFGFVPLNIGALE
NGRILEPGQEAFGAHLNKDSRLELVNQR

>RXN02556 TRANSLATE of: rxn02556.seq check: 1750 from: 1 to: 1158
LIVSTQPITDRSALSAEHAEVIKATLPLVGGKINEITPVFYNKMFAAHPELIANTFNRGN
QKQGDQQKALAASIATFATMLVTPDAPDPVQLLSRIGHKHVSLGITADQYDIVHEHLFAA
IVEVLGAETVTAPVAEAWDAVYWIMANVLIGFENNLYASNDLEPGDVFREVTVTAKKQLS
ATVWEYTLAGELVAPEPGQYTSIGVVLDDGARQLRQYSLLGGSDTEYRIAVEDNGEVSGF
LRDRVSVGDKIEATIAAGDLVLNKDTNPVVLISQGIGSTPMVGMLAGMNPERDVVVLHAD
QAESTYAQVEEVQGLVEKLPKAAFEIFYRDNDQWLEVAGRIPSGASVYLCGGVEFLKNVR
EQIEALDEQPRDVNFELFAPNDWLIS

>RXN02560 TRANSLATE of: rxn02560.seq check: 4626 from: 1 to: 867
MQGNSLNLADNSERKKPMPSPGELLAARYGQPATWTPPQWNETLDVIHQHRSVRRWLDKP

VDDDTIRTIISAAQSAGTSSNKQVISVIVVKDPELRKGLAGITRQMFPHLEQVPAVLIWL
IDYSRISAVAAREDLPTGALDYLDEAAWGFLDAGIAAQNAAIAAESLGLGTLYLGSVRND
AEAVHKLLGLPPEIVPVVGLEMGHADPPEPAGIKPPLPQEAIVHWDTYTEKNLELIDSYD
RALDTYYSRYGQHQLWSKQTAHRAASKSFSKTNRQFLRGVFERAGFGLR

>RXN02591 TRANSLATE of: rxn02591.seq check: 6816 from: 1 to: 1830
MTTAAIRGLQGEAPTKNKELLNWIADAVELFQPEAVVFVDGSQAEWDRMAEDLVEAGTLI
KLNEEKRPNSYLARSNPSDVARVESRTFICSEKEEDAGPTNNWAPPQAMKDEMSKHYAGS
MKGRTMYVVPFCMGPISDPDPKLGVQLTDSEYVVMSMRIMTRMGIEALDKIGANGSFVRC
LHSVGAPLEPGQEDVAWPCNDTKYITQFPETKEIWSYGSGYGGNAILAKKCYALRIASVM
AREEGWMAEHMLILKLINPEGKAYHIAAAFPSACGKTNLAMITPTIPGWTAQVVGDDIAW
LKLREDGLYAVNPENGFFGVAPGTNYASNPIAMKTMEPGNTLFTNVALTDDGDIWWEGMD
GDAPAHLIDWMGNDWTPESDENAAHPNSRYCVAIDQSPAAAPEFNDWEGVKIDAILFGGR
RADTVPLVTQTYDWEHGTMVGALLASGQTAASAEAKVGTLRHDPMAMLPFIGYNAGEYLQ
NWIDMGNKGGDKMPSIFLVNWFRRGEDGRFLWPGFGDNSRVLKWVIDRIEGHVGADETVV
GHTAKAEDLDLDGLDTPIEDVKEALTAPAEQWANDVEDNAEYLTFLGPRVPAEVHSQFDA
LKARISAAHA

>RXN02596 TRANSLATE of: rxn02596.seq check: 6451 from: 1 to: 1203
MTESKNYDLIVVGSGLFGLTVAERAASQLGKKVLIVERRSHLGGNAYSEAEPETGIEIHK
YGAHLFHTSNTRVWEYVNQFTSFTGYQHRVFAMHNGTAYQFPMGLGLINQFFGKYYSPDE
ARELIKEQSAEIDSSDATNLEEKAISLIGRPLYEAFIRDYTAKQWQTDPKNLPAGNITRL
PVRYNFNNRYFNDTYEGLPTDGYAAWLEKMAEHELIDVRLDTDWFDVRDDLRASNPDAPV
VYTGPLDLYFNYAEGKLGWRTLDFETEVVETGDFQGTPVMNYNDADVPFTRIHEFRHFHP
ERDDSYPKDKTVIMREFSRFADNEDEPYYPINTPDDRDMLKQYRLLAAEEAANNKVLFGG
RLGTYQYLDMHMAIGSALSMFDNKLVPFFEEGTPLEQERGH

>RXN02654 TRANSLATE of: rxn02654.seq check: 5233 from: 1 to: 885
MISLLNDPRTLFPKVDPPKQSQPEPGLDIKLSPQADIGLSSYQGSGRLKGRKALITGGDS
GIGAAVAIAYAREGADVAIAYLPEEQADADRVLQAIEETGQKAFSFPGDLRDPEYCRSLV
QETVNALGGLDILVNNASRQVWAPGLTEITDENFDQTLQVNLYGSFRVTKAAIPHLKPGS
SIIFTSSIQAYQPSETLLDYAMTKAALNNLSKGLASSLIGDGIRVNSVAPGPFWTPLQPS
HGQPQEKIEGFGQHAPIGRAGHPVELAGAYVFLASDEASYVVGETLGVTGGTPTP

>RXN02674 TRANSLATE of: rxn02674.seq check: 2941 from: 1 to: 1452
VTATFAGIDATKHLIGGQWVEGNSDRISTNINPYDDSVIAESKQASIADVDAAYEAAKKA
QAEWAATPAAERSAIIYRAAELLEEHREEIVEWLIKESGSTRSKANLEITLAGNITKESA
SFPGRVHGRISPSNTPGKENRVYRVAKGVVGVISPWNFPLNLSIRSVAPALAVGNAVVIK
PASDTPVTGGVIPARIFEEAGVPAGVISTVAGAGSEIGDHFVTHAVPKLISFTGSTPVGR
RVGELAINGGPMKTVALELGGNAPFVVLADADIDAAAQAAAVGAFLHQGQICMSINRVIV
DAAVHDEFLEKFVEAVKNIPTGDPSAEGTLVGPVINDSQLSGLKEKIELAKKEGATVQVE
GPIEGRLVHPHVFSDVTSDMEIAREEIFGPLISVLKADDEAHAAELANASDFGLSAAVWS
KDIDRAAQFALQIDSGMVHINDLTVNDEPHVMFGGSKNSGLGRFNGDWAIEEFTTDRWIG
IKRS

>RXN02675 TRANSLATE of: rxn02675.seq check: 8425 from: 1 to: 1857
MNEFDQDILQEIKTELDELILELDEVTQTHSEAIGQVSPTHYVGARNLMHYAHLRTKDLR
GLQQRLSSVGATRLTTTEPAVQARLKAARNVIGAFAGEGPLYPPSDVVDAFEDADEILDE
HAEILLGEPLPDTPSCIMVTLPTEAATDIELVRGFAKSGMNLARINCAHDDETVWKQMID
NVHTVAEEVGREIRVSMDLAGPKVRTGEIAPGAEVGRARVTRDETGKVLTPAKLWITAHG
SEPVPAPESLPGRPALPIEVTPEWFDKLEIGSVINVPDTRGSRRAFTVTRVFDGAVLAEG
PQKAYISNGTLLEHNYDRSRVYGIPAVVQRINLKVGDRLILTDEELTYDPSLGSGRTPRI
SCTLPQAVDAIKVGHRVLFDDGAIAAVCIDKTSTADGHNDVELEVTHARPQGVNLAAYKG
INLPDSELPLPSLTEEDLQHLRFVVKYADIAAISFIRNVADVEYLLQALADIGDPVAVER
LGLVLKIETIPGYEGLAQILLTGMRHENFGIMIARGDLAVELGFDRMAEVPQLIMALAEA
AHVPTILATQVLENMAKNGLPSRAEITDAAMALRAECVMLNKGPHINDAIKVLTEMSRKL
GASQRKSRLLLRKVKSWEE

>RXN02688 TRANSLATE of: rxn02688.seq check: 959 from: 1 to: 669
MAGRIILLRHGQTHNNVKHLLDTRPPGAELTDLGRKQALEVGHELATYSGERLAHVYSSI
VLRAQQTAVLATSTFEKARDMQSGAIPLDVVEGIQEINVGDFEMRGDEEAHMNYSRALNG

WLHGDPAAGLPGGETYKDVLNRYQPTLDRIMDSHDLDDDRDVAVVSHGAVIRIVATHATG
VDPNFAFNTYLGNCRFVVLEPNGKKFSQWDVVRWTDSPLPWQE

>RXN02765 TRANSLATE of: rxn02765.seq check: 9432 from: 1 to: 759
MSNQLPDHVRDAFQVGAGPAEQLGQAWDFGFRVGNTVFAKVTAPEVSGWSSKTRETLKPE
GVRVVRPIRSTDGRFVVAGWRASVFSTGTISKRVDETVVAGLRLADALVDTHAPEPVDNV
FNRADVQAWEEQPGRIGELLEPINRVNQVGHADMLATTLYAGTQPPAVTDLVPVLRPHGF
TAALVIVDGLLLGAVDEGILRRFSHLPEIEQLVLRAFLFRRNLQEFSENNDPNVISNLNR
VESTLVSYVSDKI

>RXN02803 TRANSLATE of: rxn02803.seq check: 251 from: 1 to: 657
VSGEMLAAALSAGMASQGVDVIRVGVIPTPAVAFLTDDYGADMGVMISASHNPMPDNGIK
FFSAGGHKLPDHVEDEIERVMDSLPAEGPTGHGVGRVIEEATDAQDRYLEHLKEAVPTSL
EGIKIVVDAANGAASVVAPTAYEAAGATVIAIHNKPDSYNINMDCGSTHIDQAQPPVLKH
GADLGLAHDGDADRCLAVNKDANLVDGDQIMALLAIAMK

>RXN02821 TRANSLATE of: rxn02821.seq check: 9220 from: 1 to: 240
MNEIILAQDATESTITGLGAVGYGIATIGPGLGIGILVGKALEGMARQPEMAGQLRTTMF
LGIAFVEALALIGLVAGFLF

>RXN02829 TRANSLATE of: rxn02829.seq check: 1194 from: 1 to: 273
MQKNILKSGIEISELGLGCMSLGTDYKKAQPIIESAIDNGITYFDTADIYDQGVNEEIVG
KALKKYQNRDDIVIGTKVGNRLTDDGHMTWD

>RXN02920 TRANSLATE of: rxn02920.seq check: 9771 from: 1 to: 912
MKFVMYPHLWESTTAVIEGGGHERVEDIKDADFIFFNGSAPEFPDLPENIKFVQASMAGI
DALVKRGVVNEKARWANAAGLYADTVAESTIGLILAQMHMHATTRLAKSWSVRPEVENNK
SWLHDNKTVAILGAGGIGVRLLEMLKPFNVKTIAVNNSGRPVEGADETFAMDKAEHVWAE
ADVFVLILPLTDATYQIVNAETLGKMKPSAVVVNVGRGPLINTDDLVDALNNGTIAGAAL
DVTDPEPLPDSHPLWEMDNVVITPHTANTNERIRALTGELTLRNIELFEAGEQMATEVDV
VAGY

>RXN03014 TRANSLATE of: rxn03014.seq check: 5818 from: 1 to: 906
YVGFEVLLVASYVLLTLGASPARVRSGVGYVMVSMASSMVFLFGLAMVYASVGTLNMAHV
GLRMEDVPSGTRSAIFAVLLVAFGIKAAVFPLDSWLPDSYPTAPSLVTAVFAGLLTKVGV
YSIIRARSIIFTDGSLDTMLMWVALATMLIGILGAMAQNDIKRLLSFTLVSHIGYMIFGV
ALGSAQGLSGAIFYAIHHILVQTSLFLVVGLVERQAGSSSLRRLGSLAYISPLLAILYFI
PAINLGGIPPFSGFLGKIMLIEAGARRWQLAGMGPYRRRRCHLTAHLVHHGSGLVQGLLA
RP

>RXN03015 TRANSLATE of: rxn03015.seq check: 9736 from: 1 to: 282
LGVGTPQQKGTYAADLTYVRQVVEDLVPLLEGEHIIFGKSTVPVGTAEQLQELADSLVKP
GSHVEIAWNPEFLREGYAVKDTITPDRIVVGVRE

>RXN03030 TRANSLATE of: rxn03030.seq check: 5862 from: 1 to: 564
VLPLDPAASLKIYPLVTGRTKIDEVQLQLEAAIRAELPGVTLVSSESEADLAIVWARPEI
ALFEDDLEGVSLSVDPRANGVDVERVQAVEAAVPTILAVNFTNPWVLSEIEPGAAAVVGT
FEIKPEFLLKALTGQEGGPKGKLPLTVPASMQAIADSPRDIPGKFLDESYTYVDSAGMAY
KYGHGLNF

>RXN03043 TRANSLATE of: rxn03043.seq check: 4634 from: 1 to: 1362
DLDGFRQEVSREQGGIPSYPHPHGMKDFWEFPTVSMGLGPMDAIYQARFNRYLENRGIKD
TSDQHVWAFLGDGEMDEPESRGLIQQAALNNLDNLTFVVNCNLQRLDGPVRGNTKIIQEL
ESFFRGAGWSVIKVVWGREWDELLEKDQDGALVEIMNNTSDGDYQTFKANDGAYVREHFF
GRDPRTAKLVENMTDEEIWKLPRGGHDYRKVYAAYKRALETKDRPTVILAHTIKGYGLGH
NFEGRNATHQMKKLTLDDLKLFRDKQGIPITDEQLEKDPYLPPYYHPGEDAPEIKYMKER
RAALGGYLPERRENYDPIQVPPLDKLRSVRKGSGKQQIATTMATVRTFKELMRDKGLADR
LVPIIPDEARTFGLDSWFPTLKIYNPHGQNYVPVDHDLMLSYREAPEGQILHEGINEAGS
VASFIAAGTSYATHGKAMIPLYIFYSMFGIPAHR

>RXN03044 TRANSLATE of: rxn03044.seq check: 1253 from: 1 to: 831
MARGFLLGATAGRTTLTGEGLQHMDGHSPVLASTNEGVETYDPSFAYEIAHLVHRGIDRM
YGPGKGEDVIYYITIYNEPTPQPAEPEGLDVEGLHKGIYLYSRGEGTGHEANILASGVGM
QWALKAASILEADYGVRANIYSATSWVNLARDGAARNKAQLRNPGADAGEAFVTTQLKQT
SGPYVAVSDFSTDLPNQIREWVPGDYTVLGADGFGFSDTRPAARRFFNIDAESIVVAVLN
SLAREGKIDVSVAAQAAEKFKLDDPTSVSVDPNAPEE

>RXN03056 TRANSLATE of: rxn03056.seq check: 8420 from: 1 to: 678
LDAAGISLSAVGSDFGKINITDPFEDHLERARHGVEVAKLFGAKYIRMFSFFIAEGDNPE
SFRKEVLSRTHAMVELAEAGGITLLHENEKGIYGDSPQRVKDLITSIDSPNYRAIYDAAN
YVQTGFKPFDEAWPIVKDYVDYVHIKDATIPDAEHPIGIIKPAGQGDGQYPELLAALNAD
GYNGFVSIEPHLGDFDEFGGLCGPDLWTSACDALAGILNNINAEYN

>RXN03057 TRANSLATE of: rxn03057.seq check: 8669 from: 1 to: 672
LASDLGIKFVAVVDKDLETAEKFATGLGAAGDSSESSVKAHGSLPALFSKKKIDVLHITT
PHDQHIGLALEALHHGVNVILEKPLANELDQAQRLIDYLDENPDGPKIAVCYQNRYNVSS
QELRRLLDSGDLGAINGAYSSVVWTRTPGYYTQKPWRGQQAHSGGGLLMNQAIHTLDLLQ
WFLGKATEVKGTVSTDKYADVIDVEDTAHAYIGHESGVHTSEVS

>RXN03061 TRANSLATE of: rxn03061.seq check: 2307 from: 1 to: 330
VSLTFPVINPSDGSTITELENHDSTQWMSALSDAVAAGPSWAAKTPRERSVVLTAIFEAL
TERAQELAEIIHLEAGKSDAEALGEVAYGAEYFRWFAEEAVRLPGRYGQS

>RXN03076 TRANSLATE of: rxn03076.seq check: 6328 from: 1 to: 1590
MDESRQLSFGTAGLRAPVGPARHQMNVLQVTRTTAGVASWLAERAALNPVPHLVPEDETG
IGRALYPQDGPLRVVVGYDARYGSHTFAATTAEVFAGAGFEVTLLPTPSPTPLIPWLVNK
HGLDAGVQITASHNGAADNGYKVFLSNGRQLYSELEPELEAHINAVEDPIRVPRVTVRPT
ADQLRRYVDEMVSLVTPDQADLLRVNSERGNLRVVYTALHGVGGRAMANAFQFAGFPHTH
GVKAQQYPDPTFPTVAFPNPEEPSAIELLLERAKEKNADILFALDPDADRCAVGIRTADG
GHRMLSGDEVGTLLATRLVPEYSGEGPRPVVATTVVSSQLLGIIAEDKGWDYSETLTGFK
NLSRAADGLDGPLAFAYEEAVGTCPVPDVVPDKDGISTALFMASWAAELKAQGASLQQKL
NELYRRYGYFASSQIAVRTSSPRELVDHWIAHPQQELIGVSVTPHILPEKQGIALHGQVG
HVHIRAIGRVSGTEAKAKLYLEVGQASSHDEAAQLLHQLEDEVQSWLSKL

>RXN03083 TRANSLATE of: rxn03083.seq check: 465 from: 1 to: 1023
MAKRIVIIGGGPAGYEAALAGAKYGAEVTVIEDVGVGGSAVTMDCVPSKSFIAGTGIKTD
LRRADDMGLNRGLGKAHLEIDALNIRVKDLAKAQSEDILGQLQRSDVRMINGVGRFDDYN
TKQTTHYIKVTHSDGSEETVECDLVLVATGATPRILKGAEPDGERILTWRQVYDIEELPT
HLIVVGSGVTGAEFVSAFAELGVKVTMVASRDRILPHDDADAADVLETVLAERGVSLEKH
ARVESVTRTEDGGVCVRTADGREIYGSHALMTVGSIPNTADLGLENIGVELAPSGHIKVD
RSPAPTSPVCTQQVTVLTYSHWRPLQRCRAVSPCITHSVKA

>RXN03086 TRANSLATE of: rxn03086.seq check: 7524 from: 1 to: 408
MADQAKLGGKPSDDSNFAMIRDGVASYLNDSDPEETNEWMDSLDGLLQESSPERARYLML
RLLERASAKRVSLPPMTSTDYVNTIPTSMEPEFPGDEEMEKRYRRWIRWNAAIMVHRAQR
PGIGVGGHISTYAGAA

>RXN03087 TRANSLATE of: rxn03087.seq check: 9553 from: 1 to: 213
MKIYAPFAGIVHYFVDEGDPVETGMQLGTVETIKLEAPIMAPGPGIVAKVSFDDFSDVTG
GDELLELEAKN

>RXN03096 TRANSLATE of: rxn03096.seq check: 423 from: 1 to: 402
MVLVWSKAFWRDRKDAPDGATALARPAPLVDIQDEVAVKDRNDVGRMPWGMVFSTALLVS
ASLAVSVLAGPLSSITGRAAESAQDVNIYRAAVLGPTTSTHHAHSRWSVTTPTAMTSTTA
STPMERRTNHDQWI

>RXN03101 TRANSLATE of: rxn03101.seq check: 8362 from: 1 to: 582
ILADEDDTVDVGAVIARIGDANAAAAPAEEEAAPAEEEEPVKEEPKKEAAPEAPAATGAA
TDVEMPELGESVTEGTITQWLKAVGDTVEVDEPLLEVSTDKVDTEIPSPVAGTIVEILAD

EDDTVDVGAVIARIGDANAAAAPAEEEAAPAEEEEPVKEEPKKEEPKKEEPKKEAATTPA
AASATVSASGDNVP

>RXN03112 TRANSLATE of: rxn03112.seq check: 9249 from: 1 to: 504
VEIFGKTVGIVGFGHIGQLFAQRLAAFETTIVAYDPYANPARAAQLNVELVELDELMSRS
DFVTIHLPKTKETAGMFDAHLLAKSKKGQIIINAARGGLVDEQALADAIESGHIRGAGFD
VYSTEPCTDSPLFKLPQVVVTPHLGASTEEAQDRAGTDIADSVLKALA

>RXN03117 TRANSLATE of: rxn03117.seq check: 3867 from: 1 to: 1512
MITHEVRTHRSAEEFPYKKHLAHKMARVAADPVEVAADTQEMIITRIIDNASVQAASVLR
RPVSSARAMAQVRPVTDGRGASVFGLPGRYAAEWAALANGTAVRELDFHDTFLAAEYSHP
GDNIPPILAAAQQAGKGGKDLIRGIATGYEIQVNLVRGMCLHEHKIDHVAHLGPSAAAGI
GTLLDLDVDTIYQAIGQALHTTTATRQSRKGAISSWKAFAPAFAGKMSIEAVDRAMRGEG
APSPIWEGEDGVIAWLLSGLDHIYTIPLPAEGEAKRAILDTYTKEHSAEYQSQAPIDLAR
SMGEKLAAQGLDLRDVDSIVLHTSHHTHYVIGTGSNDPQKFDPDASRETLDHSIMYIFAV
ALKDRAWHHERSYAPERAHRRETIELWNKISTVEDPEWTRRYHSVDPAEKAFGARAVITF
KDGTVVEDELAVANAHPLGARPFAREQYIQKFRTLAEGVVSEKEQDRFLDAAQRTHELED
LSELNIELDADILAKAPVIPEGLF

>RXN03144 TRANSLATE of: rxn03144.seq check: 7951 from: 1 to: 900
TTTATRQSRKGEISSWKAFAPAFAGKMAIEAMDRAMRGEGSPAPIWEGEDGVIAWLLSGK
DHVYHVPLPEHGEPKLGILETYTKEHSAEYQSQAPIDLARRMKPLVDAAGGTEHIAEIVL
RTSHHTHYVIGTGANDPQKMDPQASRETLDHSIMYIFAVALQDGVWHHEFSYTRKRSTRP
ETVELWHKIRTVEDPEWTRRYHSDDPAKKAFGAKAVITMADGTVIEDELAVADAHPLGAR
PFARENYIEKFRTLAQGIVIDSEQERFLHAVQSLPDLDDLDQLNIEVDISNQAATKAGLL

>RXN03150 TRANSLATE of: rxn03150.seq check: 9986 from: 1 to: 624
VEAQFTSPLLNNGQTCFLGTRILAPKSRYAEVVDAFTAFAGSLQVGVTSSPDTQIGPMAT
ARQRERVESYISQGKNAGARITVGGSRPRDLDAGFFVEPTVFADVDNRAAIAQDEIFGPV
PSVVSYQDDEHAIQLANDSEFGLGGTVWTSDPERGAALARRVHTGTIGINRYIPDPAAPF
GGVKNSGLGRELGPEGLASYQETQTIYL

>RXN03179 TRANSLATE of: rxn03179.seq check: 7214 from: 1 to: 666
AREAWRIFMSHWDLYAGTATGYWVEQEFEHVFGINAERLNVGTPEHADAIFDELTDILAK
PDFRPRALAEQFNLEVLATTDDPLDDLADHKALADDPTFSPRVLPTFRPDAYTKMYNAGW
AEKTTKLIDTAGDGKAGWEGYLQAMRNRRQYFINHGATSADHGLHDTDTTPLSHKDAQKI
LDKGLAGTATLAEMHAFEANTTYRSRKCPRRRLVMTIHQVCT

>RXN03180 TRANSLATE of: rxn03180.seq check: 39 from: 1 to: 510
FGENKDLISDSSFNRWLRTVSLGSTQDADMAAASNLAANSKMARQNTRDILDAVSDGGVM
LGRNGALVLGPVVGTLHIKFIAPLNKRVERVMYKTGLSEAAAAEQCALEDRLREEMAHAL
YQWNPGRDENYDLVINTGSMTYEQIVDLVVETYARKYPLHVRIIPNGKDQ

>RXN03186 TRANSLATE of: rxn03186.seq check: 9438 from: 1 to: 210
MADQAKLGGKPSDDSNFAMIRDGVASYLNDSDPEETNEWMDSLDGLLQESSPERARYLML
RLLERASAKR

>RXN03187 TRANSLATE of: rxn03187.seq check: 1211 from: 1 to: 279
VAVSDFSTDLPNQIREWVPGDYTVLGADGFGFSDTRPAARRFFNIDAESIVVAVLNSLAR
EGKIDVSVAAQAAEKFKLDDPTSVSVDPNAPEE

>RXS00584 TRANSLATE of: RXS00584.seq check: 7788 from: 1 to: 1125
MHSPERQEKMSSPVSLENAASTSNKRVVAFHELPSPTDLIAANPLTPKQASKVEQDRQDIADIFAGDDD
RLVVVVGPCSVHDPEAAIDYANRLAPLAKRLDQDLKIVMRVYFEKPRTIVGWKGLINDPHLNETYDIPE
GLRIARKVLIDVVNLDLPVGCEFLEPNSPQYYADTVAWGAIGARTTESQVHRQLASGMSMPIGFKNGTD
GNIQVAVDAVQAAQNPHFFFGTSDDGALSVVETAGNSNSHIILRGGTSGPNHDAASVEAVVEKLGENAR
LMIDASHANSGKDHIRQVEVVREIAEQISGGSEAVAGIMIESFLVGGAQNLDPAKLRINGGEGLVYGQS
VTDKCIDIDTTIDLLAELAAAVRERRAAAK

>RXS01260 TRANSLATE of: RXS01260.seq check: 3260 from: 1 to: 1182

VTFNYEDAHKRSRGVSDKIVGGVHYLMKKNKIIEIHGLGNFKDAKTLEVTDGKDAGKTITFDDCIIATG
SVVNTLRGVDFSENVVSFEEQILNPVAPKKMVIVGAGAIGMEFAYVLGNYGVDVTVIEFMDRVLPNEDA
EVSKVIAKAYKKMGVKLLPGHATTAVRDNGDFVEVDYQKKGSDKTETLTVDRVMVSVGFRPRVEGFGLE
NTGVKLTERGAIEIDDYMRTNVDGIYAIGDVTAKLQLAHVAEAQGIVAAETIAGAETQTLGDYMMMPRA
TFCNPQVSSFGYTEEQAKEKWPDREIKVASFPFSANGKAVGLAETDGFAKIVADAEFGELLGAHLVGAN
ASELINELVLAQNWDLTTEEISRSVHIHPTLSEAVKEAAHGISGHMINF

>RXS01261 TRANSLATE of: RXS01261.seq check: 5376 from: 1 to: 171
VTEHYDVVVLGAGPGGYVSAIRAAQLGKKVAVIEKQYWGGVCLNVGCIPSKVSDQKR

>RXS01758 TRANSLATE of: RXS01758.seq check: 8853 from: 1 to: 1017
MPKYIAMQVSESGAPLAANLVQPAPLKSREVRVEIAASGVCHADIGTAAASGKHTVFPVTPGHEIAGTI
AEIGENVSRWTVGDRVAIGWFGGNCGDCAFCRAGDPVHCRERKIPGVSYAGGWAQNIVVPAEALAAIPD
GMDFYEPAPMGCAGVTTFNALRNLKLDPGAAVAVFGIGGLVRLAIQFAAKMGYRTITIARGLEREELAR
QLGANHYIDSNDLHPGQALFELGGADLILSTASTTEPLSELSTGLSIGGQLTIIGVDGGDITVSAAQLM
MNRQIITGHLTGSANDTEQTMKFAHLHGVKPLIERMPLDQANEAIARISAGKPRFRIVLEPNS

>RXS02574 TRANSLATE of: RXS02574.seq check: 9855 from: 1 to: 1008
LARAQIPEQQRDQVASLMMVGVANYDQALDALNQGVGGIFIGSWTDENLLTEPGRNIEALREAVGRDFS
VSIDFEGGRVQRATNILGDFPSPRVMAQTMTPEQVEDLAEILGTGLAAHGVTVNFAPVVDVDAWGLPVV
GDRSFSNDPAVAATYATAFAKGLSKVGITPVFKHFPGHGRASGDSHTQDVVTPALDELKTYDLIPYGQA
LSETDGAVMVGHMIVPGLGTDGVPSSIDPATYQLLRSGDYPGGVPFDGVIYTDDLSGMSAISATHSPAE
AVLASLKAGADQALWIDYGSLGSAIDRVDAAVSSGEYPQEQMLASALRVQLLYITRLEQK

>RXS02735 TRANSLATE of: RXS02735.seq check: 6182 from: 1 to: 705
MVDVVRARDTEDLVAQAASKFIEVVEAATANNGTAQVVLTGGGAGIKLLEKLSVDAADLAWDRIHVFFG
DERNVPVSDSESNEGQAREALLSKVSIPEANIHGYGLGDVDLAEAARAYEAVLDEFAPNGFDLHLLGMG
GEGHINSLFPHTDAVKESSAKVIAVFDSPKPPSERATLTLPAVHSAKRVWLLVSGAEKAEAAAAAIVNGE
PAVEWPAAGATGSEETVLFLADDAAGNL

>RXS03215 TRANSLATE of: RXS03215.seq check: from: 1 to: 1008
IDVVSVVVANFLHREIVEALLASGKHVLCEKPLSDTIEDAEAMIEAAGRAATNGTIARIGLTYRRSPGV
AHIRDLVQSGELGKVLHVTGHYWTDYGSNAQAPISWRYKGPNGSGALADVGSHLTYLAEFVAGSDFAAV
RGGQLSTVITERPKPLGAIVGHEGGAVSDEYEAVENDDIASFSGSFIGGGTATLQVSRISQGHPNTLGF
EVFCEKGSVLFDFRNSGEFKIFTPATSGDISQEAGYRTITIGPKHPYWRGGLAMDAPGVGIGQNEGFVF
QARAFLEEIAGISEAESLPRCATLEEGLHNMQLIDAVSQSAAAGGETVAVPAAALIPANN

>RXS03224 TRANSLATE of: RXS03224.seq check: from: 1 to: 1158
MSFAEHAIIWHVYPLGALGAPIRPEAPAPVTHRLPNLIGWLDYVVELGCNALMLGPVFESVSHGYDTLD
FYRIDPRLGTEEDMDALLEAANQRGIGVLFDGVFNHVSSSSKYLDLTTGASFEGHDILAELDHTNPAVV
DLVVDVMNHWLDRGIAGWRLDAVYAIAPEFWEKVLPEVRRKHPHAWIVGEMIHGDYSDYVKSSGIDSVT
EYELWKAIWSSIKERNFFELEWTLSRHNEFLDTFVPQTFIGNHDVTRIATRIGQSNAILAAAILFTVGG
TPSIYYGDEQGFTGLKEDNVFGDDAIRPPLPAEFSPLGTWIENIYKALIALRRQHPWLYQAHTEVLEIA
NEAMTYKSVGLGGEELTVHLDLEEVSVRILDGEKVLFQYSA

>RXC00233 TRANSLATE of: RXC00233.seq check: 7055 from: 1 to: 417
MSVNEADLNAVEEQLGRAPRGVLDISYRSPDGVPGVVMTAPKLDDGTPFPTLYYLTDPRLTTEASRLEV
ALVMKWMTDRLSTDEELRADYQRAHEHFLAKRNAIEDLGTDFSGGGMPDRVKCLHVLIDYALAEGPHHF
L

>RXC00236 TRANSLATE of: RXC00236.seq check: 116 from: 1 to: 726
MVISFVGWALSFMDGTAPIRQLQQIPEDVPPARGVEVPQIDTEADGRTSNHLRFWAEPIAQDTGVSAQA
IAAYGNAELIASTAWPGCNLGWNTLAGIGQVETRHGTYNGKMFGGSSLDENGVATPPIIGVPLDGSPGF
AEIPDTDGGELDGDTEYDRAVGPMQFIPETWRLMGLDANGDGVADPNQIDDAALSAANLLCSNDRDLST
PEGWTAAVHSYNMSNQYLMDVRDAAASYALRQPAI

>RXC00271 TRANSLATE of: RXC00271.seq check: 7582 from: 1 to: 990
MFSSRSKVLASIFTVGALALASCSSDSSDSSTSTDAAGGDSYRVGINQLVQHPALDAATTGFKEAFEEA
GVDVTFDEQNANGEQGTALTISQQFASDNLDLVLAVATPAAQATAQNITDIPVLFTAVTDAVSAELVDS
NEAPGGNVTGTSDIAPIEQQLELLQQLVPDAKSIGIVYASGEVNSQVQVDEVTKAAEPLGLSVNTQTVT

TVNEIQQAVEALGDVDVIYVPTDNMVVSGISSLVQVAEQKQIPVIGAESGTVEGGALATLGIDYTELGR
QTGEMALRILQDGEDPATMPVETATEFTYVINEDAAERQGVEIPQEILDKAERV

>RXC00338 TRANSLATE of: RXC00338.seq check: 9343 from: 1 to: 1140
VSDVTVGDIRRILDEAYPPALAESWDKVGLICGDPTESVKRVGLALDCTQAVADKAVDMGLDMLIIHHP
LLLRGVTSVAADEPKGKVIHTLIRGGVALFSAHTNADSARPGVNDKLAELVGITAGRPIATRLLGGMDK
WGVHVLPKDAAYLKKMLFDAGAGAIGDYRECAFEIEGTGQFRPVEGANPAEGDVDKLFKSLELRIEFVA
PRNLRARLTSVLREAHPYEEPAFDIVEMHSAESLENATGLGRVGELPEPMRLADFVQQVANNLPVTEWG
VRATGDPEQMVSRVAVSSGSGDSFLNDVIKLGVDVYVTSDLRHHPVDEYLREGGPAVIDTAHWASEFPW
TSQAQEILQDKAPQVEVDVISIRTDPWTMSARAVN

>RXC00362 TRANSLATE of: RXC00362.seq check: 1707 from: 1 to: 1347
MGIIALLVFIAIAVILNVFLKRDISEALLVGLVGTALVGGVNAPTLLIDAVVDAAQSEVTFAGMAFVFM
GIVVQSTGLIDRLIAILNSIFGRLRGGAGYVSTLGSALIGLIAGSTAGNSATVGSVTIPWMKKTGWTAE
RSATLVAGNSGLGVALPPNSTMFIILALPAAAASSASQVYIALACGGAYAVLYRLAVVFYWTRKDKIPA
TPDDQRVSFGEAMKTGWRSPLIFLGILIPVILTIGPLSEWLKTHGVGESGVKSMSIIVWVPILITAIAL
IEGRKRIANNMAHFRVQISKDLPQFATVGISLFSALAAANIMEELGVGPQLSNWLDSMDLPKSVMVIIV
CIMCIVVATPLSSTATAAAIGAPAVAALAAVGIDPTVAIVVILLCTSTEGASPPVGAPIYLSAAIADAN
PTKMFVPLITYFVVPMILLAWLVGMGFLPVIVPTG

>RXC00412 TRANSLATE of: RXC00412.seq check: 7568 from: 1 to: 1080
VSHTASTPTPEEYSAQQPSTQGTRVEFRGITKVFSNNKSAKTTALDNVTLTVEPGEVIGIIGYSGAGKS
TLVRLINGLDSPTSGSLLLNGTDIVGMPESKLRKLRSNIGMIFQQFNLFQSRTAAGNVEYPLEVAKMDK
AARKARVQEMLEFVGLGDKGKNYPEQLSGGQKQRVGIARALATNPTLLLADEATSALDPETTHEVLELL
RKVNRELGITIVVITHEMEVVRSIADKVAVMESGKVVEYGSVYEVFSNPQTQVAQKFVATALRNTPDQV
ESEDLLSHEGRLFTIDLTETSGFFAATARAAEQGAFVNIVHGGVTTLQRQSFGKMTVRLTGNTAAIEEF
YQTLTKTTTIKEITR

>RXC00526 TRANSLATE of: RXC00526.seq check: 7744 from: 1 to: 690
MSLIEMRNIVKTYNIGSEGELTVLHGVDFHVDRGEFVSVVGTSGSGKSTMMNIIGLLDKPTDGTYTLDG
VDVLDISDDALASHRAKSIGFVFQNFNLIGRIDALKNVEMPMMYAGIPAKQRRSRAVELLEMVGMGERL
NHEPNELSGGQKQRVAIARALANDPEIILADEPTGALDSATGRMVMDIFHQLNKEQGKTIVFITHNPEL
ADESDRVVTMVDGRIIGSEVKHS

>RXC01004 TRANSLATE of: RXC01004.seq check: 9066 from: 1 to: 1062
VSIWATVLLIIVLLSANAFFVAAEFALISSRRDRLDSLVSQGKKGAEKVLYATEHLSIMLAGAQFGITV
CSLILGKVAEPAIAHFIEVPFTSWGVPNDLIHPISFVIALAIITWLHILFGEMVPKNIAIAGPETLGMW
LAPVLIAFVKITRPLIEFMNWIARLTLRAFGVEQKNELDSTVDPEQLASMISESRSEGLLDAEEHARLS
KALRSEQRSIKELVIKDEDVRTLAFGKSGPTLHQLEEAVRETGFSRFPVTGRDGSYLGYIHIKDILPRL
ADPEMDPSETIPRSALRPLSNVDADGLMDDVLDFMHYRSAHMAQVRLKGELLGVITLEDLIEEYVGTVN
DWTHESSDD

>RXC01017 TRANSLATE of: RXC01017.seq check: 6264 from: 1 to: 609
MAQKVTFWFDTTCPFCWVTSRWIKEVEQVRDIEIQWVPMSLAVLNEGRDLPEDYKERMKAAWGPARVFA
AVATDHADKLGDLYTAMGTRIHNDGRGPIEGSFNDVIAEALEEVGLDAALGEVADTTEWDDALRAFHQT
AMDEVGNDVGTPVVKLGDTAFFGPVLTRIPRGEEAGEIFDASFKLASYPHFFEIKRSRTENPQFD

>RXC01021 TRANSLATE of: RXC01021.seq check: 6144 from: 1 to: 522
MSSSESSRSEGSQPAPSVQPERRADSTGAPAAASKEASQQMDAAGVLEWARTAVEQLSERRAEINALNV
FPVPDADTGSNMTYTMTAALDEALKLGELGDVARITEALAVGSVRGARGNSGVVLSQVLRAIAQAAADG
VIDGHTIQEALSIARSLVDRAITDPVEGTVVTVLRS

>RXC01212 TRANSLATE of: RXC01212.seq check: 3583 from: 1 to: 924
MPMTTTPAIDVTDLVRTYGDYTAVKGLNFHVQRGEVFGLLGTNGAGKTSTLEVIEGLSAPSSGTVRISG
LDPVADRAILRPELGIMLQSGGLPSQLTVAETMDMWHGTCTYPRAIKDVLADVDLLHRENVKVGALSGG
EQRRLDLACALLGDPSILFLDEPTTGLDPESRRHTWQLLLDLKQRGVTMMLTTHYLEEAEFLCDRIAIM
NAGEIAVEGTLDELVAREKSIISFVLRGGQVELPVLSGAEIIRDNNHVRIATTTLQQHTLEILTWAAET
GIALEGFAAKPATLESVFMDIASLENTSLQTA

>RXC01306 TRANSLATE of: RXC01306.seq check: 7259 from: 1 to: 1008

MTEWYVVLPATILLIALSAFFVIIEFALLAARRNRLEETVETSRSSRAALRSLNELTLMLAGAQLGITM
VTFALGAITKPWVHYALMPLFEWARIPLVMADVIAFILSLFIVTFLHLVIGEMAPKSWAIAHPETALRT
IAIPARGFINLFRPLLQWINKMANDLVRKVGETPVDRAAAGGYDTDTLHALIEHSRETGALDQQSAAQI
SGIIKLDKITVGQTLTASPFTHSASATVAEVQAAAQRSGSLRVLIDAPSHLFPHVIHVRDTLGASPDEK
ASKWSRPILTVAETDTLHQALEYMREHNEQISAVLSADGKTVLGVITWDHILKYLWPASV

>RXC01366 TRANSLATE of: RXC01366.seq check: 5562 from: 1 to: 390
VSQFRRCSRPGCGKPAVATLTYAYSDSTAVVGPLAPAAEPHSWDLCEHHAERITAPLGWEMLRVNDIKV
DDDEDLTALAQAVREAGRTVSGLVPEDEVGGNHPVNRSARIAEQKVHRRGHLYVVPDQDES

>RXC01372 TRANSLATE of: RXC01372.seq check: 5614 from: 1 to: 591
QDTFVLPTLPTAAGLSPARIVASISTLLDLLEADPSIISDRLEHLADCIDEEVESLSPERDELVNPGRK
LRAYVDHARIVHTGRTDVGLAIANVIAPIWTRRGLVSAVLDFPELMESLPELRGPEPITDDIFHDPFID
DEPGVVPFRAVVWAEEEPGIPDAMAQSCDGPSKGALTQALRLLVRGQSATTYSIEEKDL

>RXC01659 TRANSLATE of: RXC01659.seq check: 8569 from: 1 to: 546
VAGVAQRFVDERIHVGLDSMPEAVTAVWMESDWVLAETIKGSTPSDWEEILRPLALLTDASFTLPPRST
RAQTLDLKHLEPSRLKPEQPEKPAFTPNASEEDLSQPLVIRPEEPLQMPVRGVQESRGVVEPRSLGADD
VESIAEGDPERPSDLYGTRVLRDLNGQSSIFQDSTDADEPPKKW

>RXC01663 TRANSLATE of: RXC01663.seq check: 7844 from: 1 to: 858
MEISVLIIAALILVAGIVLWRADSSKQAAKKAESPVGSVAPAPVLVEEEPDPEFEPELDPEPEAQPEPE
LEVAPRFAPEPVQDLEPDQAEDIYFDDSPELDADVENALAELTEVEDYPEEPVQSEQPQAPATAEVAAD
EEQRGVDKHSFLSSLPGSQRRERRNWAAKHHFDFIKEDAFLTDEWSRGAASTGAVARDVVSGMAEGYET
HLVDLAGVPVMAMRRGITSDVVIDARRGEQPADPEREESDDLVEIDTVSGFRLLSTWRGLRSVLSTSAF
TSVWIPCQKL

>RXC01693 TRANSLATE of: RXC01693.seq check: 6379 from: 1 to: 1422
MNTAPFKLEADFASALPTMAAPWQGEEAPNPELVILNDDLAYSLGLDPTWLRTPEGVQFLLGLNPEPLT
KAVAQAYSGHQFGQFVASLGDGRALLLGEARSADGVLHDIHLKGSGRTQFSRGADGRAVLGPVLREYII
SEAMHALGVPTTRSLAVISTGRKIQRGSVAPGAVLVRVATSLIRVGSFQYSNISGGIELSQHLANYTIT
RHFPSLVAELSAPTPATYVSLFKAILQRQADTVGKWTRLGFVHGALNTDNTLISGETVDYGPCAFMERY
RGDAKFSSIDTYGRYKFENQPMILGWNMARLVETLLPLLGATPDEGMTAAQEALVEFDDLCEQAIRKEF
ATALGLDESDTGTVEQFRELLYLHNPDITTLLRALTDNTAPPSGFEAFVHDWKTQDPDIEAMRAVNPLF
IPRNHLVEAALADAVEGNLEKFHELLAAVTNPFDPTAGPDELRLPSEEGFEEDYMTFCGT

>RXC01703 TRANSLATE of: RXC01703.seq check: 3504 from: 1 to: 1113
VAWPSNAKEKLFIHWHYWWQAHYLDCLVDAARRRTTKARRDRIRDTIRGISVRNVGKLTSNRYYDDKAW
LALALGRAGKVRKVRTPKSLPSLEQNIVDGIDSLTGVLPWRSGETFYNVPSNGPAAIMMARTDRLDEAM
KITDWIFDNLIDGDGLVMDGLRMRMHGPELVRSIHPYCQGVAIGACLEIALKLRERAGLTTTVVDHWSD
ADKAEDSLKYFAHIHAVVQAVSRKMTNFHGVIDWDTGDGDGGLFKGILVRYLADVAIRLPDDSPTNRET
KKIAARLVLESAESVWNHRLEVDGLPVFATDWTTDARLPQNFGLSSSSLSDLVSVVRVDERDLSVQLSG
WMLMEAAAKVAEELENNGNSYTGRSR

>RXC02254 TRANSLATE of: RXC02254.seq check: 1030 from: 1 to: 777
IAVAEEGGLWENLLQHRFGGHGALAGHALGNLVIAALTDILGTSQHALDQIAQLAGAKGRIIPVCAEPL
DLEAEVSGLDSDARVMRQVRGQVAVAATPGQVRRVRIIPDNPEPNPAAIEAILDADLVTLGPGSWFSSV
IPHILVPGIVDALAQTKATKTVVLNLTSEPGETAGFSAERHIHVLRQHARNLQVDQVIVDAKTLSSQTE
RNHVERAARTLGAEVSFHDVQAEDGRGRFTSIHDPAKLCAALLASFAGARKR

>RXC02255 TRANSLATE of: RXC02255.seq check: 729 from: 1 to: 936
VAKNSVRAAEVSAILRFAGEMQAVGGKLVIEANLDSMQVGMRLQEFIQGLYNSRVDVHTVNPTVSRKTP
RYLVRIIDNADEIARRTGLVTRSGHVVKGLAPSVVSGTISDAEAAWRGAFLANGSLSDPGRSSSLEVLC
PGQESALALVGCARRIGIAAKTKDSRGFDRVNVRDAEAIGALLTRMGAQKTRMLWEEKRIKRESRTPQT
GLANFDDANLRRSARAAVAAAARVERAMKILGDDVPEHLAEAGQLRVQHRQASLEELGRLADPQMTKDA
VAGRIRRLLTMADKRAEDLKIPDTNSVVTEDLLEEI

>RXC02435 TRANSLATE of: RXC02435.seq check: 470 from: 1 to: 558

VTDNLGSTSIGDAWILYAPLMDDGGFGPLRAIGGMFLHIGPGHMLLNLVLLWLLGREIERDFGSALFTA
MYFVGGIGASAAVIWMDPYSPTAGASGAIYAMMAILVGLFVLRSADIRAPLILIAINIAYTLMSTNVSL
WGHLGGLITGALITWPMVKAKTQRTRWIIVLIGFAVVVAAVILGIDRV

>RXC03216 TRANSLATE of: RXC03216.seq check: 470 from: 1 to: 558
MKLGLYNAIFHDRTLPEALAAIKAAGLTGIELNTGGFLPATHIPTIDDILVSDDARDEFLGIFEGTGVD
IYGLNCNGNPLHPNKAIGDKHAEDIRRSIRLAERLGQNRVVTMSGLPGGEPGAKYTNWVVNAWNSAALD
VLDYQWDIAAEFWRETDRFAADHGVKVALELHPQNIVFNSADVHKLIDLTGATHVGVELDASHLFWQQM
DPIAVIDHLGELIFHAAAKDVRVNKEWAQLNGVLDNSFRRLDPSENRTNLGGDEWANEWPKNSAWDFVA
LGRGHDVAYWTEFLRALHRVDPNMLVNIEHEDVSLGREEGVNEAAKVLIEANKALEESLVS